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NOVEL COMPOSITIONS AND METHODS FOR CANCER

The present application is a continuing application of U.S.S.N.s 09/747,377, filed December 22, 2000 and 09/798,586, filed March 2, 2001, and applications entitled Novel Compositions and Methods for Cancer filed October 23, 2001, November 8, 2001, November 30, 2001, and December 20, 2001, all of which are expressly incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates to novel sequences for use in diagnosis and treatment of cancer, especially carcinomas, as well as the use of the novel compositions in screening methods.

BACKGROUND OF THE INVENTION

Oncogenes are genes that can cause cancer. Carcinogenesis can occur by a wide variety of mechanisms, including infection of cells by viruses containing oncogenes, activation of protooncogenes in the host genome, and mutations of protooncogenes and tumor suppressor genes.

There are a number of viruses known to be involved in human cancer as well as in animal cancer. Of particular interest here are viruses that do not contain oncogenes themselves; these are slow-transforming retroviruses. They induce tumors by integrating into the host genome and affecting neighboring protooncogenes in a variety of ways, including promoter insertion, enhancer insertion, and/or truncation of a protooncogene or tumor suppressor gene. The analysis of sequences at or near the insertion sites led to the identification of a number of new protooncogenes.

With respect to lymphoma and leukemia, murine leukemia retrovirus (MuLV), such as SL3-3 or Akv, is a potent inducer of tumors when inoculated into susceptible newborn mice, or when carried in the germline. A number of sequences have been identified as relevant in the induction of lymphoma and leukemia by analyzing the insertion sites; see Sorensen et al., J. of Virology 74:2161 (2000); Hansen et al., Genome Res. 10(2):237-43 (2000); Sorensen et al., J. Virology 70:4063 (1996); Sorensen et al., J. Virology 67:7118 (1993); Joosten et al.,

Virology 268:308 (2000); and Li et al., Nature Genetics 23:348 (1999); all of which are expressly incorporated by reference herein.

Lymphomas are a collection of cancers involving the lymphatic system and are generally categorized as Hodgkin's disease and Non-Hodgkin lymphoma. Hodgkin's lymphomas are of B lymphocyte origin. Non-Hodgkin lymphomas are a collection of over 30 different types of cancers including T and B lymphomas. Leukemia is a disease of the blood forming tissues and includes B and T cell lymphocytic leukemias. It is characterized by an abnormal and persistent increase in the number of leukocytes and the amount of bone marrow, with enlargement of the spleen and lymph nodes.

Breast cancer is one of the most significant diseases that affects women. At the current rate, American women have a 1 in 8 risk of developing breast cancer by age 95 (American Cancer Society, 1992). Treatment of breast cancer at later stages is often futile and disfiguring, making early detection a high priority in medical management of the disease.

Accordingly, it is an object of the invention to provide sequences involved in cancer and in particular in oncogenesis.

SUMMARY OF THE INVENTION

In accordance with the objects outlined above, the present invention provides methods for screening for compositions which modulate carcinomas, especially lymphoma and leukemia. Also provided herein are methods of inhibiting proliferation of a cell, preferably a lymphoma cell. Methods of treatment of carcinomas, including diagnosis, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses a carcinoma associated (CA) gene or fragments thereof. Preferred embodiments of CA genes are genes which are differentially expressed in cancer cells, preferably lymphatic, breast, prostate or epithelial cells, compared to other cells. Preferred embodiments of CA genes used in the methods herein include, but are not limited to the nucleic acids selected from Tables 1-112. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the CA gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate.

Also provided herein is a method of screening for a bioactive agent capable of binding to a CA protein (CAP), the method comprising combining the CAP and a candidate bioactive agent, and determining the binding of the candidate agent to the CAP.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CAP. In one embodiment, the method comprises combining the CAP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CAP.

Also provided is a method of evaluating the effect of a candidate carcinoma drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile of the patient to an expression profile of a heathy individual.

In a further aspect, a method for inhibiting the activity of an CA protein is provided. In one embodiment, the method comprises administering to a patient an inhibitor of a CA protein preferably selected from the group consisting of the sequences outlined in Tables 1-112 or their complements.

A method of neutralizing the effect of a CA protein, preferably a protein encoded by a nucleic acid selected from the group of sequences outlined in Tables 1-112, is also provided. Preferably, the method comprises contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a CA protein, preferably selected from the sequences outlined in Tables 1-112.

Also provided herein is a method for diagnosing or determining the propensity to carcinomas, especially lymphoma or leukemia by sequencing at least one carcinoma or lymphoma gene of an individual. In yet another aspect of the invention, a method is provided for determining carcinoma including lymphoma and leukemia gene copy number in an individual.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to a number of sequences associated with carcinomas,

especially lymphoma, breast cancer or prostate cancer. The relatively tight linkage between clonally-integrated proviruses and protooncogenes forms "provirus tagging", in which slow-transforming retroviruses that act by an insertion mutation mechanism are used to isolate protooncogenes. In some models, uninfected animals have low cancer rates, and infected animals have high cancer rates. It is known that many of the retroviruses involved do not carry transduced host protooncogenes or pathogenic *trans*-acting viral genes, and thus the cancer incidence must therefor be a direct consequence of proviral integration effects into host protooncogenes. Since proviral integration is random, rare integrants will "activate" host protooncogenes that provide a selective growth advantage, and these rare events result in new proviruses at clonal stoichiometries in tumors.

The use of oncogenic retroviruses, whose sequences insert into the genome of the host organism resulting in carcinoma, allows the identification of host sequences involved in carcinoma. These sequences may then be used in a number of different ways, including diagnosis, prognosis, screening for modulators (including both agonists and antagonists), antibody generation (for immunotherapy and imaging), etc. However, as will be appreciated by those in the art, oncogenes that are identified in one type of cancer such as lymphoma or leukemia have a strong likelihood of being involved in other types of cancers as well. Thus, while the sequences outlined herein are initially identified as correlated with lymphoma, they can also be found in other types of cancers as well, outlined below.

Accordingly, the present invention provides nucleic acid and protein sequences that are associated with carcinoma, herein termed "carcinoma associated" or "CA" sequences. In a preferred embodiment, the present invention provides nucleic acid and protein sequences that are associated with carcinomas which originate in lymphatic tissue, herein termed "lymphoma associated" , "leukemia associated" or "LA" sequences.

Suitable cancers which can be diagnosed or screened for using the methods of the present invention include cancers classified by site or by histological type. Cancers classified by site include cancer of the oral cavity and pharynx (lip, tongue, salivary gland, floor of mouth, gum and other mouth, nasopharynx, tonsil, oropharynx, hypopharynx, other oral/pharynx); cancers of the digestive system (esophagus; stomach; small intestine; colon and rectum; anus, anal canal, and anorectum; liver; intrahepatic bile duct; gallbladder; other biliary; pancreas; retroperitoneum; peritoneum, omentum, and mesentery; other digestive); cancers of the respiratory system (nasal cavity, middle ear, and sinuses; larynx; lung and bronchus; pleura; trachea, mediastinum, and other respiratory); cancers of the mesothelioma; bones and joints; and soft tissue, including heart; skin cancers, including melanomas and other non-epithelial skin cancers; Kaposi's sarcoma and breast cancer; cancer of the female genital system (cervix uteri; corpus uteri; uterus, nos; ovary; vagina; vulva; and other female genital); cancers

of the male genital system (prostate gland; testis; penis; and other male genital); cancers of the urinary system (urinary bladder; kidney and renal pelvis; ureter; and other urinary); cancers of the eye and orbit; cancers of the brain and nervous system (brain; and other nervous system); cancers of the endocrine system (thyroid gland and other endocrine, including thymus); cancers of the lymphomas (hodgkin's disease and non-hodgkin's lymphoma), multiple myeloma, and leukemias (lymphocytic leukemia; myeloid leukemia; monocytic leukemia; and other leukemias).

Other cancers, classified by histological type, that may be associated with the sequences of the invention include, but are not limited to, Neoplasm, malignant; Carcinoma, NOS; Carcinoma, undifferentiated, NOS; Giant and spindle cell carcinoma; Small cell carcinoma, NOS; Papillary carcinoma, NOS; Squamous cell carcinoma, NOS; Lymphoepithelial carcinoma; Basal cell carcinoma, NOS; Pilomatrix carcinoma; Transitional cell carcinoma, NOS; Papillary transitional cell carcinoma; Adenocarcinoma, NOS; Gastrinoma, malignant; Cholangiocarcinoma; Hepatocellular carcinoma, NOS; Combined hepatocellular carcinoma and cholangiocarcinoma; Trabecular adenocarcinoma; Adenoid cystic carcinoma; Adenocarcinoma in adenomatous polyp; Adenocarcinoma, familial polyposis coli; Solid carcinoma, NOS; Carcinoid tumor, malignant; Branchiolo-alveolar adenocarcinoma; Papillary adenocarcinoma, NOS; Chromophobe carcinoma; Acidophil carcinoma; Oxyphilic adenocarcinoma; Basophil carcinoma; Clear cell adenocarcinoma, NOS; Granular cell carcinoma; Follicular adenocarcinoma, NOS; Papillary and follicular adenocarcinoma; Nonencapsulating sclerosing carcinoma; Adrenal cortical carcinoma; Endometroid carcinoma; Skin appendage carcinoma; Apocrine adenocarcinoma; Sebaceous adenocarcinoma; Ceruminous adenocarcinoma; Mucoepidermoid carcinoma; Cystadenocarcinoma, NOS; Papillary cystadenocarcinoma, NOS; Papillary serous cystadenocarcinoma; Mucinous cystadenocarcinoma, NOS; Mucinous adenocarcinoma; Signet ring cell carcinoma; Infiltrating duct carcinoma; Medullary carcinoma, NOS; Lobular carcinoma; Inflammatory carcinoma; Paget"s disease, mammary; Acinar cell carcinoma; Adenosquamous carcinoma; Adenocarcinoma w/ squamous metaplasia; Thymoma, malignant; Ovarian stromal tumor, malignant; Thecoma, malignant; Granulosa cell tumor, malignant; Androblastoma, malignant; Sertoli cell carcinoma; Leydig cell tumor, malignant; Lipid cell tumor, malignant; Paraganglioma, malignant; Extra-mammary paraganglioma, malignant; Pheochromocytoma; Glomangiosarcoma; Malignant melanoma, NOS; Amelanotic melanoma; Superficial spreading melanoma; Malig melanoma in giant pigmented nevus; Epithelioid cell melanoma; Blue nevus, malignant; Sarcoma, NOS; Fibrosarcoma, NOS; Fibrous histiocytoma, malignant; Myxosarcoma; Liposarcoma, NOS; Leiomyosarcoma, NOS; Rhabdomyosarcoma, NOS; Embryonal rhabdomyosarcoma; Alveolar rhabdomyosarcoma; Stromal sarcoma, NOS; Mixed tumor, malignant, NOS; Mullerian mixed tumor; Nephroblastoma; Hepatoblastoma; Carcinosarcoma, NOS; Mesenchymoma, malignant; Brenner tumor, malignant; Phyllodes

tumor, malignant; Synovial sarcoma, NOS; Mesothelioma, malignant; Dysgerminoma; Embryonal carcinoma, NOS; Teratoma, malignant, NOS; Struma ovarii, malignant; Choriocarcinoma; Mesonephroma, malignant; Hemangiosarcoma; Hemangioendothelioma, malignant; Kaposi's sarcoma; Hemangiopericytoma, malignant; Lymphangiosarcoma; Osteosarcoma, NOS; Juxtacortical osteosarcoma; Chondrosarcoma, NOS; Chondroblastoma, malignant; Mesenchymal chondrosarcoma; Giant cell tumor of bone; Ewing's sarcoma; Odontogenic tumor, malignant; Ameloblastic odontosarcoma; Ameloblastoma, malignant; Ameloblastic fibrosarcoma; Pinealoma, malignant; Chordoma; Glioma, malignant; Ependymoma, NOS; Astrocytoma, NOS; Protoplasmic astrocytoma; Fibrillary astrocytoma; Astroblastoma; Glioblastoma, NOS; Oligodendroglioma, NOS; Oligodendroblastoma; Primitive neuroectodermal; Cerebellar sarcoma, NOS; Ganglioneuroblastoma; Neuroblastoma, NOS; Retinoblastoma, NOS; Olfactory neurogenic tumor; Meningioma, malignant; Neurofibrosarcoma; Neurilemmoma, malignant; Granular cell tumor, malignant; Malignant lymphoma, NOS; Hodgkin's disease, NOS; Hodgkin's; paragranuloma, NOS; Malignant lymphoma, small lymphocytic; Malignant lymphoma, large cell, diffuse; Malignant lymphoma, follicular, NOS; Mycosis fungoides; Other specified non-Hodgkin's lymphomas; Malignant histiocytosis; Multiple myeloma; Mast cell sarcoma; Immunoproliferative small intestinal disease; Leukemia, NOS; Lymphoid leukemia, NOS; Plasma cell leukemia; Erythroleukemia; Lymphosarcoma cell leukemia; Myeloid leukemia, NOS; Basophilic leukemia; Eosinophilic leukemia; Monocytic leukemia, NOS; Mast cell leukemia; Megakaryoblastic leukemia; Myeloid sarcoma; and Hairy cell leukemia.

In addition, the genes may be involved in other diseases, such as but not limited to diseases associated with aging or neurodegenerative diseases.

Association in this context means that the nucleotide or protein sequences are either differentially expressed, activated, inactivated or altered in carcinomas as compared to normal tissue. As outlined below, CA sequences include those that are up-regulated (i.e. expressed at a higher level), as well as those that are down-regulated (i.e. expressed at a lower level), in carcinomas. CA sequences also include sequences which have been altered (i.e., truncated sequences or sequences with substitutions, deletions or insertions, including point mutations) and show either the same expression profile or an altered profile. In a preferred embodiment, the CA sequences are from humans; however, as will be appreciated by those in the art, CA sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CA sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). In some cases, prokaryotic CA sequences may be useful. CA sequences from other organisms may be obtained using the techniques outlined below.

CA sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CA sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of an CA protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CA sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CA sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CA sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below (for example in antisense

applications or when a candidate agent is a nucleic acid), nucleic acid analogs may be used that have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Lett. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Lett. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments for use in anti-sense applications or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand "Watson" also defines the sequence of the

other strand "Crick"; thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

An CA sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CA sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

The CA sequences of the invention were initially identified as described herein; basically, infection of mice with murine leukemia viruses (MLV) resulted in lymphoma, although many of these sequences will also be involved in other cancers as is generally outlined herein.

The CA sequences outlined herein comprise the insertion sites for the virus. In general, the retrovirus can cause carcinomas in three basic ways: first of all, by inserting upstream of a normally silent host gene and activating it (e.g. promoter insertion); secondly, by truncating a host gene that leads to oncogenesis; or by enhancing the transcription of a neighboring gene. For example, retrovirus enhancers, including SL3-3, are known to act on genes up to approximately 200 kilobases of the insertion site.

In a preferred embodiment, CA sequences are those that are up-regulated in carcinomas; that is, the expression of these genes is higher in carcinoma tissue as compared to normal tissue of the same differentiation stage. "Up-regulation" as used herein means at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

In a preferred embodiment, CA sequences are those that are down-regulated in carcinomas; that is, the expression of these genes is lower in carcinoma tissue as compared to normal I tissue of the same differentiation stage. "Down-regulation" as used herein means at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

In a preferred embodiment, CA sequences are those that are altered but show either the

same
expression profile or an altered profile as compared to normal lymphoid tissue of the same differentiation stage. "Altered CA sequences" as used herein refers to sequences which are truncated, contain insertions or contain point mutations.

CA proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins.

In a preferred embodiment the CA protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or disregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CA sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases

have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin_like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL_1 receptor, IL_2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CA proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CA proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CA proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

An CA sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CA sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

As used herein, a nucleic acid is a "CA nucleic acid" if the overall homology of the nucleic acid sequence to one of the nucleic acids of Tables 1-112 is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from those of the nucleic acids of Tables 1-112. In another embodiment, the sequences are naturally occurring allelic variants of the sequences of the nucleic acids of Tables 1-112. In another embodiment, the sequences are sequence variants as further described herein.

Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of

Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.
Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); http://blast.wustl]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the nucleic acids of Tables 1-112. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids of Tables 1-112, it is understood that the percentage of homology will be

determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acids identified in the figures, or their complements, are considered CA sequences. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al., both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.
In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, supra, and Tijssen, supra.

In addition, the CA nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. Alternatively, the CA nucleic acid sequences can serve as indicators of oncogene position, for example, the CA sequence may be an enhancer that activates a protooncogene. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CA genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., supra, hereby expressly incorporated by reference. In general, this is done using PCR, for example, kinetic

PCR.

Once the CA nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CA nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CA nucleic acid can be further used as a probe to identify and isolate other CA nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CA nucleic acids and proteins.

The CA nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CA nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy and/or antisense applications. Alternatively, the CA nucleic acids that include coding regions of CA proteins can be put into expression vectors for the expression of CA proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to CA nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CA nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon™, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica_based materials including silicon and modified silicon, carbon, metals, inorganic glasses, etc. In general, the substrates allow optical detection and do not appreciably fluoresce.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross_linkers, pages 155_200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip technology.

In addition to the solid-phase technology represented by biochip arrays, gene expression can also be quantified using liquid-phase arrays. One such system is kinetic polymerase chain reaction (PCR). Kinetic PCR allows for the simultaneous amplification and quantification of specific nucleic acid sequences. The specificity is derived from synthetic oligonucleotide primers designed to preferentially adhere to single-stranded nucleic acid sequences bracketing the target site. This pair of oligonucleotide primers form specific, non-covalently bound complexes on each strand of the target sequence. These complexes facilitate *in vitro* transcription of double-stranded DNA in opposite orientations. Temperature cycling of the reaction mixture creates a continuous cycle of primer binding, transcription, and re-melting of the nucleic acid to individual strands. The result is an exponential increase of the target

dsDNA product. This product can be quantified in real time either through the use of an intercalating dye or a sequence specific probe. SYBR® Greene I, is an example of an intercalating dye, that preferentially binds to dsDNA resulting in a concomitant increase in the fluorescent signal. Sequence specific probes, such as used with TaqMan® technology, consist of a fluorochrome and a quenching molecule covalently bound to opposite ends of an oligonucleotide. The probe is designed to selectively bind the target DNA sequence between the two primers. When the DNA strands are synthesized during the PCR reaction, the fluorochrome is cleaved from the probe by the exonuclease activity of the polymerase resulting in signal dequenching. The probe signaling method can be more specific than the intercalating dye method, but in each case, signal strength is proportional to the dsDNA product produced. Each type of quantification method can be used in multi-well liquid phase arrays with each well representing primers and/or probes specific to nucleic acid sequences of interest. When used with messenger RNA preparations of tissues or cell lines, and an array of probe/primer reactions can simultaneously quantify the expression of multiple gene products of interest. See Germer, S., et al., Genome Res. 10:258-266 (2000); Heid, C. A., et al., Genome Res. 6, 986-994 (1996).

In a preferred embodiment, CA nucleic acids encoding CA proteins are used to make a variety of expression vectors to express CA proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CA protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be

appropriate to the host cell used to express the CA protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CA protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CA proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an CA protein, under the appropriate conditions to induce or cause expression of the CA protein. The conditions appropriate for CA protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial

for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect, plant and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CA proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlytion signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CA proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CA protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been

transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CA proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CA protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CA protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies. If the desired epitope is small, the CA protein may be fused to a carrier protein to form an immunogen. Alternatively, the CA protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CA protein is an CA peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CA nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CA nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^{3}H, ^{14}C, ^{32}P, ^{35}S, or ^{125}I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962);

David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CA protein sequences. An CA protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CA protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CA proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CA proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CA proteins are portions or fragments of the wild type sequences herein. In addition, as outlined above, the CA nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the CA proteins are derivative or variant CA proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CA peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CA peptide.

Also included in an embodiment of CA proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CA protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CA protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CA protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CA variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and LAR mutagenesis. Screening of the mutants is done using assays of CA protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CA protein are desired, substitutions are generally made in accordance with the following chart:

Chart I

Original Residue	Exemplary Substitutions

Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CA proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CA protein is altered. For example, glycosylation sites may be altered or removed, dominant negative mutations created, etc.

Covalent modifications of CA polypeptides are included within the scope of this invention, for example for use in screening. One type of covalent modification includes reacting targeted amino acid residues of an CA polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an CA polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CA polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-CA antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the a-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CA polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CA polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CA polypeptide.

Addition of glycosylation sites to CA polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CA polypeptide (for O-linked glycosylation sites). The CA amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CA polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CA polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, LA Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CA polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of CA comprises linking the CA polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CA polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising an CA polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an CA polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the CA polypeptide, although internal fusions may also be tolerated in some instances. The presence of such epitope-tagged forms of an CA polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CA polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an CA polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of CA protein in one embodiment are other CA proteins of the

CA family, and CA proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CA proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CA nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CA proteins can be made that are longer than those encoded by the nucleic acids of the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CA proteins may also be identified as being encoded by CA nucleic acids. Thus, CA proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, the invention provides CA antibodies. In a preferred embodiment, when the CA protein is to be used to generate antibodies, for example for immunotherapy, the CA protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CA protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab_2, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of

such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-112, or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a protein encoded by a nucleic acid of Tables 1-112, or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CA are capable of reducing or eliminating the biological function of CA, as is described below. That is, the addition of anti-CA antibodies (either polyclonal or preferably monoclonal) to CA (or cells containing CA) may reduce or eliminate the CA activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially

preferred.

In a preferred embodiment the antibodies to the CA proteins are humanized antibodies. Humanized forms of non_human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen binding subsequences of antibodies) which contain minimal sequence derived from non_human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non_human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non_human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non_human immunoglobulin and all or substantially all of the framework residues (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522_525 (1986); Riechmann et al., Nature, 332:323_329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593_596 (1992)].

Methods for humanizing non_human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non_human. These non_human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co_workers [Jones et al., Nature, 321:522_525 (1986); Riechmann et al., Nature, 332:323_327 (1988); Verhoeyen et al., Science, 239:1534_1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non_human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also

available for the preparation of human monoclonal antibodies [Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86_95 (1991)]. Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779_783 (1992); Lonberg et al., Nature 368 856_859 (1994); Morrison, Nature 368, 812_13 (1994); Fishwild et al., Nature Biotechnology 14, 845_51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65_93 (1995).

By immunotherapy is meant treatment of a carcinoma with an antibody raised against an CA protein. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment, oncogenes which encode secreted growth factors may be inhibited by raising antibodies against CA proteins that are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CA protein.

In another preferred embodiment, the CA protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CA protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CA protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CA protein. The antibody is also an antagonist of the CA protein. Further, the antibody prevents activation of the transmembrane CA protein. In one aspect, when the antibody prevents the binding of other molecules to the CA protein, the antibody prevents growth of the cell. The antibody may also sensitize the cell to cytotoxic

agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, carcinomas may be treated by administering to a patient antibodies directed against the transmembrane CA protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CA protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CA protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with carcinoma.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with carcinomas, including lymphoma. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CA proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CA proteins not only serves to increase the local concentration of therapeutic moiety in the carcinoma of interest, i.e., lymphoma, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CA protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CA protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CA antibodies of the invention specifically bind to CA proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^{-4}- 10^{-6} M^{-1}, with a preferred range being 10^{-7} - 10^{-9} M^{-1}.

In a preferred embodiment, the CA protein is purified or isolated after expression. CA

proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CA protein may be purified using a standard anti-CA antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CA protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CA proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the carcinoma phenotype; that is, the expression levels of genes in normal tissue and in carcinoma tissue (and in some cases, for varying severities of lymphoma that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or carcinoma tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus carcinoma tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via

standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip® expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CA protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CA genes, i.e. those identified as being important in a particular carcinoma phenotype, i.e., lymphoma, can be evaluated in a diagnostic test specific for that carcinoma.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CA nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of CA sequences in a particular cell. The assays are done as is known in the art. As will be appreciated by those in the art, any number of different CA sequences may be used as probes, with single sequence assays being used in some cases, and a plurality of the sequences described herein being used in other embodiments. In addition, while solid-phase assays are described, any number of solution based assays may be done as well.

In a preferred embodiment, both solid and solution based assays may be used to detect CA sequences that are up-regulated or down-regulated in carcinomas as compared to normal tissue. In instances where the CA sequence has been altered but shows the same expression profile or an altered expression profile, the protein will be detected as outlined herein.

In a preferred embodiment nucleic acids encoding the CA protein are detected. Although DNA or RNA encoding the CA protein may be detected, of particular interest are methods

wherein the mRNA encoding a CA protein is detected. The presence of mRNA in a sample is an indication that the CA gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CA protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5_bromo_4_chloro_3_indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CA proteins, antibodies, nucleic acids, modified proteins and cells containing CA sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level, or as sets of assays.

As described and defined herein, CA proteins find use as markers of carcinomas, including lymphomas such as, but not limited to, Hodgkin's and non-Hodgkin lymphoma. Detection of these proteins in putative carcinoma tissue or patients allows for a determination or diagnosis of the type of carcinoma. Numerous methods known to those of ordinary skill in the art find use in detecting carcinomas. In one embodiment, antibodies are used to detect CA proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CA protein is detected by immunoblotting with antibodies raised against the CA protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the CA protein find use in *in situ* imaging techniques. In this method cells are contacted with from one to many antibodies to the CA protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CA protein(s) contains a detectable label. In another preferred embodiment

each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CA proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing carcinomas from blood samples. As previously described, certain CA proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CA proteins. Antibodies can be used to detect the CA proteins by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, *in situ* hybridization of labeled CA nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CA tissue and/or normal tissue, are made. *In situ* hybridization as is known in the art can then be done.

It is understood that when comparing the expression fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the CA proteins, antibodies, nucleic acids, modified proteins and cells containing CA sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to carcinoma, especially lymphoma, severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CA probes are attached to biochips for the detection and quantification of CA sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the CA sequences as described herein are used in drug screening assays. The CA proteins, antibodies, nucleic acids, modified proteins and cells containing CA sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In one embodiment, the expression profiles are used, preferably in conjunction with high throughput

screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, et al., Genome Res., 6:986-994 (1996).

In a preferred embodiment, the CA proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CA proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the carcinoma phenotype. As above, this can be done by screening for modulators of gene expression or for modulators of protein activity. Similarly, this may be done on an individual gene or protein level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the CA genes herein, a variety of assays to evaluate the effects of agents on gene expression may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as aberrantly regulated in carcinoma, candidate bioactive agents may be screened to modulate the genes response. "Modulation" thus includes both an increase and a decrease in gene expression or activity. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired, etc. Alternatively, where the CA sequence has been altered but shows the same expression profile or an altered expression profile, the protein will be detected as outlined herein.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the level of the gene product itself can be monitored, for example through the use of antibodies to the CA protein and standard immunoassays. Alternatively, binding and bioactivity assays with the protein may be done as outlined below.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CA nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CA sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates a particular type of carcinoma, modulates CA proteins, binds to a CA protein, or interferes between the binding of a CA protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic or inorganic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the carcinoma phenotype, binding to and/or modulating the bioactivity of an CA protein, or the expression of a CA sequence, including both nucleic acid sequences and protein sequences. In a particularly preferred embodiment, the candidate agent suppresses a CA phenotype, for example to a normal tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CA phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of an CA protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic or inorganic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic

or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

In assays for altering the expression profile of one or more CA genes, after the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR occurring as needed, as will be appreciated by those in the art. For example, an *in vitro* transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with a label as defined herein, with biotin-FITC or PE, cy3 and cy5 being particularly preferred.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, chemiluminescent, chemical, or radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin

which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target. In addition, either solid phase or solution based (i.e., kinetic PCR) assays may be used.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed gene(s) or mutated gene(s) important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In addition, screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CA expression pattern leading to a normal expression pattern, or modulate a single CA gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CA tissue reveals genes that are not expressed in normal tissue or CA tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CA genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CA tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CA cells, that thus has an associated CA expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, CA tissue may be screened for agents that reduce or suppress the CA phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CA activity. By defining such a signature for the CA phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor

does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CA proteins" or an "CAP". The CAP may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of Tables 1-112. Preferably, the CAP is a fragment. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the CAP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine.

In one embodiment the CA proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the CA protein is conjugated to BSA.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the CA gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to CA proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate the CAP activity and the carcinoma phenotype. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more CA nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CA proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CA protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CA

protein. Preferred embodiments utilize the human or mouse CA protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CA proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CA protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, Teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CA protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CA protein is added. Novel binding agents include specific antibodies, non_natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein_protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CA protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CA protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present

on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I, or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CA protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CA protein and thus is capable of binding to, and potentially modulating, the activity of the CA protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CA protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CA protein.

In a preferred embodiment, the methods comprise differential screening to identity bioactive agents that are capable of modulating the activity of the CA proteins. In this embodiment, the methods comprise combining a CA protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CA protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CA protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CA protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CA protein, but cannot bind to modified CA proteins. The structure of the CA protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CA bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non_specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein_protein binding and/or reduce non_specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti_microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CA proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CA proteins comprise the steps of adding a candidate bioactive agent to a sample of CA proteins, as above, and determining an alteration in the biological activity of CA proteins. "Modulating the activity of an CA protein" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CA proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both *in vitro* screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CA proteins.

Thus, in this embodiment, the methods comprise combining a CA sample and a candidate bioactive agent, and evaluating the effect on CA activity. By "CA activity" or grammatical equivalents herein is meant one of the CA protein's biological activities, including, but not limited to, its role in tumorigenesis, including cell division, preferably in lymphatic tissue, cell proliferation, tumor growth and transformation of cells. In one embodiment, CA activity includes activation of or by a protein encoded by a nucleic acid of Tables 1-112. An inhibitor of CA activity is the inhibition of any one or more CA activities.

In a preferred embodiment, the activity of the CA protein is increased; in another preferred embodiment, the activity of the CA protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CA protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CA proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CA protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are

able to enhance or interfere with the activity of the CA protein.

In one embodiment, a method of inhibiting carcinoma cancer cell division, is provided. The method comprises administration of a carcinoma cancer inhibitor.

In a preferred embodiment, a method of inhibiting lymphoma carcinoma cell division is provided comprising administration of a lymphoma carcinoma inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a carcinoma cancer inhibitor. In a particularly preferred embodiment, a method of inhibiting tumor growth in lymphatic tissue is provided comprising administration of a lymphoma inhibitor.
In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a carcinoma cancer inhibitor. Preferably, the carcinoma is a lymphoma carcinoma.

In one embodiment, a carcinoma cancer inhibitor is an antibody as discussed above. In another embodiment, the carcinoma cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for carcinoma cancer molecules. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen, Cancer Res. 48:2659, (1988) and van der Krol et al., BioTechniques 6:958, (1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1_100% wgt/vol. The agents may be administered alone or in combination with other treatments, i.e., radiation.

The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically_active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various CA sequences are important in carcinomas. Accordingly, disorders based on mutant or variant CA genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CA genes comprising determining all or part of the sequence of at least one endogenous CA genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CA genotype of an individual comprising determining all or part of the sequence of at least one CA gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced CA gene to a known CA gene, i.e., a wild-type gene. As will be appreciated by those in the art, alterations in the sequence of some oncogenes can be an indication of either the presence of the disease, or propensity to develop the disease, or prognosis evaluations.

The sequence of all or part of the CA gene can then be compared to the sequence of a known CA gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CA gene of the patient and the known CA gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CA genes are used as probes to determine the number of copies of the CA gene in the genome. For example, some cancers exhibit chromosomal deletions or insertions, resulting in an alteration in the copy number of a gene.

In another preferred embodiment CA genes are used as probes to determine the chromosomal location of the CA genes. Information such as chromosomal location finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CA gene loci.

Thus, in one embodiment, methods of modulating CA in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CA antibody that reduces or eliminates the biological activity of an endogenous CA protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CA protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CA sequence is down-regulated in carcinoma, the activity of the CA gene is increased by increasing the amount of CA in the cell, for example by overexpressing the endogenous CA or by administering a gene encoding the CA sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CA sequence is up-regulated in carcinoma, the activity of the endogenous CA gene is decreased, for example by the administration of a CA antisense nucleic acid.

In one embodiment, the CA proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CA proteins, which are useful as described herein. Similarly, the CA proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CA antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CA protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CA antibodies may be coupled to standard affinity chromatography columns and used to purify CA proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CA protein.

In one embodiment, a therapeutically effective dose of a CA or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose

of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CA degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

The administration of the CA proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CA proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a CA protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p_toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non_toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier

proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol. Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CA proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CA genes (including both the full-length sequence, partial sequences, or regulatory sequences of the CA coding regions) can be administered in gene therapy applications, as is known in the art. These CA genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

In a preferred embodiment, CA genes are administered as DNA vaccines, either single genes or combinations of CA genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

In one embodiment, CA genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CA gene or portion of a CA gene under the control of a promoter for expression in a patient with carcinoma. The CA gene used for DNA vaccines can encode full-length CA proteins, but more preferably encodes portions of the CA proteins including peptides derived from the CA protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CA gene. Similarly, it is possible to immunize a patient with a plurality of CA genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CA proteins.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CA polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

In another preferred embodiment CA genes find use in generating animal models of carcinomas, particularly lymphoma carcinomas. As is appreciated by one of ordinary skill in the art, when the CA gene identified is repressed or diminished in CA tissue, gene therapy technology wherein antisense RNA directed to the CA gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CA that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for

example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CA protein. When desired, tissue-specific expression or knockout of the CA protein may be necessary.

It is also possible that the CA protein is overexpressed in carcinoma. As such, transgenic animals can be generated that overexpress the CA protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CA and are additionally useful in screening for bioactive molecules to treat carcinoma.

The CA nucleic acid sequences of the invention are depicted in Tables 1-112. The sequences in Tables 1 and 2 depict mouse tags, i.e. the genomic insertion sites. The sequences in Tables 3-102 include genomic sequence, mRNA and coding sequences for both mouse and human. N/A indicates a gene that has been identified, but for which there has not been a name ascribed. The different sequences are assigned the following SEQ ID Nos:

Table 3 (mouse gene: Fscn1; human gene SNL)
Mouse genomic sequence (SEQ ID NO: 1)
Mouse mRNA sequence (SEQ ID NO: 2)
Mouse coding sequence (SEQ ID NO: 3)
Human genomic sequence (SEQ ID NO: 4)
Human mRNA sequence (SEQ ID NO: 5)
Human coding sequence (SEQ ID NO: 6)

Table 4 (mouse gene Map3k6; human gene MAP3K6)
Mouse genomic sequence (SEQ ID NO: 7)
Mouse mRNA sequence (SEQ ID NO: 8)
Mouse coding sequence (SEQ ID NO: 9)
Human genomic sequence (SEQ ID NO: 10)
Human mRNA sequence (SEQ ID NO: 11)
Human coding sequence (SEQ ID NO: 12)

Table 5 (mouse gene Fosb; human gene FOSB)
Mouse genomic sequence (SEQ ID NO: 13)
Mouse mRNA sequence (SEQ ID NO: 14)
Mouse coding sequence (SEQ ID NO: 15)

Human genomic sequence (SEQ ID NO: 16)
Human mRNA sequence (SEQ ID NO: 17)
Human coding sequence (SEQ ID NO: 18)

Table 6 (mouse gene cmkbr7; human gene: CCR7)
Mouse genomic sequence (SEQ ID NO: 19)
Mouse mRNA sequence (SEQ ID NO: 20)
Mouse coding sequence (SEQ ID NO: 21)
Human genomic sequence (SEQ ID NO: 22)
Human mRNA sequence (SEQ ID NO: 23)
Human coding sequence (SEQ ID NO: 24)

Table 7 (mouse gene: Ccnd1; human gene: CCND1)
Mouse genomic sequence (SEQ ID NO: 25)
Mouse mRNA sequence (SEQ ID NO: 26)
Mouse coding sequence (SEQ ID NO: 27)
Human genomic sequence (SEQ ID NO: 28)
Human mRNA sequence (SEQ ID NO:29)
Human coding sequence (SEQ ID NO: 30)

Table 8 (mouse gene: Ccnd3; human gene: CCND3)
Mouse genomic sequence (SEQ ID NO: 31)
Mouse mRNA sequence (SEQ ID NO: 32)
Mouse coding sequence (SEQ ID NO: 33)
Human genomic sequence (SEQ ID NO: 34)
Human mRNA sequence (SEQ ID NO: 35)
Human coding sequence (SEQ ID NO: 36)

Table 9 (mouse gene: Wnt3; human gene: WNT3)
Mouse genomic sequence (SEQ ID NO: 37)
Mouse mRNA sequence (SEQ ID NO: 38)
Mouse coding sequence (SEQ ID NO: 39)
Human genomic sequence (SEQ ID NO: 40)
Human mRNA sequence (SEQ ID NO: 41)
Human coding sequence (SEQ ID NO: 42)

Table 10 (mouse gene: Batf; human gene: BATF)
Mouse genomic sequence (SEQ ID NO: 43)
Mouse mRNA sequence (SEQ ID NO: 44)

Mouse coding sequence (SEQ ID NO: 45)
Human genomic sequence (SEQ ID NO: 46)
Human mRNA sequence (SEQ ID NO: 47)
Human coding sequence (SEQ ID NO: 48)

Table 11 (mouse gene: Irf4; human gene: IRF4)
Mouse genomic sequence (SEQ ID NO: 49)
Mouse mRNA sequence (SEQ ID NO: 50)
Mouse coding sequence (SEQ ID NO: 51)
Human genomic sequence (SEQ ID NO: 52)
Human mRNA sequence (SEQ ID NO: 53)
Human coding sequence (SEQ ID NO: 54)

Table 12 (mouse gene: Notch1; human gene: NOTCH1)
Mouse genomic sequence (SEQ ID NO: 55)
Mouse mRNA sequence (SEQ ID NO: 56)
Mouse coding sequence (SEQ ID NO: 57)
Human genomic sequence (SEQ ID NO: 58)
Human mRNA sequence (SEQ ID NO: 59)
Human coding sequence (SEQ ID NO: 60)

Table 13 (mouse gene: Myc; human gene MYC)
Mouse genomic sequence (SEQ ID NO: 61)
Mouse mRNA sequence (SEQ ID NO: 62)
Mouse coding sequence (SEQ ID NO: 63)
Human genomic sequence (SEQ ID NO: 64)
Human mRNA sequence (SEQ ID NO: 65)
Human coding sequence (SEQ ID NO: 66)

Table 14 (mouse gene Bach2; human gene BACH2)
Mouse genomic sequence (SEQ ID NO: 67)
Mouse mRNA sequence (SEQ ID NO: 68)
Mouse coding sequence (SEQ ID NO: 69)
Human genomic sequence (SEQ ID NO: 70)
Human mRNA sequence (SEQ ID NO: 71)
Human coding sequence (SEQ ID NO: 72)

Table 15 (mouse gene Wnt1; human gene WNT1)
Mouse genomic sequence (SEQ ID NO: 73)

Mouse mRNA sequence (SEQ ID NO: 74)
Mouse coding sequence (SEQ ID NO: 75)
Human genomic sequence (SEQ ID NO: 76)
Human mRNA sequence (SEQ ID NO: 77)
Human coding sequence (SEQ ID NO: 78)

Table 16 (mouse gene Rasgrp1; human gene: RASGRP1)
Mouse genomic sequence (SEQ ID NO: 79)
Mouse mRNA sequence (SEQ ID NO: 80)
Mouse coding sequence (SEQ ID NO: 81)
Human genomic sequence (SEQ ID NO: 82)
Human mRNA sequence (SEQ ID NO: 83)
Human coding sequence (SEQ ID NO: 84)

Table 17 (mouse gene: Nmyc1; human gene: MYCN)
Mouse genomic sequence (SEQ ID NO: 85)
Mouse mRNA sequence (SEQ ID NO: 86)
Mouse coding sequence (SEQ ID NO: 87)
Human genomic sequence (SEQ ID NO: 88)
Human mRNA sequence (SEQ ID NO:89)
Human coding sequence (SEQ ID NO: 90)

Table 18 (mouse gene: Myb; human gene: MYB)
Mouse genomic sequence (SEQ ID NO: 91)
Mouse mRNA sequence (SEQ ID NO: 92)
Mouse coding sequence (SEQ ID NO: 93)
Human genomic sequence (SEQ ID NO: 94)
Human mRNA sequence (SEQ ID NO: 95)
Human coding sequence (SEQ ID NO: 96)

Table 19 (mouse gene: Sox4; human gene: SOX4)
Mouse genomic sequence (SEQ ID NO: 97)
Mouse mRNA sequence (SEQ ID NO: 98)
Mouse coding sequence (SEQ ID NO: 99)
Human genomic sequence (SEQ ID NO: 100)
Human mRNA sequence (SEQ ID NO: 101)
Human coding sequence (SEQ ID NO: 102)

Table 20 (mouse gene: Tcof1; human gene: TCOF1)

Mouse genomic sequence (SEQ ID NO: 103)
Mouse mRNA sequence (SEQ ID NO: 104)
Mouse coding sequence (SEQ ID NO: 105)
Human genomic sequence (SEQ ID NO: 106)
Human mRNA sequence (SEQ ID NO: 107)
Human coding sequence (SEQ ID NO: 108)

Table 21 (mouse gene: Pim1; human gene: PIM1)
Mouse genomic sequence (SEQ ID NO: 109)
Mouse mRNA sequence (SEQ ID NO: 110)
Mouse coding sequence (SEQ ID NO: 111)
Human genomic sequence (SEQ ID NO: 112)
Human mRNA sequence (SEQ ID NO: 113)
Human coding sequence (SEQ ID NO: 114)

Table 22 (mouse gene: Wnt3a; human gene: WNT3A)
Mouse genomic sequence (SEQ ID NO: 115)
Mouse mRNA sequence (SEQ ID NO: 116)
Mouse coding sequence (SEQ ID NO: 117)
Human genomic sequence (SEQ ID NO: 118)
Human mRNA sequence (SEQ ID NO: 119)
Human coding sequence (SEQ ID NO: 120)

Table 23 (mouse gene: Ly6e; human gene LY6E)
Mouse genomic sequence (SEQ ID NO: 121)
Mouse mRNA sequence (SEQ ID NO: 122)
Mouse coding sequence (SEQ ID NO: 123)
Human genomic sequence (SEQ ID NO: 124)
Human mRNA sequence (SEQ ID NO: 125)
Human coding sequence (SEQ ID NO: 126)

Table 24 (mouse gene: Rasa2; human gene RASA2)
Mouse genomic sequence (SEQ ID NO: 127)
Mouse mRNA sequence (SEQ ID NO: 128)
Mouse coding sequence (SEQ ID NO: 129)
Human genomic sequence (SEQ ID NO: 130)
Human mRNA sequence (SEQ ID NO: 131)
Human coding sequence (SEQ ID NO: 132)

Table 25 (mouse gene: Gata1; human gene GATA1)
Mouse genomic sequence (SEQ ID NO: 133)
Mouse mRNA sequence (SEQ ID NO: 134)
Mouse coding sequence (SEQ ID NO: 135)
Human genomic sequence (SEQ ID NO: 136)
Human mRNA sequence (SEQ ID NO: 137)
Human coding sequence (SEQ ID NO: 138)

Table 26 (mouse gene: Fkbp5; human gene FKBP5)
Mouse genomic sequence (SEQ ID NO: 139)
Mouse mRNA sequence (SEQ ID NO: 140)
Mouse coding sequence (SEQ ID NO: 141)
Human genomic sequence (SEQ ID NO: 142)
Human mRNA sequence (SEQ ID NO: 143)
Human coding sequence (SEQ ID NO: 144)

Table 27 (mouse gene: Rel; human gene REL)
Mouse genomic sequence (SEQ ID NO: 145)
Mouse mRNA sequence (SEQ ID NO: 146)
Mouse coding sequence (SEQ ID NO: 147)
Human genomic sequence (SEQ ID NO: 148)
Human mRNA sequence (SEQ ID NO: 149)
Human coding sequence (SEQ ID NO: 150)

Table 28 (mouse gene: Icsbp; human gene ICSBP1)
Mouse genomic sequence (SEQ ID NO: 151)
Mouse mRNA sequence (SEQ ID NO: 152)
Mouse coding sequence (SEQ ID NO: 153)
Human genomic sequence (SEQ ID NO: 154)
Human mRNA sequence (SEQ ID NO: 155)
Human coding sequence (SEQ ID NO: 156)

Table 29 (mouse gene: Bmi1; human gene BMI1)
Mouse genomic sequence (SEQ ID NO: 157)
Mouse mRNA sequence (SEQ ID NO: 158)
Mouse coding sequence (SEQ ID NO: 159)
Human genomic sequence (SEQ ID NO: 160)
Human mRNA sequence (SEQ ID NO: 161)
Human coding sequence (SEQ ID NO: 162)

Table 30 (mouse gene: Runx1; human gene RUNX1)
Mouse genomic sequence (SEQ ID NO: 163)
Mouse mRNA sequence (SEQ ID NO: 164)
Mouse coding sequence (SEQ ID NO: 165)
Human genomic sequence (SEQ ID NO: 166)
Human mRNA sequence (SEQ ID NO: 167)
Human coding sequence (SEQ ID NO: 168)

Table 31 (mouse gene: Il2ra; human gene IL2RA)
Mouse genomic sequence (SEQ ID NO: 169)
Mouse mRNA sequence (SEQ ID NO: 170)
Mouse coding sequence (SEQ ID NO: 171)
Human genomic sequence (SEQ ID NO: 172)
Human mRNA sequence (SEQ ID NO: 173)
Human coding sequence (SEQ ID NO: 174)

Table 32 (mouse gene: Nfkb1; human gene NFKB1)
Mouse genomic sequence (SEQ ID NO: 175)
Mouse mRNA sequence (SEQ ID NO: 176)
Mouse coding sequence (SEQ ID NO: 177)
Human genomic sequence (SEQ ID NO: 178)
Human mRNA sequence (SEQ ID NO: 179)
Human coding sequence (SEQ ID NO: 180)

Table 33 (mouse gene: Fyn; human gene FYN)
Mouse genomic sequence (SEQ ID NO: 181)
Mouse mRNA sequence (SEQ ID NO: 182)
Mouse coding sequence (SEQ ID NO: 183)
Human genomic sequence (SEQ ID NO: 184)
Human mRNA sequence (SEQ ID NO: 185)
Human coding sequence (SEQ ID NO: 186)

Table 34 (mouse gene: Nfkbil1; human gene NFKBIL1)
Mouse genomic sequence (SEQ ID NO: 187)
Mouse mRNA sequence (SEQ ID NO: 188)
Mouse coding sequence (SEQ ID NO: 189)
Human genomic sequence (SEQ ID NO: 190)
Human mRNA sequence (SEQ ID NO: 191)

Human coding sequence (SEQ ID NO: 192)

Table 35 (mouse gene: Flt3; human gene FLT3)
Mouse genomic sequence (SEQ ID NO: 193)
Mouse mRNA sequence (SEQ ID NO: 194)
Mouse coding sequence (SEQ ID NO: 195)
Human genomic sequence (SEQ ID NO: 196)
Human mRNA sequence (SEQ ID NO: 197)
Human coding sequence (SEQ ID NO: 198)

Table 36 (mouse gene: Dntt; human gene DNTT)
Mouse genomic sequence (SEQ ID NO: 199)
Mouse mRNA sequence (SEQ ID NO: 200)
Mouse coding sequence (SEQ ID NO: 201)
Human genomic sequence (SEQ ID NO: 202)
Human mRNA sequence (SEQ ID NO: 203)
Human coding sequence (SEQ ID NO: 204)

Table 37 (mouse gene: Znfn1a1; human gene ZNFN1A1)
Mouse genomic sequence (SEQ ID NO: 205)
Mouse mRNA sequence (SEQ ID NO: 206)
Mouse coding sequence (SEQ ID NO: 207)
Human genomic sequence (SEQ ID NO: 208)
Human mRNA sequence (SEQ ID NO: 209)
Human coding sequence (SEQ ID NO: 210)

Table 38 (mouse gene: Tbx21; human gene TBX21)
Mouse genomic sequence (SEQ ID NO: 211)
Mouse mRNA sequence (SEQ ID NO: 212)
Mouse coding sequence (SEQ ID NO: 213)
Human genomic sequence (SEQ ID NO: 214)
Human mRNA sequence (SEQ ID NO: 215)
Human coding sequence (SEQ ID NO: 216)

Table 39 (mouse gene: Stat5b; human gene STAT5B)
Mouse genomic sequence (SEQ ID NO: 217)
Mouse mRNA sequence (SEQ ID NO: 218)
Mouse coding sequence (SEQ ID NO: 219)
Human genomic sequence (SEQ ID NO: 220)

Human mRNA sequence (SEQ ID NO: 221)
Human coding sequence (SEQ ID NO: 222)

Table 40 (mouse gene: Sema4d; human gene SEMA4D)
Mouse genomic sequence (SEQ ID NO: 223)
Mouse mRNA sequence (SEQ ID NO: 224)
Mouse coding sequence (SEQ ID NO: 225)
Human genomic sequence (SEQ ID NO: 226)
Human mRNA sequence (SEQ ID NO: 227)
Human coding sequence (SEQ ID NO: 228)

Table 41 (mouse gene: Mdm2; human gene MDM2)
Mouse genomic sequence (SEQ ID NO: 229)
Mouse mRNA sequence (SEQ ID NO: 230)
Mouse coding sequence (SEQ ID NO: 231)
Human genomic sequence (SEQ ID NO: 232)
Human mRNA sequence (SEQ ID NO: 233)
Human coding sequence (SEQ ID NO: 234)

Table 42 (mouse gene: Prlr; human gene PRLR)
Mouse genomic sequence (SEQ ID NO: 235)
Mouse mRNA sequence (SEQ ID NO: 236)
Mouse coding sequence (SEQ ID NO: 237)
Human genomic sequence (SEQ ID NO: 238)
Human mRNA sequence (SEQ ID NO: 239)
Human coding sequence (SEQ ID NO: 240)

Table 43 (mouse gene: Top1; human gene TOP1)
Mouse genomic sequence (SEQ ID NO: 241)
Mouse mRNA sequence (SEQ ID NO: 242)
Mouse coding sequence (SEQ ID NO: 243)
Human genomic sequence (SEQ ID NO: 244)
Human mRNA sequence (SEQ ID NO: 245)
Human coding sequence (SEQ ID NO: 246)

Table 44 (mouse gene: Dusp10; human gene DUSP10)
Mouse genomic sequence (SEQ ID NO: 247)
Mouse mRNA sequence (SEQ ID NO: 248)
Mouse coding sequence (SEQ ID NO: 249)

Human genomic sequence (SEQ ID NO: 250)
Human mRNA sequence (SEQ ID NO: 251)
Human coding sequence (SEQ ID NO: 252)

Table 45 (mouse gene: Fli1; human gene FLI1)
Mouse genomic sequence (SEQ ID NO: 253)
Mouse mRNA sequence (SEQ ID NO: 254)
Mouse coding sequence (SEQ ID NO: 255)
Human genomic sequence (SEQ ID NO: 256)
Human mRNA sequence (SEQ ID NO: 257)
Human coding sequence (SEQ ID NO: 258)

Table 46 (mouse gene: Tk2; human gene TK2)
Mouse genomic sequence (SEQ ID NO: 259)
Mouse mRNA sequence (SEQ ID NO: 260)
Mouse coding sequence (SEQ ID NO: 261)
Human genomic sequence (SEQ ID NO: 262)
Human mRNA sequence (SEQ ID NO: 263)
Human coding sequence (SEQ ID NO: 264)

Table 47 (mouse gene: Nupr1)
Mouse genomic sequence (SEQ ID NO: 265)
Mouse mRNA sequence (SEQ ID NO: 266)
Mouse coding sequence (SEQ ID NO: 267)
Human genomic sequence (SEQ ID NO: 268)
Human mRNA sequence (SEQ ID NO: 269)
Human coding sequence (SEQ ID NO: 270)

Table 48 (mouse gene: Zfhx1b; human gene ZFHX1B)
Mouse genomic sequence (SEQ ID NO: 271)
Mouse mRNA sequence (SEQ ID NO: 272)
Mouse coding sequence (SEQ ID NO: 273)
Human genomic sequence (SEQ ID NO: 274)
Human mRNA sequence (SEQ ID NO: 275)
Human coding sequence (SEQ ID NO: 276)

Table 49 (mouse gene: Vdac1; human gene VDAC1)
Mouse genomic sequence (SEQ ID NO: 277)
Mouse mRNA sequence (SEQ ID NO: 278)

Mouse coding sequence (SEQ ID NO: 279)
Human genomic sequence (SEQ ID NO: 280)
Human mRNA sequence (SEQ ID NO: 281)
Human coding sequence (SEQ ID NO: 282)

Table 50 (mouse gene: Nfatc1; human gene NFATC1)
Mouse genomic sequence (SEQ ID NO: 283)
Mouse mRNA sequence (SEQ ID NO: 284)
Mouse coding sequence (SEQ ID NO: 285)
Human genomic sequence (SEQ ID NO: 286)
Human mRNA sequence (SEQ ID NO: 287)
Human coding sequence (SEQ ID NO: 288)

Table 51 (mouse gene: Syk; human gene SYK)
Mouse genomic sequence (SEQ ID NO: 289)
Mouse mRNA sequence (SEQ ID NO: 290)
Mouse coding sequence (SEQ ID NO: 291)
Human genomic sequence (SEQ ID NO: 292)
Human mRNA sequence (SEQ ID NO: 293)
Human coding sequence (SEQ ID NO: 294)

Table 52 (mouse gene: Gnb1; human gene GNB1)
Mouse genomic sequence (SEQ ID NO: 295)
Mouse mRNA sequence (SEQ ID NO: 296)
Mouse coding sequence (SEQ ID NO: 297)
Human genomic sequence (SEQ ID NO: 298)
Human mRNA sequence (SEQ ID NO: 299)
Human coding sequence (SEQ ID NO: 300).

Table 53 (mouse gene: Ccnd2; human gene CCND2)
Mouse genomic sequence (SEQ ID NO: 301)
Mouse mRNA sequence (SEQ ID NO: 302)
Mouse coding sequence (SEQ ID NO: 303)
Human genomic sequence (SEQ ID NO: 304)
Human mRNA sequence (SEQ ID NO: 305)
Human coding sequence (SEQ ID NO: 306)

Table 54 (mouse gene Tnfrsf6; human gene TNFRSF6)
Mouse genomic sequence (SEQ ID NO: 307)

Mouse mRNA sequence (SEQ ID NO: 308)
Mouse coding sequence (SEQ ID NO: 309)
Human genomic sequence (SEQ ID NO: 310)
Human mRNA sequence (SEQ ID NO: 311)
Human coding sequence (SEQ ID NO: 312)

Table 55 (mouse gene Irf2; human gene IRF2)
Mouse genomic sequence (SEQ ID NO: 313)
Mouse mRNA sequence (SEQ ID NO: 314)
Mouse coding sequence (SEQ ID NO: 315)
Human genomic sequence (SEQ ID NO: 316)
Human mRNA sequence (SEQ ID NO: 317)
Human coding sequence (SEQ ID NO: 318)

Table 56 (mouse gene Morf; human gene: MORF)
Mouse genomic sequence (SEQ ID NO: 319)
Mouse mRNA sequence (SEQ ID NO: 320)
Mouse coding sequence (SEQ ID NO: 321)
Human genomic sequence (SEQ ID NO: 322)
Human mRNA sequence (SEQ ID NO: 323)
Human coding sequence (SEQ ID NO: 324)

Table 57 (mouse gene: Runx3; human gene: RUNX3)
Mouse genomic sequence (SEQ ID NO: 325)
Mouse mRNA sequence (SEQ ID NO: 326)
Mouse coding sequence (SEQ ID NO: 327)
Human genomic sequence (SEQ ID NO: 328)
Human mRNA sequence (SEQ ID NO:329)
Human coding sequence (SEQ ID NO: 330)

Table 58 (mouse gene: Bcl11b; human gene: BCL11B)
Mouse genomic sequence (SEQ ID NO: 331)
Mouse mRNA sequence (SEQ ID NO: 332)
Mouse coding sequence (SEQ ID NO: 333)
Human genomic sequence (SEQ ID NO: 334)
Human mRNA sequence (SEQ ID NO: 335)
Human coding sequence (SEQ ID NO: 336)

Table 59 (mouse gene: Arhgef1; human gene: ARHGEF1)

Mouse genomic sequence (SEQ ID NO: 337)
Mouse mRNA sequence (SEQ ID NO: 338)
Mouse coding sequence (SEQ ID NO: 339)
Human genomic sequence (SEQ ID NO: 340)
Human mRNA sequence (SEQ ID NO: 341)
Human coding sequence (SEQ ID NO: 342)

Table 60 (mouse gene: Ptprk; human gene: PTPRK)
Mouse genomic sequence (SEQ ID NO: 343)
Mouse mRNA sequence (SEQ ID NO: 344)
Mouse coding sequence (SEQ ID NO: 345)
Human genomic sequence (SEQ ID NO:346)
Human mRNA sequence (SEQ ID NO: 347)
Human coding sequence (SEQ ID NO: 348)

Table 61 (mouse gene: Mcmd5; human gene: MCM5)
Mouse genomic sequence (SEQ ID NO: 349)
Mouse mRNA sequence (SEQ ID NO: 350)
Mouse coding sequence (SEQ ID NO: 351)
Human genomic sequence (SEQ ID NO: 352)
Human mRNA sequence (SEQ ID NO: 353)
Human coding sequence (SEQ ID NO: 354)

Table 62 (mouse gene: Matn4; human gene: MATN4)
Mouse genomic sequence (SEQ ID NO: 355)
Mouse mRNA sequence (SEQ ID NO: 356)
Mouse coding sequence (SEQ ID NO: 357)
Human genomic sequence (SEQ ID NO: 358)
Human mRNA sequence (SEQ ID NO: 359)
Human coding sequence (SEQ ID NO: 360)

Table 63 (mouse gene: Tnfsf11; human gene TNFSF11)
Mouse genomic sequence (SEQ ID NO: 361)
Mouse mRNA sequence (SEQ ID NO: 362)
Mouse coding sequence (SEQ ID NO: 363)
Human genomic sequence (SEQ ID NO: 364)
Human mRNA sequence (SEQ ID NO: 365)
Human coding sequence (SEQ ID NO: 366)

Table 64 (mouse gene: Itk; human gene ITK)
Mouse genomic sequence (SEQ ID NO: 367)
Mouse mRNA sequence (SEQ ID NO: 368)
Mouse coding sequence (SEQ ID NO: 369)
Human genomic sequence (SEQ ID NO: 370)
Human mRNA sequence (SEQ ID NO: 371)
Human coding sequence (SEQ ID NO: 372)

Table 65 (mouse gene: Fish; human gene: N/A)
Mouse genomic sequence (SEQ ID NO: 373)
Mouse mRNA sequence (SEQ ID NO: 374)
Mouse coding sequence (SEQ ID NO: 375)
Human genomic sequence (SEQ ID NO: 376)
Human mRNA sequence (SEQ ID NO: 377)
Human coding sequence (SEQ ID NO: 378)

Table 66 (mouse gene: Egr2; human gene EGR2)
Mouse genomic sequence (SEQ ID NO: 379)
Mouse mRNA sequence (SEQ ID NO: 380)
Mouse coding sequence (SEQ ID NO: 381)
Human genomic sequence (SEQ ID NO: 382)
Human mRNA sequence (SEQ ID NO: 383)
Human coding sequence (SEQ ID NO: 384)

Table 67 (mouse gene: Sos1; human gene SOS1)
Mouse genomic sequence (SEQ ID NO: 385)
Mouse mRNA sequence (SEQ ID NO: 386)
Mouse coding sequence (SEQ ID NO: 387)
Human genomic sequence (SEQ ID NO: 388)
Human mRNA sequence (SEQ ID NO: 389)
Human coding sequence (SEQ ID NO: 390)

Table 68 (mouse gene: Pou2af1; human gene POU2AF1)
Mouse genomic sequence (SEQ ID NO: 391)
Mouse mRNA sequence (SEQ ID NO: 392)
Mouse coding sequence (SEQ ID NO: 393)
Human genomic sequence (SEQ ID NO: 394)
Human mRNA sequence (SEQ ID NO: 395)
Human coding sequence (SEQ ID NO: 396)

Table 69 (mouse gene: Mef2c; human gene MEF2C)
Mouse genomic sequence (SEQ ID NO: 397)
Mouse mRNA sequence (SEQ ID NO: 398)
Mouse coding sequence (SEQ ID NO: 399)
Human genomic sequence (SEQ ID NO: 400)
Human mRNA sequence (SEQ ID NO: 401)
Human coding sequence (SEQ ID NO: 402)

Table 70 (mouse gene: Map3k8; human gene MAP3K8)
Mouse genomic sequence (SEQ ID NO: 403)
Mouse mRNA sequence (SEQ ID NO: 404)
Mouse coding sequence (SEQ ID NO: 405)
Human genomic sequence (SEQ ID NO: 406)
Human mRNA sequence (SEQ ID NO: 407)
Human coding sequence (SEQ ID NO: 408)

Table 71 (mouse gene: Fgfr3; human gene FGFR3)
Mouse genomic sequence (SEQ ID NO: 409)
Mouse mRNA sequence (SEQ ID NO: 410)
Mouse coding sequence (SEQ ID NO: 411)
Human genomic sequence (SEQ ID NO: 412)
Human mRNA sequence (SEQ ID NO: 413)
Human coding sequence (SEQ ID NO: 414)

Table 72 (mouse gene: Cbx8; human gene CBX8)
Mouse genomic sequence (SEQ ID NO: 415)
Mouse mRNA sequence (SEQ ID NO: 416)
Mouse coding sequence (SEQ ID NO: 417)
Human genomic sequence (SEQ ID NO: 418)
Human mRNA sequence (SEQ ID NO: 419)
Human coding sequence (SEQ ID NO: 420)

Table 73 (mouse gene: Lmo2; human gene LMO2)
Mouse genomic sequence (SEQ ID NO: 421)
Mouse mRNA sequence (SEQ ID NO: 422)
Mouse coding sequence (SEQ ID NO: 423)
Human genomic sequence (SEQ ID NO: 424)
Human mRNA sequence (SEQ ID NO: 425)

Human coding sequence (SEQ ID NO: 426)

Table 74 (mouse gene: Itpr1; human gene ITPR1)
Mouse genomic sequence (SEQ ID NO: 427)
Mouse mRNA sequence (SEQ ID NO: 428)
Mouse coding sequence (SEQ ID NO: 429)
Human genomic sequence (SEQ ID NO: 430)
Human mRNA sequence (SEQ ID NO: 431)
Human coding sequence (SEQ ID NO: 432)

Table 75 (mouse gene: Sell; human gene SELL)
Mouse genomic sequence (SEQ ID NO: 433)
Mouse mRNA sequence (SEQ ID NO: 434)
Mouse coding sequence (SEQ ID NO: 435)
Human genomic sequence (SEQ ID NO: 436)
Human mRNA sequence (SEQ ID NO: 437)
Human coding sequence (SEQ ID NO: 438)

Table 76 (mouse gene: Dpt; human gene DPT)
Mouse genomic sequence (SEQ ID NO: 439)
Mouse mRNA sequence (SEQ ID NO: 440)
Mouse coding sequence (SEQ ID NO: 441)
Human genomic sequence (SEQ ID NO: 442)
Human mRNA sequence (SEQ ID NO: 443)
Human coding sequence (SEQ ID NO: 444)

Table 77 (mouse gene: Pap; human gene PAP)
Mouse genomic sequence (SEQ ID NO: 445)
Mouse mRNA sequence (SEQ ID NO: 446)
Mouse coding sequence (SEQ ID NO: 447)
Human genomic sequence (SEQ ID NO: 448)
Human mRNA sequence (SEQ ID NO: 449)
Human coding sequence (SEQ ID NO: 450)

Table 78 (mouse gene: Blm; human gene BLM)
Mouse genomic sequence (SEQ ID NO: 451)
Mouse mRNA sequence (SEQ ID NO: 452)
Mouse coding sequence (SEQ ID NO: 453)
Human genomic sequence (SEQ ID NO: 454)

Human mRNA sequence (SEQ ID NO: 455)
Human coding sequence (SEQ ID NO: 456)

Table 79 (mouse gene: Blr1; human gene BLR1)
Mouse genomic sequence (SEQ ID NO: 457)
Mouse mRNA sequence (SEQ ID NO: 458)
Mouse coding sequence (SEQ ID NO: 459)
Human genomic sequence (SEQ ID NO: 460)
Human mRNA sequence (SEQ ID NO: 461)
Human coding sequence (SEQ ID NO: 462)

Table 80 (mouse gene: Ptp4a2; human gene PTP4A2)
Mouse genomic sequence (SEQ ID NO: 463)
Mouse mRNA sequence (SEQ ID NO: 464)
Mouse coding sequence (SEQ ID NO: 465)
Human genomic sequence (SEQ ID NO: 466)
Human mRNA sequence (SEQ ID NO: 467)
Human coding sequence (SEQ ID NO: 468)

Table 81 (mouse gene: Mcm3ap; human gene MCM3AP)
Mouse genomic sequence (SEQ ID NO: 469)
Mouse mRNA sequence (SEQ ID NO: 470)
Mouse coding sequence (SEQ ID NO: 471)
Human genomic sequence (SEQ ID NO: 472)
Human mRNA sequence (SEQ ID NO: 473)
Human coding sequence (SEQ ID NO: 474)

Table 82 (mouse gene: Jak2; human gene JAK2)
Mouse genomic sequence (SEQ ID NO: 475)
Mouse mRNA sequence (SEQ ID NO: 476)
Mouse coding sequence (SEQ ID NO: 477)
Human genomic sequence (SEQ ID NO: 478)
Human mRNA sequence (SEQ ID NO: 479)
Human coding sequence (SEQ ID NO: 480)

Table 83 (mouse gene: Fus1; human gene FUS1)
Mouse genomic sequence (SEQ ID NO: 481)
Mouse mRNA sequence (SEQ ID NO: 482)
Mouse coding sequence (SEQ ID NO: 483)

Human genomic sequence (SEQ ID NO: 484)
Human mRNA sequence (SEQ ID NO: 485)
Human coding sequence (SEQ ID NO: 486)

Table 84 (mouse gene: Rassf1; human gene RASSF1)
Mouse genomic sequence (SEQ ID NO: 487)
Mouse mRNA sequence (SEQ ID NO: 488)
Mouse coding sequence (SEQ ID NO: 489)
Human genomic sequence (SEQ ID NO: 490)
Human mRNA sequence (SEQ ID NO: 491)
Human coding sequence (SEQ ID NO: 492)

Table 85 (mouse gene: Pik3r1; human gene PIK3R1)
Mouse genomic sequence (SEQ ID NO: 493)
Mouse mRNA sequence (SEQ ID NO: 494)
Mouse coding sequence (SEQ ID NO: 495)
Human genomic sequence (SEQ ID NO: 496)
Human mRNA sequence (SEQ ID NO: 497)
Human coding sequence (SEQ ID NO: 498)

Table 86 (mouse gene: Braf; human gene BRAF)
Mouse genomic sequence (SEQ ID NO: 499)
Mouse mRNA sequence (SEQ ID NO: 500)
Mouse coding sequence (SEQ ID NO: 501)
Human genomic sequence (SEQ ID NO: 502)
Human mRNA sequence (SEQ ID NO: 503)
Human coding sequence (SEQ ID NO: 504)

Table 87 (mouse gene: Tle3; human gene: TLE3)
Mouse genomic sequence (SEQ ID NO: 505)
Mouse mRNA sequence (SEQ ID NO: 506)
Mouse coding sequence (SEQ ID NO: 507)
Human genomic sequence (SEQ ID NO: 508)
Human mRNA sequence (SEQ ID NO: 509)
Human coding sequence (SEQ ID NO: 510)

Table 88 (mouse gene: Nek2; human gene NEK2)
Mouse genomic sequence (SEQ ID NO: 511)
Mouse mRNA sequence (SEQ ID NO: 512)

Mouse coding sequence (SEQ ID NO: 513)
Human genomic sequence (SEQ ID NO: 514)
Human mRNA sequence (SEQ ID NO: 515)
Human coding sequence (SEQ ID NO: 516)

Table 89 (mouse gene: Nr3c1; human gene NR3C1)
Mouse genomic sequence (SEQ ID NO: 517)
Mouse mRNA sequence (SEQ ID NO: 518)
Mouse coding sequence (SEQ ID NO: 519)
Human genomic sequence (SEQ ID NO: 520)
Human mRNA sequence (SEQ ID NO: 521)
Human coding sequence (SEQ ID NO: 522)

Table 90 (mouse gene: Dad1; human gene DAD1)
Mouse genomic sequence (SEQ ID NO: 523)
Mouse mRNA sequence (SEQ ID NO: 524)
Mouse coding sequence (SEQ ID NO: 525)
Human genomic sequence (SEQ ID NO: 526)
Human mRNA sequence (SEQ ID NO: 527)
Human coding sequence (SEQ ID NO: 528)

Table 91 (mouse gene: Lck; human gene LCK)
Mouse genomic sequence (SEQ ID NO: 529)
Mouse mRNA sequence (SEQ ID NO: 530)
Mouse coding sequence (SEQ ID NO: 531)
Human genomic sequence (SEQ ID NO: 532)
Human mRNA sequence (SEQ ID NO: 533)
Human coding sequence (SEQ ID NO: 534)

Table 92 (mouse gene: Git2; human gene GIT2)
Mouse genomic sequence (SEQ ID NO: 535)
Mouse mRNA sequence (SEQ ID NO: 536)
Mouse coding sequence (SEQ ID NO: 537)
Human genomic sequence (SEQ ID NO: 538)
Human mRNA sequence (SEQ ID NO: 539)
Human coding sequence (SEQ ID NO: 540).

Table 93 (mouse gene: Anp32; human gene N/A)
Mouse genomic sequence (SEQ ID NO: 541)

Mouse mRNA sequence (SEQ ID NO: 542)
Mouse coding sequence (SEQ ID NO: 543)
Human genomic sequence (SEQ ID NO: 544)
Human mRNA sequence (SEQ ID NO: 545)
Human coding sequence (SEQ ID NO: 546).

Table 94 (mouse gene: Map2k5; human gene MAP2K5)
Mouse genomic sequence (SEQ ID NO: 547)
Mouse mRNA sequence (SEQ ID NO: 548)
Mouse coding sequence (SEQ ID NO: 549)
Human genomic sequence (SEQ ID NO: 550)
Human mRNA sequence (SEQ ID NO: 551)
Human coding sequence (SEQ ID NO: 552).

Table 95 (mouse gene: Cd28; human gene CD28)
Mouse genomic sequence (SEQ ID NO: 553)
Mouse mRNA sequence (SEQ ID NO: 554)
Mouse coding sequence (SEQ ID NO: 555)
Human genomic sequence (SEQ ID NO: 556)
Human mRNA sequence (SEQ ID NO: 556)
Human coding sequence (SEQ ID NO: 558).

Table 96 (mouse gene: Sept9; human gene Msf)
Mouse genomic sequence (SEQ ID NO: 559)
Mouse mRNA sequence (SEQ ID NO: 560)
Mouse coding sequence (SEQ ID NO: 561)
Human genomic sequence (SEQ ID NO: 562)
Human mRNA sequence (SEQ ID NO: 563)
Human coding sequence (SEQ ID NO: 564).

Table 97 (mouse gene: Fzd10; human gene FZD10)
Mouse genomic sequence (SEQ ID NO: 565)
Mouse mRNA sequence (SEQ ID NO: 566)
Mouse coding sequence (SEQ ID NO: 567)
Human genomic sequence (SEQ ID NO: 568)
Human mRNA sequence (SEQ ID NO: 569)
Human coding sequence (SEQ ID NO: 570).

Table 98 (mouse gene: Calm2; human gene CALM2)

Mouse genomic sequence (SEQ ID NO: 571)
Mouse mRNA sequence (SEQ ID NO: 572)
Mouse coding sequence (SEQ ID NO: 573)
Human genomic sequence (SEQ ID NO: 574)
Human mRNA sequence (SEQ ID NO: 575)
Human coding sequence (SEQ ID NO: 576).

Table 99 (mouse gene: Ncf4; human gene NCF4)
Mouse genomic sequence (SEQ ID NO: 577)
Mouse mRNA sequence (SEQ ID NO: 578)
Mouse coding sequence (SEQ ID NO: 579)
Human genomic sequence (SEQ ID NO: 580)
Human mRNA sequence (SEQ ID NO: 581)
Human coding sequence (SEQ ID NO: 582).

Table 100 (mouse gene: Rac2; human gene RAC2)
Mouse genomic sequence (SEQ ID NO: 583)
Mouse mRNA sequence (SEQ ID NO: 584)
Mouse coding sequence (SEQ ID NO: 585)
Human genomic sequence (SEQ ID NO: 586)
Human mRNA sequence (SEQ ID NO: 587)
Human coding sequence (SEQ ID NO: 588).

Table 101 (mouse gene: Mbnl; human gene MBNL)
Mouse genomic sequence (SEQ ID NO: 589)
Mouse mRNA sequence (SEQ ID NO: 590)
Mouse coding sequence (SEQ ID NO: 591)
Human genomic sequence (SEQ ID NO: 592)
Human mRNA sequence (SEQ ID NO: 593)
Human coding sequence (SEQ ID NO: 594).

Table 102 (mouse gene: mCG10516; human gene N/A)
Mouse genomic sequence (SEQ ID NO: 595)
Mouse mRNA sequence (SEQ ID NO: 596)
Mouse coding sequence (SEQ ID NO: 597)
Human genomic sequence (SEQ ID NO: 598)
Human mRNA sequence (SEQ ID NO: 599)
Human coding sequence (SEQ ID NO: 600)

Table 103 (mouse gene: Rorc; human gene RORC)
Mouse genomic sequence (SEQ ID NO: 601)
Mouse mRNA sequence (SEQ ID NO: 602)
Mouse coding sequence (SEQ ID NO: 603)
Human genomic sequence (SEQ ID NO: 604)
Human mRNA sequence (SEQ ID NO: 605)
Human coding sequence (SEQ ID NO: 606)

Table 104 (mouse gene mCG15938; human gene BAT1)
Mouse genomic sequence (SEQ ID NO: 607)
Mouse mRNA sequence (SEQ ID NO: 608)
Mouse coding sequence (SEQ ID NO: 609)
Human genomic sequence (SEQ ID NO: 610)
Human mRNA sequence (SEQ ID NO: 611)
Human coding sequence (SEQ ID NO: 612)

Table 105 (mouse gene: Iqgap1; human gene IQGAP1)
Mouse genomic sequence (SEQ ID NO: 613)
Mouse mRNA sequence (SEQ ID NO: 614)
Mouse coding sequence (SEQ ID NO: 615)
Human genomic sequence (SEQ ID NO: 616)
Human mRNA sequence (SEQ ID NO: 617)
Human coding sequence (SEQ ID NO: 618)

Table 106 (mouse gene Zpf29; human gene: hCG27579)
Mouse genomic sequence (SEQ ID NO: 619)
Mouse mRNA sequence (SEQ ID NO: 620)
Mouse coding sequence (SEQ ID NO: 621)
Human genomic sequence (SEQ ID NO: 622)
Human mRNA sequence (SEQ ID NO: 623)
Human coding sequence (SEQ ID NO: 624)

Table 107 (mouse gene: Kcnj9; human gene: KCNJ9)
Mouse genomic sequence (SEQ ID NO: 625)
Mouse mRNA sequence (SEQ ID NO: 626)
Mouse coding sequence (SEQ ID NO: 627)
Human genomic sequence (SEQ ID NO: 628)
Human mRNA sequence (SEQ ID NO:629)
Human coding sequence (SEQ ID NO: 630)

Table 108 (mouse gene: Ppp3cc; human gene: PPP3CC)
Mouse genomic sequence (SEQ ID NO: 631)
Mouse mRNA sequence (SEQ ID NO: 632)
Mouse coding sequence (SEQ ID NO: 633)
Human genomic sequence (SEQ ID NO: 634)
Human mRNA sequence (SEQ ID NO: 635)
Human coding sequence (SEQ ID NO: 636)

Table 109 (mouse gene: mCG9110; human gene: hCG27579)
Mouse genomic sequence (SEQ ID NO: 637)
Mouse mRNA sequence (SEQ ID NO: 638)
Mouse coding sequence (SEQ ID NO: 639)
Human genomic sequence (SEQ ID NO: 640)
Human mRNA sequence (SEQ ID NO: 641)
Human coding sequence (SEQ ID NO: 642)

Table 110 (mouse gene: mCG2257; human gene: PRDM11)
Mouse genomic sequence (SEQ ID NO: 643)
Mouse mRNA sequence (SEQ ID NO: 644)
Mouse coding sequence (SEQ ID NO: 645)
Human genomic sequence (SEQ ID NO: 646)
Human mRNA sequence (SEQ ID NO: 647)
Human coding sequence (SEQ ID NO: 648)

Table 111 (mouse gene: mCG17918; human gene: hCG23764)
Mouse genomic sequence (SEQ ID NO: 649)
Mouse mRNA sequence (SEQ ID NO: 650)
Mouse coding sequence (SEQ ID NO: 651)
Human genomic sequence (SEQ ID NO: 652)
Human mRNA sequence (SEQ ID NO: 653)
Human coding sequence (SEQ ID NO: 654)

Table 112 (mouse gene: Lfng; human gene: LFNG)
Mouse genomic sequence (SEQ ID NO: 655)
Mouse mRNA sequence (SEQ ID NO: 656)
Mouse coding sequence (SEQ ID NO: 657)
Human genomic sequence (SEQ ID NO: 658)
Human mRNA sequence (SEQ ID NO: 659)
Human coding sequence (SEQ ID NO: 660).

Table 1

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000619	GATCAAAGCAATCTCTATGTCTTTCTCTGCTG TCCTCCTCAGACATCTCCAGAGAGCTGGGAT ATTTTTCTTTCCCATTTGAGATTATGAAGTTG TTTCTAGAGTGCATGACGCAGGTTGAAGGAT AAGTACACAGGTCCCAAGGAACCAAGCGTTT TCACTGACGGTGATGAGTCTTGTTCGTGAGA TTGTTGTGATTCTCAGCCTTTCTCTTCCCCTG TGTGTGCTCTTCATTTTCTGGTTCTGTCTGCC TAGCACCTCCTGGGGAAGCTGCTGTGCTTT	p000632	A	*Spr*
IM000620	GATCTTTGGAGCCCAGTTGTTAATCATAAGA GCTGATATTTTGAAAGAGTGTGTCAACCTAG ATGCACAGGGAAGCCAAAGCATTCAGCC	p000633	D	--
IM000621	ATATGACCACAAGGAAATAAGATAAAGTGTT CATACTGAATTTATAATGAAAAGTGATC	p000634	C	--
IM000622	GAACAGGCATGGCTTTACTTGTACAATGAGG AAACCAAGGCAGAGATTGCAAAGCGGGTCC TACACGTTTGCTCCATGCCCTGCTTCTCTGA CCACAGTGTACTGAGAATATGCTGAGCCCTA GTTCCTGGGGAGGAGGCAGAAGAGAGCAGC ATCCTGCCCACTTGAAGGCGTGCACACATAG TTCCTGTCTGATC	p000638	D	--
IM000623	GATCAGGAGACCACACCCAGCTAGCCTTCTC TGACTGGGTATCCTTGGTCAGCCAGCCTTTC TTCACCTCATGTTCTCATTTGCAAACTCACAT GAACACTATTTGACCTACACACTTCATAAAGC TGTTTTTAGAAAGACGAGATAATACAGGAGG AACGCTACAATATTAAATGATATGTATTTATA T	p000639	D	--
IM000624	AGTGTTTAGGTCAGCTGGTGCAGGAGAAGC TTCTTGAGGAAGACGACCATCTGGCAAGGC CTGATGGTAGAAAATAATGGACTTCTCTCCA ACTGAGTAGGAACTTGATGATC	p000640	D	--
IM000625	ATCAGTAAGTTAATCCTAAGAATTACTATGCA TTTTTCCCCTCTTTTTTAACAACATTCCTCCTT AGCTTATATGAGGCTCTAGTGCCCGGAGACT TTAATACTGCCCTAACATGATGGTGGCTCTTT GTCCCTCTTTCTCAGCCACTGAAATCTGACA GTTTGGGGAAGAATAATAAGAATTTAAGAAA CTAGATGGTTTTAAATATAGATATAAAAACAG TTCTTCGACTATTCTCAATAAAGAAATTCAGT CAAAAGAATTTCAGTCCTAACACAATGATC	p000641	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000626	GATCATCAGAGTCCTGCATCTTATGTGTGCA GTGTTTTCAGCAATACAGGCTTACCTTCAAC CTCTAACAGGCAACCAGATGCTACAATAGCT TATATTGTTTTAGAAATCACTTGGACTACTCT AAACAACAACTTGAGTGAAGGCTCTTTGTAT CTGATACTGGAGTTTGTTAGTCTATGACACTT GTGGGGAGACATGTCTGCACAAGTAGCATAT GTGTGTACATGTATATTGTATACATATATAGT TTTGCTCTATGTATGTATGTGTATATGTATGT ATGTATATGTATATGTATGTATATATATAG	p000642	D	--
IM000627	AAGGGACCTGATAATCGTGTTGGCAACTGG GCTACAATTAGTTATCAATTGCTTGCTTGCCA CCTGCCCTGCTCCATAGAGAATCATAGTCTG GGGAGTGTGGAGGAATAGCGGAGTCATCTA AACACATCACTGCTGCCCCCACCATTTGCCT GCCACCAGGCCCCTGCCTTTCATTTTGCATT TCTCCCTCTTACAAGCAAATGGCGCTCACTG ATC	p000643	D	--
IM000628	GTTTGGGGATTGTACAGAATGCACAGCGTAG TATTCAGGAAAAAGGAAACTGGGAAATTAAT GTATAAATTAAAATCAGCTTTTAATTAGCTTA ACACACACATACGAAGGCAAAAATGTAACGT TACTTTGATC	p000644	K	*Myc*
IM000629	GATCTCATTACAGATGGTTGTGAGCTACCAT GTGG	p000647	R	--
IM000630	GATCTCAGGAGGCACCGAGAGACTCAGCAT GGACTCAAATGAGTACCCTGGCAGCCCGCA ACACCAGCTGTGTAACACTACCGTGAGGGAT GTCTTCCCTGCCTCCCTCCAGCCCCTTCTCA GGCCCTGAGTCCAGTGTGCAAAGCTCATCAT GGTTAGTCCCCTTCACCT	p000649	K	*Gfi1*
IM000631	AGAGCACCCGACTGCTCTTCCGAAGGTCCA GAGTTCAAATCCCAGCAACCACATGGTGGCT CACAACCATCCGTAACAAGATC	p000650	R	--
IM000632	GATCAAATCCTGTCAGGGAGAGGGGCTCCT CCCAGTAGTGCCATCCCATAATAATAAGAAG GACTCCTGGGCCTCAGTGAAGTCAGGCTGA CCACTACTGCAGGTTAGTCATGACCAGTAGC CAGAATGGAACGAAGGGTGACCCAGTGTGA GGACACAGCCCCAGGCAACTGCTTCTGCTTT GAGCCAAGTTGTTACCCCAAAGCTCGTCATT CCGCTTGGTTTCTCATGTGTGTGAGCTGCAC ATATGGAGGTCCCCCTTTGTTCCCTT	p000651	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000633	GTGAGGAAGGTCCCTCTGCATTCTAACCTTC CTCAACTCCACCAGCCTCGGCGTTTAAGGGA GAAATATTACCGTTCCCTTTGGGCCAAGTTG GAGCCAGTGAAGTAGTCGGAAATGTACAGTC ACAGGAAATTGCTGCTACCAAGGCTGGAGG AACAAAGAGAAGACTTGTCACAAGAGGCCAG AGAGGAAGTCACCCAGTACAAACTGAAGCG CGCGCGCACACACACACACACACACACACA CACGCACACACACACACACACGATC	p000652	D	--
IM000634	TGGCCGCCTAGACAAGCTGACCATCACCTC CCAGAACCTGCAACTGGAGAGCCTTCGCAT GAAGCTTCCGAAATGTGCGTGCTCCACCTGT CCCTCACCTCACAGACATCATTTCTCCATTTA GCCCCTCCCGATC	p000654	A	*Ii*
IM000635	GATCCCCTGGAATTTACAGTCGGTTCCAACA ATCATGTAGATG	p000656	C	--
IM000636	GATCGGCTATAGCATTTGTCAATGTTTACCCA GAAGAATAGCACAGATATATTTGCACATCAAT GCTTATTGCAGTATTATTCACAGTGGCTATGT AATGGAACCAACCTACATGGCCAGCAACTGA ATAGATTAAGAAAATATATATACACAATGGTG CTTTTTTCGGCTATAAAGAAGAATGAAGTTAT GTTGTTTGTTAGAAGATGGATGAAAGTGGAG ATGATAATATCAAGTGCACAGTCAACCTCTCT CTCTCACCTCCCCCGCCCCGCTCTTTCTCTC TCATATACATTTGAGAGTAGCAGTAAACTGTC TGAGAACAAAGGGGATTAATGGGAGGGGAG AAGATTAAGGAGCGGAAGGGTAGTAGGTAG TAT	p000659	A	*Cr2*
IM000637	GATCGGCTTCTATGGACTGAGTGTGTAAGAA AACATT	p000661	D	--
IM000638	TTAGGAGGGTAGAGAACATTCAGGAATCAAG AACAAGCATTTTAACACCCACTGAGCTATCC TGTGGATGGTGGTGGTTTTGTTTGTTTGTTG GTTTTGTTTTAGGAAGTCAGGGATGGGGTGG GAATCTCACTCTGTGGCTTAGACTTGCAACA ATCCCAAATTCTGGAATGATAAGCAAGAGAG CTGTCTAGTCCCAGTCTCAGATACATGCTGT TAATTTTCTACTACTGCTATAACACATAGGCT CAAATGCGGTGGCTTACCTAACACACCCTGT GCAGTTCTGAAAGTCGTAACTCTGGCACGAT C	p000662	D	--
IM000639	ATGCTAAGCTGTGACTCCTCTCGATACGAGA CCCTGGCTGCCCTCCTTTCCCGATC	p000663	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000640	GATCGTCTGGAAGAGCAGTCAGTATTCTTAA CTGCTGAGCCATCTTTGCAGCCCCCAGTTCT TTGGGGTTTTTTGTTTGTTTGTTTGGTTGGTT GGTTGGTTTGGTTTAGTTTGGTTTGGTTCAA GACAGGGTTTCTCTGTGTTGCCCTGGATGTC CTGGAACTCTCTTTGTAGACCAGGGTGGCCT TTAACTCACAGAAATGCGCCTGCTAGGATTA AAGCTGTGTCCCACCACTATATATATATGTGT G	p000665	R	--
IM000641	GTCACAGTGTTAGAGCCACAGACGGGGGAA CCTACTGGCTGTCCTGGGTTCCTGTAAACTA GGGGACAAAGCTGCCACAGCCAGACTTAGC TGCGATC	p000666	D	--
IM000642	GATCGCTGCTTCTGTAAATCCGCAACGACAA TTGTTATCTTCTCCTTTTCTTTCTTTTATTTGT TTTATTCTATTTTATTTTTCAGATGAACTCTCA TGTAGCCCAGGCTGGTCTCAAACTCCCTCTG TAGCTGACGGCAACCTTGAAC	p000668	R	--
IM000643	TTCCTACACCATAGCATTTAGTTGTAGGCAG AAGCGATC	p000669	D	--
IM000644	GATCGGCTCAAGGGCTCTAATTTAGTCTAGG AAGTCCTTAGGAAACATGAAAATCTCCGAGA TAAGACCCGGGGTAAAAAGCTTGAGCCACG GAGTTAGACATGCCCAGGGTGGAGTCATGTT CAGAGGTTCAAGACCCGAATCAGCTACGTAA ATAAAGCATTTGAGGCCTACCTGGGCTACAA GAGAGTATCTTTAAATAAATAAGATGATTTAA AAAAAACTGTTTTCCCCTTAGATGGATTAAAA AAACAAGACAAAACAAAACAAAACAAAAACC CGTCTTTCCTTCTTAA	p000672	D	--
IM000645	CTGTCCGTGTGGGAAACGTTTAGCAAGTCCG AGCGTGTTCGATC	p000673	K	*Nmyc*
IM000646	ATGCGTTCGTATGACAGTTCTCCAAATGACT GTCCCAAAGTCCCAGATTCCTGGAAACAGTA AAGACTGCCTCAAACTGTAGTCACTAGTCTA TTATCTTAATCATAGTAACCATTTGGGTTTGA CTTGAAAACCTGTGACAGGGAGATAAATTTC TGCCACTGTAGGTGAAGCTTGGAAGGGCTA ACCCAATGAATATGCTCAGTCGATC	p000676	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000647	AGATGAAGCTATCCCCAGTCCCTAAGCTGAG TTCTGCCTGAGACTATTTGAAACAGGGTACC CCTGGGTCCCAGTTCAGTTGACAGGTAGTG GACGCATGAGAACGCCATACCTGGTGGCCG TGCCCGAGAGTGCTGTCCCTGACCTGCCAC TGTGTTCTCCAGAGCAGCTTTCCAATCTGCC TGCTCCTGTCTCCCCTGCCTGTTGGCACCAG GCAGCCAGAATTCCATTTGTTTGTTTGCTTCG CGATAGGCTCTTGCCATGTAGTCCTTCCTGG CCTAGAACTTGATATGTAGACTTCCCCCCTT GGATC	p000678	C	--
IM000648	CCGTGTCCGTGGGCATGTGCGTGTACAGAC AGACATACATGCCCCCGCATGAGTGTGAACA CCAGAGGTCAACCTCAGGTGTCCTTTTGATG TTATCTACCTTGTTTTTTGAAGCAAGGTCTAG GATTGACCAATGAGCCCCAAGTAGGGATC	p000679	D	--
IM000649	GATCCATAGGCAGAGAAGGCAGTAATAGGA CATTGGTCATTGTACCTCATTTGTGAGGGGT CACCTTGGAAATGTGCTGAGACTAGGTTCTA GGAGAAGCTCGCCA	p000682	D	--
IM000650	CTGGCACTGTGTGGCAGAAACAGTGAACAG TGTAGCGGTGCAGAATGTGTGTGCTGTGGG TTTTAGCACCAGGGCTGCATGAGACTGCAGA CATGCTTATGACGCAGGAAGGCTCAGGACA CAGCACACATGTGTGCTAACATACATGTTTC ACCTCAGACTCAGCTCCCATTTGACTTTTAAT TAATTTTTGGCCATTCCACAACAGAACCTTTT CTTGCTCCCTTTTTTCAATCTTATGTATATATC TCCTACATTTAGTTACAGGACTGTGACCTAC AGTTTAAAACTCGGGGATC	p000684	D	--
IM000651	GATCCCTCCCCTCCCTTCTTTTTCCCGCCAA GCGTCGGCGAAGCCCTGCCCTTCAGGAGGC AGGAGGGGAGCTGAGTGAGGCGAGTCGGA CCCAGCAGCTGAGAGCAGCGCAGCCCAGG GGTCCTCGGCCGCGCAGACCCCCGGAATAA	p000685	K	*Myc*
IM000652	CTACCACAGCCCCAGTGCTCTGGAGGGACT CTAGTAGCCAGGGCTGGCAGCTTGGTTTGG GCCAGCATCTCACTATGTAGCCTAGTTGTCC TGGAATTTGCTATGTAAATGTGGCTACCCTC AAACTCATAGAGAGCCTCCCACCTCTCCTGA GATTATAGGCACATGCTACCATGCCCTAAGT GGATC	p000686	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000653	GGAGCAGGCCCTTCTGAATCAACTTGGCAG AGTGAAGGAGGCACTCTCCACACAAACAGG AAAAGGGCAGTGGTGACTTTCTAGGCAGGG AACTGGTTACATTTTGTTTATTTGAAGGTGAA GAGTCGTGACATTCTGGGAAATAGGCAAGAT GGCCGTTTCCCCTCAGCTACAACCAGCCATG CAGACCTCCTTGCAGGGACCTGGCTATCTAC ACTGGAACCAGAAAGGCACGCCCTGCTTTA GCCTCAGGCAGAACGATAATAACAGCGTGCT AGCTCAGTAGTCTGTGTGCTGGAAGGGTTTA TGAGGAGGAAGTCCGCAATTACATATTTCTG GGCAAACATTAACCAAGATTGAAACCTAGAT TTGAAGAGAAGTAGCAGGCTGGGATC	p000687	D	--
IM000654	AGATGAACTTATAAATGCATCTGCAGTCCTC AAATAAAGATGAATAGTAACCCAGAGGCGTG GTAGTGCGCTCTTCAAACCCAGTGCTCAGAA GGTGCAAACAAAAGGACCGGGAGTCCAAGG CTAGCCTTGACTAGAAGGGGCCATGTCTCAA AGAACAACAACCAAGAGCTGCTTATGGAGGT CAGTCTGTGTTCCCAGGGGGACAGCATCAG TCTAAGTTGGCGGTTGTTGTTGGCTGAGCAT GCACAAATCCCTAACAGCACATAAAGCAAGT TGTGTCACACACTCACAGTGCCCAGATTCAC TGGATC	p000688	B	Mm.13133 6
IM000655	GTCCATTGTGTACTGAGAGAGGAGTTAGGTT TAGAAAGCCTTCCTCAGATGTCCCTCAAAGA AGCTGCTACAACTGCCCTCATCCCACGTTGC CAAGGATC	p000689	D	--
IM000656	AGCTGTAGGGAAGCCCAAAGCACAGACGAC TGCTGCTGCTGCTGCGGTTCCCACTCTGGGT TGACCTTAGAAACGGGGGTTCATCTCCTCCA GCAGCTCCGGGAAGGAAGGTGAAGGGGACT AACCATGATGAGCTTTGCACACTGGACTCAG GGCCTGAGAAGGGGCTGGAGGGAGGCAGG GAAGACATCCCTCACGGTAGTGTTACACAGC TGGCGTTGCGGGCTGCCAGGGTACTCATTT GAGTCCATGCTGAGTCTCTCGGTGCCTCCTG AGATC	p000694	K	*Gfi1*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000657	GATCGCCCCAGTTACCTCAAATTGTGTGAGT GTGTGTGTGTGTGTGTATGCATATATGCATA CAAGCATATACATGCATGCATATATATAATAC ACATAGACATATATACACACATATAGACGCAT ACATGCATTTGTATGCATGCATCTATGTATGT ACATATCCACAACCAAATATACCAAACACGC AGACACAGCACACATAGGACAATAGTAATTG TGAATCTAACTGGTGGGGTTTATGGGTCAAG AGCCAGGGTAGAGGAAACTGGCTAAGGCTC TAACCATCCTAGAGCAGGCACATCTACCAGG AAAAGAAACAAGGAAAAGAGCAGAGTTGAG GGTTACTTAACATG	p000695	D	--
IM000658	ACAGAATCTGTGGGTCATTATTACGTTTATAG GAACAGGATTTTCTTTCCTTTCTGACTCTACC TTCTAGAAAGGCCGACTTTTAAATCCTCATG CTCTTGTCTATTGACAGGAAAAGATGGGCTT CCACACTGATC	p000700	D	--
IM000659	GATCAGGCTGGCCTTGAACTCACAGAGACC CACCTGCCTCTGCCTCCTGCATGCTGGGATT AAAGGTGTGTGCCACCACTGCCCAGCTCAC AAAGTAGTAGTAGGACTAGTACTAGTACTAA TAATAACAAACATTACAACAATCTTAATTATTT TTGTTTCTACCTTTAAAATCTCCCAACTGTCT TTTTATATTGCCTCAAGTCTTCCCTCAGTCCC TGGCCTTCATAGCTTGACTTTTTTGCTAGAG GTTATCAGTGGCTCATCTCTCTCCTGAGATT GAGCTGGCTAAGACCACTATTCAGAGGGAG AATGTAATGTCTCAGACATCATAGCCAGTCC TCAGTTCTCCTTTTGCTGACTGACCACTTTGC CAAACTAGTTTTCCTAAGCCATACCTTTTCTT TTTAAAAAAATAGTCTTTCTTATAGTGGGTGCT GGCTTTGAACTTCTGTCCTCTTGCCTCACCTT GCACTGGTAGTAGAGGCTTGCAATTTCACCG	p000702	C	--
IM000660	GATCAAGAACGAAACCCCTGAAAACATAAAA CAGTAAGATAACAATAGCGTGCCTGATTTTG TCCAAACCTTCTTGTCACCTGTCACTGAGATT GTCAACTCCTTTTCACCACCCTACATACGTTA GTTAGCTCAGTTTACGAGAGTTTGCAAAGGC CCCCACCAGTACCCTGCAACTTTACCCACCC CTGCATGGGACTGTGAGAAAATGGGACTGG AGAGTAACCCTCTTCAGGCTCACAATCTGAG CTAGTCAGAGCATCTCACGGGTCCCGGGAC TTTCAGTGTGCTTTCCTCTTGGGTATTGGACT TTAAACAATGTGTACCGATATGGGTGAATAAT ACAACATCCATGGAGAAATAAGCCAAATCAA GACACTTCTTCAGAGG	p000703	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000661	GATCAAAAACATCAACGTAAGGAGCCCTTAA TGACGCTTTGTGACGGTTTAGAATGGTCTAC CCAAACCTAGCCAAGTCTAACTATGTTATGG AGGTGGTAAAAGCAGTTAACCTAAACATCTG GGACACTCACAGAATGATAGGTAGGTAGGTA GATAGATAGATAGATAGATAGATAGATAGAT AGACAGACAGACAGACAGATGTTGAATAAAA AGTGACGTTTACAGTGATGTTAGCTCAAGGC AGGGCTTTTCAGGCCATTTCCCCTGGTCTCA CCC	p000704	D	--
IM000662	CTACTAAGTCCAGAGCAGAGAAGGAGGCGC CGCCTGTGTGCACAGCGGAGTCTGGGAGAG ACCACCGGCCCAAACCAGTAAACACAGGGC ACCCACCGTGCTCCGATC	p000706	D	--
IM000663	ACAGTAATCTGATTATCTTGCAGTAGATAATT TGTCTACCTGTTAATGACTCTGCTTCTTGAAC TACGTCCCAGTAGATGCCATGCTTTCAGCCT GGTAAGTGACACTAATACTACCTCCAAACTG TCACTTGGATTGTCAGGGTTTTGGTGTGGTG ATGATACAGGAGAAATGTAAAACACGGAGTT GATGATAGAAAGGAGTCACTAATACATTTTCT TAGGAAAAGTCAAGTGACACACAGCAGAATC TAGCTGAAGGAGCTCCGCCAATAGGGCTGG AAGATAACTCTCGCACTAACCTGCTTTATTAG GAACTGTAGGAAAGGCAGGTCTGCAGCACA GTTGAAGTTTAGGTTGCTGAGAAAGTTTCTG CTCATATTTATTCACCAGTGATGATC	p000708	D	--
IM000664	GTTTAGCAAGTCCGAGCGTGTTCGATC	p000709	K	*Nmyc*
IM000665	AGGCAAACCCATGTGAGGCCTTCTCACATCT TTCCTTGGATGCCTGCACACACCTGACTTGA CAGACTTCAAATCAGACTTATCAACTCACCTC TTCAGTCCTGGGCCTCTTCCTGTATTTCAATC TTAGATAGAAAATTGGTTCCACTGTCTACCA GCCTTGAACCAGGAATGCAGAGCCAACCAC CCCTGGGGTGTCCCAGGCAGCTGGGCTGGA TGCTACCTGTCATGCTCTTGATC	p000710	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000666	ATGTATGAGTGTGGGGCTGGGTTTGAACCTG TGTCACCTTAGGACTCTCTGAACCTCGGTTT CCTATTAGACGGAGGGGCTATTCGGAGTCCT CATCTAATGGAGACACTTTGTGGGTATCAGA GGGCAACACTGTGGTATTGGGGGTGGGGGG TTGCTGCTTAGAGCTCAGAGAAGAGGAGTTT GGCTTGCTCTACAGAACATGCAGGCTGAGG TGTGGGTGCAGGGTTTCCCTGAGGCCCCGG CTCTGACCCTCTCCCCACTCCATTTCCTGCG CAGGTGAGCGACAAACGTTCCAACAGCTTCC GCCAGGCCATCCTTCAGGGAAACCGCAGGC TGAGCAGCAAGGCCCTGCTGGAGGAGAAGG GGCTGAGCCTCTCTCAGCGGCTCATCCGCC ACGTGGCCTACGAGACTCTGCCCCGGGAGA TTGACCGCAAGTGGTACTATGACAGCTACAC CTGCTGCCTCCGCCCGGTTCATGATC	p000711	C	--
IM000667	GATCATTTTTCTCTCGAGATGGATTAAAGCTA TGCTGCAGAAGGACCCGTGTGTGTCCTGTGT GTGTGTGTCCTCGCCGGCGAGACTCCTTATC ACACATGACAGCTTCAAAGCCCCCAGATTCA ATAGGTTCCAGGAGTTCACATTTAACACTCAT GGGGTCAAAGTGCAGGCAGATGGTGGAGCC TGTGGAAGGTCATCAGACAAACAACCTGGTG GTTGCAGCAGAAATCACCAGGCAAGTAG	p000712	R	--
IM000668	GATCTGGCTAGCAGGGAGCCATTTACAGCTC AGACATCTATCATCCTTA	p000713	D	--
IM000669	GATCATTGTACCTCACCTGTCAGTTTGACAG GTGGGAGGTGATATCTCTTTTCATTCATGTAT TCTTTGAAAGTTTGTTCATGCATATAATACAT TCTGGTTCAATTCACCACTCCACCCTTTTGTA TCCCCTGCGTACCGAGCCCCCATTTTCTCAC CAAGTCTTACTGTTATCTCAGTTTTGGGGCTT AGTTTTTTGTTTGTCTTGTTTTGTTGTTTTTGA AACAGGGTCCCGTTATGCAGCCCTGGCCCT GAACTTGCTAAATAAACCAGGTTGGCTTTGA ATTCAGAGTTCTGCACACCTCTGTTACCCAA GTGCTCAGATTAAAGGCGTATACTACCAC	p000714	C	--
IM000670	GATCAATTCAATCTATTGCAATAACCTGGTTT TTTTTTTCCGCAACTCCAAGATGGGGGGGGG GGGGCCCAGTCAGGAGAGGTTTCAACACAA ACGCACTAGTATTTACACACAGAATCTCCTC CACTGTTCTTCTTCTTTGCTTTAAAAGTCTTT GTTCCGGAATCTATAGATAGGGAGACAGATG GCTAGCTCCCCAAGGCTGAGAGCAGAGGAG AGTATAAACAGGGAAGTCAAGGGGTCTGGG AGGGCAAGGTAAGGAAGCCACAG	p000715	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000671	CAATGCCTTCCCCGCGAGATGGAGTGGCTG TTTATCCCTAAGTGGCTCTCCAAGTATACGT GGCAGTGAGTTGCCGAGCAATTTTAATAAAA TTCCAGACATCGTTTTTCCTGCATAGACCTCA TCTGCGGTTGATC	p000716	K	*Myc*
IM000672	TAGTATTCAGGAAAAAGGAAACTGGGAAATT AATGTATAAATTAAAATCAGCTTTTAATTAGC TTAACACACACATACGAAGGCAAAAATGTAA CGTTACTTTGATC	p000718	K	*Myc*
IM000673	GATCAGAAAAACAGCCCATTATTCAAGATTC AGGT	p000719	D	--
IM000674	TAACTTCAATTTAATAATTATCACATGCTAGG AACTAAAGAGGTGCACAAAACAAACCAACAG TGGTTCCTATCCTGTCTAACAGAAGAAACTA CAATTGTGGTTTGGGATGCCACATAAATGAC AGCAACGGGACCTACAGAAAATTAAGTCACA GAGAGAATGGACCATTTCTGCAGAGACCTG GAAAACAGACAAGGGAAGAAACATGGTGTGT CTAAGTGATGGGGCAGGTGGTGCAAACGCT AGAGGCAAGCAGAGGGGATATGAAACTGTG CTGCACAGCTGGACAGAAGGGAGGCTGGAA GGGAAGAGAGGACCCTCTGTTTTGACTCAAT GGCTAGATGCCATGTGCCAAATAAGAAAGCA CTTGGGGGGTTCTGTGGGAAATCGGAACAG AGGGACTGGAATCAAACCTCAACGTTCCTTG CATACTCCAGATAAGAACCAGGCTTTGAGCC AGGGCCTGGGAAGAGGGCTGGCCTACATAT CTCATTTTAGAGATGAGCAAACAGGACTGGG AGCTCTAGGTCTTCAGTGACACGCTTGCTTG GCCCGCAGGAGACCCTGGGTTTGATC	p000720	D	--
IM000675	GATCATGTCATGGGTCAACAGAAATAATTCT GAAAGGCTAAGTCATTTCTTCTACCCCCAAG AAAAATCAAGAACACCCCACATTACAAACCTT CCGTAGTAAACTGAGAATGGAGCCATGGCC AGAGCCCCTCTGCTCTCCCATCCCCCAACCA AGAACCAAAC	p000721	D	--
IM000676	ATATAACTTCTTTTTTTTTAAAAAAGAATTATT TATTTTATGTATATAAGTTCCTTATAGCTGTAT TCAGAGACGCCAGAAGAGAGCATCTGATC	p000722	R	--
IM000677	GATCATAGCACACTGGGGTGCCATCTGTCAC CCCTAGACAAACATCTTTAACCNGCATCTCTT CCTGAAGCCCACTTGGACCACCCTTTGGAAA ACCATCACCAAGGCCAGTAAGGTACCCGTG GTGACTCACCTCAGCCTAGCCCACCATAGAC GCTTAGCAGAGCAGGTGTGTGTAAGTCAGA GCCAGACAATCAGAACACTCTCCCTGCTCCA AAGTAGCAATGTAAAAAATTGAACCCAAAGTT G	p000724	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000678	GATCAAAGTAACGTTACATTTTTGCCTTCGTA TGTGTGTGCTAAGCTAATTAAAAGCTGATTTT AATTTATACATTAATTTCCCAGTTTCCTTTTTC CTGAATACTACGCTGTGCATTCTGTACAATC CCCAAACGTATACATACACACTTTATATATAC ACGATAATCTAGCTTATTAACCAACCAGAAAC ATGAGTCTTTTGCTCTGTGCATTGGTTCTAGA TTTATTATATAATGCATATTCCCTCGGGATTT GCTTATCC	p000727	K	*Myc*
IM000679	GATCATTTGATGCTTCAGATAAATATGTAAAT GGTGAC	p000728	B	Mm.12788 1
IM000680	GATCAAGATAATCCCCCACAGGCATGCCCAG AGGCCCATTTCCTAGGTGAGACTATAGTCTG TCAAGTTGACAATGCTAACCATTGCAGTGAG GGAGAGAAAGAAGGCCAGGATGGTGCCTCT CTGTTACTCTGCTTACCCACGGGGTGCAAGG ACAGTGGGGGATGGGCCTGAGCTTCCTCAT GAACACACACATGAGAGCAGTCAGCACATG GCCTCTTCCTCTAAGCTTCACAGTGGCAGCC GCACCTCTGCTGTTAAGACCTAACATGTGGC CGGGCAGTGGTGGCACACGCCTTTAATCCC AGCACTCGGGAGGCAGAGGCAGGTGGATTT CTGAGTTCGAGGCCAGCCTGGTCTCCAGAG TGAGTTCCAGGACAGCCAGGGCTACACAGA GAAACCCTGTCTTGAAAAACCAAAACCAAAA CCAACCAACCAACCAACCAAACAAACCATCT AACATGTACATCCTATCCATGTGCACGAATC ATAC	p000729	R	--
IM000681	AGACCAGTGCCGGAGCCGTTCCTGGCTGAG GCAGCCCAAGTCCTTGAAGAGCTTGAAGAG GTCGCTGCGGAACTTGACGCCGATGAAGGC ATACAAGAAAGGGTTGACGCAGCAGCGGAC GGAGGCCAGGCTGTAGGTGACGTCATAGGC AATGTTGAGCTGCTTGCTGGTTTCGCAGCTG CTATTGGTGATGTTGAAGTTGGCCACCGTCT GAGCCAGGACCACCCCATTGTAGGGCAGCT GGAAGACTATGAAGACTACCACCACGGCAAT GATC	p000730	A	*Cmkbr7*
IM000682	CCCTCTCAAGCCTTCCTTGTTACTTAGCCTCT ATAGGTCTGTGCATTATACCATCATTCTTTTA ATTTACAGCTAATATCCATTTATATATGATTAT GTACCATATTTGCCTTTTGGGGTCTGGATTG CCCTACTCAGGATGACCTTTTCTAGTTTGATC	p000731	D	--
IM000683	GATCATGATGTTTGTTGAAGCAACAGAAACT ATAAGACAGTGCCCAAGAGCCTCTCTGGAGA TAGCC	p000732	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000684	GATCGTGTTAGACACAAGTAAGAAATGAATG AGTCTTCCTGATTTTTTAAATTAACTTCTCCC CATATTGGCTGTCACTACTTTTTAAATCAGAA AGGAGAATCTGGACGGTTCCAGGCCTGCAG CGCCATGCTTGCAAAAGGTTTACAGAATCGC TCTGGACAACT	p000734	D	--
IM000685	CTACCACAGCATCTTTTGAGTGTATATAGTCA GTGTGCTACATGTTATCTATGAACATATGCAA ATGAGGTTTGAGAATTAAAGTTGCTGATAGA CTCATGGGTTAGGGGTTTGATTGCCTGCTAA TGATC	p000735	D	--
IM000686	GATCACGAAACGGTTGACTAAAGCAAGACTG AACCACAGGCAGATACCAAACCCAAAGCTCT ATGTCTAGTGTCTAGAATACATAGGTTTGGG TAGCCATGCCCCTGTGACCCTGCCACCTGCA GCACACATAAGACAATACTATAGACAACCAC TTCTGAGTCAGAATTGCAATGATGTCTTTGG CAAACTACTCTAGTCTCCTTTGGCCAGGAGC TGCTAAGTGGTTCAGGCTGAGGTACAATCAA CCTAGGTAGGTGGGACTGTGTGCCCCTGTG CTCCTGGGTGGCCTTCATGTCTGCTATGCTT GCCCTTT	p000736	D	--
IM000687	GATCATGTCAACTATACCTGGACACGGACCT TCATCCTTGCTGGTTTCACTACCTCTGGCAC CCTGCAACATCTTGCAGTTTTTGGAACCCTG TGCATCTATCTCCTCACACTGGCAGGGAACT TGTTCATCATTGTCTTGGTCCAGGCAGATTC AGGGCTGTCCACTCCCATGTACTTCTTTATC AGTGTCCTCTCCTTCCTGGAACTCTGGTATG TCAGCACCACAGTGCCCACCTTGCTGCATAC CTTGCTCCATGGGCCTTCACCCATCCCCTCG TCTGCATGCTTTGTCCAGCTGTATGTCTTCCA CTCCTTGGGCATGACCGAGTGCTACCTGCTA GGTGTCATGGCTCTGGACCGCTACCTTGCTA TCTGTCGTCCACTGCACTACCATGCACTCAT GAGCAGACAGGTACAGAAACAGTTAGTTGG GGTTACATGGTTGGCTGGTTTTTCAGCTGCC TGGTGCCTGCAGGTCTCACTGCCTCTTTACC TTATTGTTTGAAAGAAGTGGCCCATTACTT	p000737	C	--
IM000688	CTGTCAATTCATCCAGCTCTAGGCCGCTGTC TGGCTCGATGCTTATTGGTTTAACAGTGCCG ATGCATAGGATTCTACAGTCAGAGTGGCCTA AGCAACAGCTAAATATTGTTTTCTTGCTGTTC TGGGAACTAGATGTTCAAGGTCAAGGCGTCA GTAGCTCTGTTATGAGACCTCTCTGCTGTCG GGCTGTGTCTTCAAGTTTTTTCCCCCCTCTGT GCATGTGTGTTCCTATTTCCTCTGCATGAAA GACCAGTAGAGCCAAGTGGTGGCACACACC TTTGATC	p000738	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000689	GATCATGAGAGGCGAGAAACCCAGACATCT CTAACTCTTCTTGCCAACTCAGGAGCCACCT GTGGCCCCAGCTGGCCACCAGCCGTTCCTC CCTCAGAGGCCTCCATTTCCACAAAAGGCCT TCCTGGTTGTTCAGGACAGAGCCTGGTTTCC CTGATACCCCTTCTCTCAGTGGCCACTGAAG TTACAGGGATGCAGCCAGCCGTGGTTGCCA TGTCTGTATATGCTAATCTCCGAATTCCACTT CCTGTTTAGATTCTCAG	p000739	D	--
IM000690	GTTTGTCCGCATGAGTCCCAGGGACCACTCA GAGTGGCTGGCAGGCATTGTGGAGTGGAAT GTGGGAAGACACATTCCCAGCCTTGTTTGCA GCTTGGGACTGTCTGTGTTTTGGGATGATC	p000740	D	--
IM000691	GATCACCTGGGAAGGGGGAAAAGGACAAGT CTGAGCTCCCAGCCCACATTCTCCTAGGGTA GCAGCTCCCTCACTTAGTGT	p000741	D	--
IM000692	GATCAGTTCTTATTAAACAATACAGACTTAGG CAAAATGAGTCAGAAATAAGGATATCGCATA TCCCGAGACCATTTGAACTCTAAGAAGTATTT TCTATTATTAAAGTAGTTCACCAGGCAGTGG TGGCACACACCTTTAATCCCAGCACTCGGGA GGCAGAGGCAGGTGGATTTCTCAGTTTGAG GCCAGCCTGGTCTACAGAGTGAGTTCCAGG ACAGCCAGGGCTACACAGAGAAACCCTGTC TGGACAAACCAAAAAAAAAAAAAAAAAAAA G	p000744	R	--
IM000693	GATCATCACAGATGACATAGAACCAAACTGT AACTTTCTAGACTACATGTAGCAGACATTT	p000745	D	--
IM000694	GATCATACATGAATACAAGCAGGCTTCTGGT ATACTCTTAAGTTGAATTCTGTTTTCTGTAGT CGTAGTCTTGTCTTTTCCAGTTTTAAATTCTA GAACAGGTATACTGTAGAGCACCCGCCTCC CCTTGCTCTGGAGGTAGGGTAGAGTGGGAG TTAAGGTCAGTTCC	p000746	B	AA657028
IM000695	ATTTCTCTTGTAAAACTCACTTTCTGTTCACC CATTTTGTCTGTGTCCTTACTAAATTATTTCTA TATAGGAATCTTTGTATCTTCTGATATAAGCT AGCGCATGGGTACCACCAGCACCCAAGTCA TCTGCTGAGGTGCTTCTAACCTTGCTTGATT CAGTGTCTTCAACAGAAGGTGGAGTAAACAG GTCATTTTTTTACCCTAGAGAGTTCAGATC	p000748	D	--
IM000696	GATCTCCGGGTGCCAGACTTGCCCAGCAAG CACTCTTACCTGCTGAGCCATCCTGAGGGCC TGGATTTAAAAAAAAAAAATATTGACATATTG TTC	p000749	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000697	GATCTCCTAAAACTCCCTGTGTCAGGAAACT TTCTGTGCTTTTGTATTGCGTTCCTGTGTTCG TGGAAGGCCCCCACGCCTTCATCCTTGCTAA TTCTTTTTGGATAGCTTGTTGCTTTAACTAGA TTGGCCCTTTCTTGGCTAGTATTTTCTGCTGT ACCTATGAGTGGTGTGGGAGAACTGTGCAG ACTTCCAGGAAGCGCAGCCATGAAGCTACAT GTGCCTATGTGTAGACACATCATGGATTTTCT TACTAGTTTACTAGTGGGTGATAATCTGTCCT TTTGAGCTCTCCAGAACGTTCTAGAAGCTTA AGGAGAGAAATCACTTAAGAGAG	p000752	D	--
IM000698	ATCTGATAGTAAGTAAAAGGACAGCTAAAGA TGAAGGGAAAGCAGGAGAGTCCTGGAAGAA GAAACTAGTGTTTCTAAGAGTTCATCATTGAT AAAATGCAAAAGAAGTCAATTACATACATGTT TAGGAAACTGAATCCTCTTGTTTTGGGGGAT GTTTGTTTTGAGGCAAAGGCTCTCTTACAGA GCCCTGGCTGTTCTGGAGTTCTGTATATCAG GCTCTGGCCTCAAACTCAAGAGATC	p000753	D	--
IM000699	ACATCAAGAGGAAGTTGGAAATGTCATCTTT AGCTATCTTATATCCTGGTAGCTTTAAGATTT CCTTTGTGTGACTTTATAGTTCTCAAAATATT TTTAAGGGTCAGGGGAGGAAGCACTTTCAAG AAATGAGATGGGAGAGGGAATGTCTTTGTGT TGGCCTGGAGATC	p000755	D	--
IM000700	AGCTATACCTGAAATTTGGCCAAGAACAGAA GCTCAGGAAATAGTGTGATTTAAAAACCAAA ACCAATTTACAAAAGGAAGACTGTGGTGTAG ATC	p000756	D	--
IM000701	CCACAACTGAAAGCAACACACACAGTATTTT TCTGTGGGTTTTAGGATGTATCCACACTCCC GAACTTCCTTTCCCTGAAGCACCCCTCAGTT TACTCTGAAGCATGGTTTGAGTCCCAAGGCC AGTGTCAACTTTCTGCCAAGTCTCAATGGCA AAAGTCTGTTTTAATCTGCTCAGGCTAATGTA GATC	p000757	D	--
IM000702	CTTCCAGTCTTTTTAGCTATTTATTGATATGA ATTCCCTGCCTTATGTATCATCCAAGATTCTA CCTAAAATACTTCCAATAAGTATCAAGGACCA CTCAAATATTCACTATTGGACTTAGAAGCTCC ACTCTTAAAAATAGATTCTATAGAAAGAGCCT GAAATGGGGGCATGAAATGGGTCCATCTCC ACCATCACGCACACATGAACAAAGAAAAGGA GGAAATGGTGTTAAGAAAACTTACATCATACT ATTTAAAAATAAGGAGGAAGGAGGGAGGGA GAGAAAGAGAGAAAGCTCAATGCTTAGGCAA GAGTGCTTAAGAAAATTACAGTTAACAGATC	p000758	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000703	GATCTCCTAAAACTCCCTGTGTCAGGAAACT TTCTGTGCTTTTGTATTGCGTTCCTGTGTTCG TGGAAGGCCCCCACGCCTTCATCCTTGCTAA TTCTTTTTGGATAGCTTGTTGCTTTAACTAGA TTGGCCCTTTCTTGGCTAGTATTTTCTGCTGT ACCTATGAGTGGTGTGGGAGAACTGTGCAG ACTTCCAGGAAGCGCAGCCATGAAGCTACAT GTGCCTATGT	p000759	D	--
IM000704	GATCTGAGTGCTGGGAACCAAACCTGGGTC CTCTGCAACAGTTTGTGCTCTTAGCTGCCGA GCTTT	p000760	R	--
IM000705	GTACGGCGATGGGCACAGGCTTCGGGACAG TCCGCGCGACGCTCAGGCGGACAACGGGA GGCGGGCGGGGAAGGCAGGGGCTGCAGTG TCAAGTCCCTGACCCGGGAGGCTCGGAAAC TTCACTGCCTCTGCGCATCCGGCATGGCCC CTCCCACTCGGACTTCGTCAAAAAACCGCCA CCGTGGAGTGTCCCAGTATGTGCGGTGTGG GACAAACTATCGCACTGTTGCCCTGGCTCTT CTCCTAGACCCCCTTTGTGAGCCAAAAGAGA AACGCTGGGCAGATC	p000761	B	Mm.27393
IM000706	GATCTCGTTACGGATGGTTGTGAGCCACCAT GTGGTTGCTGGGATAA	p000762	R	--
IM000707	CTGGGTTGACCTTAGAAACGGGAGTTCATCT CCTCCAGCAGCTCCGGGAAGGAAGGTGAAG GGGACTAACCATGATGAGCTTTGCACACTGG ACTCAGGGCCTGAGAAGGGGCTGGAGGGA GGCAGGGAAGACATCCCTCACGGTAGTGTT ACACAGCTGGTGTTGCGGGCTGCCAGGGTA CTCATTTGAGTCCATGCTGAGTCTCTCGGTG CCTCCTGAGATC	p000763	K	*Gfi1*
IM000708	GATCTCAGGAGGCACCGAGAGACTCAGCAT GGACTCAAATGAGTACCCTGGCAGCCCGCA ACACCAGCTGCGTAACACTACCGTGAGGGA TGTCTTCCCTGCCTCCCTCCAGCCCCTTCTC AGGCCCTGAGTCCAGTGTGCAAAGCTCATCA TGGTTAGTCCCCTTCACCTTCCTTCCCGGAG CTGCTGGAGGAGATGAACTCCCGTTTCTAAG GTCAACCCAGAGTGGGAACCGCAGCAGCAG CAGCAGTCGTCTGTGCTTTGGGCTTCCCTA	p000764	K	*Gfi1*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000709	GGAAGAAGTGTGTGCAGGCCATGGTCAAGT CCTGCATGGCTCCCATCTGGGTCCAGCAGC ACCCAGCCTCCAGTGCTTGCTCCTGATGTCC CAGTGAACTCAGGTCCTGAGCAGCAAATCCC AGGGGCCAGTCCTAGGGAGAAAAAGAACAC ACTGCCATCTCAGTGCCTCAACAGAAGCAAA CCTAGGCGTCAGGTCATGTCCTTGTTACCCA CATCACACCTAGACTTCCCTGGGTATCATGC TCTGTGTGAGATC	p000765	B	Mm.153512
IM000710	GATCTAAGGATATATCATTCCTAGGAGAAAAT GAATATTTATGACCTTGGATTTGTCAATGTTT TTTTAAATATGGCATTAAGCCACAGAGATAAA AATAAGAAAATAGATACATCGAATTTCAGTAA AATGAGGAAGTTCTTGTGATTCAACAGAAAC	p000766	A	*Mtm1*
IM000711	GAGGTAAGTCTGTTCAGTGTAGCTATCCTTA GCAGCTAACAGTCCTCAAAACTTTTTAGAGA TC	p000767	D	--
IM000712	CTACAGATGCATTATTAATATTACTTTTTAAAA AAACCCAGTATACTGCTTGAAAACAGTGAAT GCAATGGGTTCTCATTCACCTTCCTGCTCTC AATCAATCTCCATCTCTAAAGCAAGAAGTGG GGGCCCTTCTGGCTGAGCGAGGGGTGAAGG GAGGGGAAGAGATC	p000768	D	--
IM000713	GATCTGGAGAAGATGTCAAGTTTTAAAATGA GGCAG	p000769	D	--
IM000714	GAGTGAAGCAAGAATTTGGAGCCCAGCTGC CGCAGCCTTTTTCCTTTCAGCAAAGCTCGGG AGTGATAGATATGCATGAACCAAAGCAAAGC CTTGAGAGTGCCACTTGGCCCTGCCTCCTGA GGGTCTCAGGGCATCAGCTGGAGACCACCC TGTGACCCACACATCACCGACTATGAAAACA GCTCATCAGAGTAATAAAGATC	p000770	D	--
IM000715	CAATGAACAGGACACATGCTTCACACGACAG TCCAAAAATGCAAAGTGTGGAAGAATTCCAC AGCCATAGCCTTCATTACTAGATC	p000771	D	--
IM000716	ATGCCTTCCTGGTAGAAGAGGGCCATGCTGT GGCGGGGAGGGGCCACTCAATTTTTCCTGC TCCCTTTCCCTGTCCCATATTCTCAGGAGCTT CTAGAAGCGTAGCCTGCATCTCATGCCCTGA CTTGGCACCAAATGCTTGCTTTGTATCAACA CCGCTTTCTCTTCTGCTCTTTCCAGCTCGCA GCCATTCAAATAATACCACCCGGTACCCGTG GAATCAGGAGCAGAGATTCCAAATTGAGTCC TAAAATCAAATCCAAATGGGCCCGTCAGCTA GATC	p000773	D	--

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IM000717	AGGCGAGCGGATTACTAAGGACTGAAAGAC TCCTAAGACTTGTCTCCTGCTCCCTGGCCAG CGGTGGAGCTCAAGCAGAATTGCAAGCTCA GCTCAGGTCTCAGTGATGCAAAGCACCCTC GTTACTCCAATGTGTGTTACTCCTACAGGTG GGCTGCCTTCCACTTTCAAACACCCGCACAA ACAGACCTCCCACCGTATGCCAGAGCATCTG TTCGATGCTTTCTGGAAACTATGCAAGCCCA AATTTAATATCCAATCAGATC	p000774	D	--
IM000718	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTTACAAGGTCTCATACAGAATCCAGGCTG GTCTCAAACTACTGGAGTCAAGCCATCTTCT CACCTGGCTTAGCTGGGGTCACAGACTTGTG CCATCATGCCCAATGGAATGCTGTTCCTTTT GGAAAGCCTGCTACTGTCATATACTGTCATA GGAGTTAGCGACTGCTGGCTTATTCCTTCGC TTTGCTTGGAGATC	p000776	R	--
IM000719	CCCCCTTCCTGTCACCTCCTGACCCCTTGCG CAAAGGAGGCTCGTGGCCCGCTGTCCCACT GGGGGATGGGGCTGGGGTTGAGAAGGCTA GTGAGCGCCTCTAACGCTCAGGAAGTGAAG TTTGTGGTTTTGGGGGCTGAGCTCCGAAGGA GATTAAAAAAAAAAAAAAAAAGTCAGAGAGA CAGATC	p000777	D	--
IM000720	CTTTGTATAAGCAGCAAACAAAAAGCCAGAG GCAGTCCACAGATC	p000778	D	--
IM000721	ATACAACAGGAGCAAAGCTGGAGGGGAACA GATATAGAGGACAGTTCAGGGCATCTGCAGA GGTGCTGTGGAATGGGGAGGGGACAGTGGA TAAGGGGACTTACCCTGAGCATCTCGGTAAT AAGCATGGGTCACACTGCGGAAGCGCTCCT GTCCTGCAGTGTCCCAGATC	p000780	A	*Rab37*
IM000722	GATCTATGTCATCTTCCAGGACTCAGAGTTA AGAGAGTTACCAAGTGAGAGCTCTCATCACC TTCTGAAGCAGTTGAGAATTGGAACCCAGAA AGATGCACATGCACGGGCACACACACACCC ACGGGCACACACCCACCCACCCATGCAGAG AGAGAGAGAGAGAGAGAGAGAGAGAACT CACACTGGTACTGCAGTAAACGGGAGCTTGT TT	p000781	D	--
IM000723	GATCTTCTTTCTCTGCTCAATTAGTTCACTTC TGCTTTCATCTCCTTTTCTTTTGATAAACCAT GAGTTTCATTAGGGCTATTACAATCACATGC AGTTTTTCCTTATAGTA	p000782	D	--
IM000724	GAATTAGGCCTAGAAACATTAGAATCCAGAC CACGGAGCTCCCCAGATC	p000783	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000725	GATCTTGTTCTAGAACGACCCTGAAGGCAGC AGAACAGAGCAGGACTGAAGGCCACCAAGG GGATTTCAACTCTTCAGAAAAAATAAGTGACT CACCTTCTCACAAAGAGCAAGAATCACAGAG GTCAGATTGTCTCCTCCTGCCCATCAGGGAC AGAGTCCCCCATCTTTGCCTTGCTCCATCTG GCAGGTAAGAGATGGGAAGTCTCCTTTCCCT CGGTCTGCAGCATCCCTGGCATCCCTGGGG AGTGTTGGCACAGAACCCCCCTCCCAA	p000784	C	--
IM000726	GATCTGTGTGGGCAAAGCCCATGTGCTGCA GTGTGTCTGGGTAGAAATGAGTTGTGTGGTG CTCAAATGTAAATGAAGTCCCTGTGTT	p000785	D	--
IM000727	GATCTCATTACAGATGGATGTGAGCCACCAT GTGGTTGCTGGGAATTGAACTCAGGACCTTT GGAAGAGCAGTCAGTGCCCTTAACTGCTGA GCCATCTCTCCAGCCCCCCACCTTTTTTTTTA AAAGATTTATTTTATAGTTTTTGCTTTTTTAAC AGTACTGGAACATCTCAGTAATTGCTAAGTT GTCCTTGCTCCAGGTGAGCAGTCATATTTTC TCCAATTCTGGTTTCCTTACTTGTGTCAGAGA CCAAAATAGCTTGTTTAATCAGTTAGAGCTCT TTAGTTACCCATATCTGTGTAGTAA	p000787	R	--
IM000728	TAAGAACATAAAAGCAAAATTTGGAGGCTCA AGATTCAGTTTAGTTGCTAGAGGGCTCACAT AGCATGCCCTCCCCACCCGGGATTCCATTCT CATTTATCGAGGCATAAGGCCAGGTGTGGTG GGATATGTGCTGGGATGCATAAGATC	p000788	D	--
IM000729	GAAAGGCACACTGGTGAAGGCTGAGGACCA CCAAAGCTGCATTTCTGCTAGGCTAGGTAGA ACAAGAATGGTGCTCCACTAAGAACTCAAAA AGCCACAGCCCACCCCTGAGGCCCTCCATC TGACACATGCCGGTCACCTGTCCTCCCACAG CCCAGCACAGAGAAGCCACCATCCCTCCCC TTCCCACCTCCTGCAGCTGACAGTGTGCATC TTTCCGCACATTCCTCTCTCCTCAATCAGGTC AGAATGTATTCCAAAGATC	p000789	D	--
IM000730	CACTGAAAATGGCTAGAATTCTGGTGATGGG TGAGCCGATC	p000793	D	--
IM000731	GATCGGAGTCCCTCGTTTCAGAGGCCCCACT TCTATGGCTCCTGCCTTCCTTGGCTACATCC ATTCCTGCTGAGCTCCTGGAAACCTGTGTAT CAAGTCTTTTCCAGTTAGTGCGTTCTGAGTG GCTCTAGAAACCGCTTCCCATTACAGCGAAA GACCCGTATAAACCATGTTCTCTTCCTCTGT GACAAGAGACAACAGACACCGCACAAAGGA CTGTCTGGCCTGGGGGGGGGTCCCTGGTTC ACAGCTTCAGTCCTGA	p000794	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000732	GATCGCTCAATATAACAGCAACATGCCAAGT GCCACTTGTAAAATTTGTTGTTGAGCAGTCTC ATTATCAACTGAAGCACAATGTCAGGCTAGC AAGAGGCAGGTTCAGTTGTTGATTAGCGATA GCACACACAAGCCAGCACATGCTTTTTCTGT GAGTTCTAT	p000795	D	--
IM000733	GATCGCTGAGTTTGTTTACAGAGCAGGGACG CCTCAGCTCGGATGCCAAAGCTACCAAGAG CTGCAAACGCAAACTTAGCAGAAGCACACGT ACTCCC	p000796	A	*Cited2*
IM000734	GATCGCACAGGTAAAATGGGGACTCACTTTA GCTAAAACAACAACAACAAACAGCCTGATGA GTCGAAAGTCTCTTTAGGTTGCCCTCTGTTC TCCAGCCCCACATCCTGAAGGCTGTGCATTC CTCCCACAGCAGTCTCAAAATAACCATAGTG CTCAAGTCCCCTGTATCAAATGGTGGTATCT GCATCCACCCTACAGGTGTTCTTTGATTCTTT CTTTTCTTTGTAAGTGTGTCTGGGTGTTTTGC CTGAGCGTATGTATGCGCCTAGTACCTGCAG AGGCCAGAATAAGGTGTCAG	p000797	D	--
IM000735	GATCGTGAGAGGCGAGAAACCCAGACATCT CTAACCCTTCTTGCCAACTCAGGAGCCACCT GTGGCCCCAGCTGGCCACCAGCCGTTCCTC CCTCAGAGGCCTCCATTTCCACAAAAGGCCT TCCTGGTTGTTCAGGACAGAGCCTGGTTTCC CTGATACCCCTTCTCTCAGTGGCCACTGAAG TTACAGGGATGCAGCCAGCCGTGGTTGCCA TGTCTGTATATGCTAATCTCCGAATTCCACTT CCTGTTTAGATTCTCGG	p000798	D	--
IM000736	ACTGTCCGTGTGGGAAACGTTTAGCAAGTCC GAGCGTGTTCGATC	p000799	K	*Nmyc*
IM000737	ATTTCTTTTTGAGTACTTCATATAAGAGCTTC GCATCTACACCACTCTTGCTCGCCACTCCTC TTTTCTTCTTTCATTAACTACTGTCCACTCTC CAAACTTCATAATCTCTCTAATTACTATTGTTA TTTACACACACACACACACACACACACACAC ACACACACACACGTATATGTAACCTACTGAA TCTTACTAAATAGCTTTACTATCTTCCAAGTA ACAGGCACTTGATAAATCTTCTGTCAATCTCC CAGAACAGAAGCCTTAAGAGTCATTTAAGTT CTTTTATCTCAGGCTGTTCTGTTCTATGCCTT TTGCTTTTAATCCATCACCGATC	p000801	D	--
IM000738	GAATGTCTAGATGGAGACTGGACAGAGTTG GATTCCTAGACACCTAACAGAAGCGAAAGCA GGGGATGGATAAGGTGGGTGCCTCGTCCTA CAGCAGGTTCTGAGTGTCCGCAGAGACTCC CATGGCTTGGCACCATGGTTGAAGCTTTCCA TCGATC	p000803	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000739	CTATTTTCGTTCTCTCCGATC	p000804	D	--
IM000740	GATCCTCATGTCAAGGCAGGGGCAGACCAG GGTCAAGGGAAAAACACCTGCTTTCCTGGGT TGTAAATGCCAGAAAGGGAAGGCACGGGGT GGGTAGGGTGGAGAACATGGCCCAGACCCC TGTCTCTTCTCT	p000806	D	--
IM000741	GCACCTGACTTCCTCATATAAGACACAAACA TCTTGAGTGCTGCGCAGGTGTACCAGGATAC AGGTGAATCCAATCTGGTGGAGATTTGCCCC TGCTGCCCTGATTAGCTGAAGCTGCGTGCCT GGTGAGGTGGCATGGCCTGCTGTGCGTGGA TGGGAACTGAGAGTATAAAAGAGCGAGAGG CCCGGGTTAGAGGAGGATTATTATTCGAGAG AGGATTGTTATTATTGGGAGATATGAACAAG GGAGATATAAACAGGGGAGATATAAACAAGG GAGATATATGGAGAAAGAAGAAACAGGACTG AATAAATGTGTGCAGAAGGATC	p000808	R	--
IM000742	GATCCTTCTCCTGTCTTCTCTTCTGGAAGGC TGGGCTACATGCCAACATGTCAGAGTTTTAC CTGGGTTCCTTCCAGAGGTTTGAACTCAGGT CCTTGTACTTACACAGCAGCTACTTTGCCTAT TGAGTCAATATTTTGTGTGTGTTTGTGTAGGT GTGTTCATGTCTGTATACTTG	p000809	D	--
IM000743	GATCGTGCATGCATGGGTGTGTTTTGGGGA GAGGTTCTGTCCTTGCTAAG	p000811	D	--
IM000744	AGCTCAGCTTGTCAGGCCTGATTGTGAACAC TTCACCAACCGAGCCATCTCGTCAGCACAGC CCTGTTTTTTATTCCCATTTTCTTTTCTGTATT TCTGTTGAATTTCTCACATACTCTCCTTTCTC TTCTGCCTTCTTCTGGTTTCTGCATCATTTCT ATATTGACATTTAAACAACCCCCAAAATTCAA GATACATCAACAAAAATTTATTCAACTAGTCT TTCTTACTTCCATATCAATAATGAAAGAAAAT TAAAACCTTTCAAATTCAACAAATCCCTACAC TACATATAATCACTTTCCTCTATGCTAAATCC AACTTGAAATTATATCCTCAATACCCTGCTGG TATTTTTACTGTCTACATCACTGCCTAGTCTT CGATC	p000812	D	--
IM000745	CTGGTATATGAACGAAGTTGGTCTCTAAAGG CCGTCTAGAACAACGGTTCTCAACCCGAGG GTCGCACCGGGGTCACCTAAGACTACTGGG AAAGCACAAATATTTACATTACGACTCATAAC AGTAGCAAAATTACAGTTATGAACTAGCAAC AAAAAATAGTTTTATGGTTGGGGATTACCACA ACATGAGGAACTGTATTCAAGGGTCGCAGCA TTAGGAAGGTTGAGAACCACCGATC	p000815	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000746	TTCTAACCTGCTAGGGTTTTCTCACGTGGGT TCTTCTTTGAGGGCTCTCTGGCTTCCCTACT GAGCTGTAGCTGCCAAAGTTGAAGGGCTGC GTCTCCCTTGCGTCTCCCCAGTCTTTACAGC TCCTGAAACACACTAAGGTATTTATTCAAATC CCTGTTTTGTGTGCGATC	p000819	D	--
IM000747	AGGGCCCTTCCACCTCTTCTAGAATTCGGTA AGCTAAAAGTACATGTATCCGATTAATCTGAA ATAATTTTGTAGACAGTTTGGTGACGGGTGG AGGGTGTGTGGTTGCGCGATC	p000820	C	--
IM000748	GATCGGCGAGACCACGATTCGGATGCAACA GCAAAAGGCTTTATTGGATACACGGGTACCC GGGCGACTCAGTCTATCGGAGGACTGGCGC GCCGAGTGTGGGGTTCGGACCAA	p000823	R	--
IM000749	TTGGCTGTGGAGATGAACGTGGGAACCGTG GAAATGACCCTAGAATGGGGCTCAAATGTGA AAGGCATGCCAGAGGTTGCTCTGTTGTTTTA AGTCCCTGCCGAACATTAGAATTTAGCCTCA GTTTTAAAAGCTGTTACTGCCTAGTTGGGTG CTTCTTTCTTAAAAAGCAACCAAAAAAAAAAA AGCCGTTTTCACTCTGAAATGTATTAGAAATT TGCATTAGCCCAATGGCTAATAAGCGATC	p000824	D	--
IM000750	GTTATAAGGATTGCATACAAATGGCATCAGG ACTGGATGTGGTGGCACATGTCTTGTATCAC AGCACTTGGTGAACAGAGGCAGGGGAATCT CTTTGAGTTACAGGCTAGCCAGCATGACACG GTGAGACTCTGTCTTAAACAAACAAACAAAC AAAAAAACAAACAAAGGTAGCATAAGAGCGA TC	p000825	D	--
IM000751	ACCTGAATCTTGAATAATGGGCTGTTTTTCCG ATC	p000827	D	--
IM000752	AACTAATACCTTTCCTTCCGCTGCGATGTTTC ATGAGACTCTGGGTTAGTGCATGGTCAGGG GCCCAGGCAAACAGTGGCAGTTCTGCCCAG GATC	p000831	D	--
IM000753	GTTTAAAGAGCCGGTTCGACCCGCTTTCCGT TTCGCTCCGGGTCAGCTAGTACTGTGAACCG CTCGGTCGGGTCCGGCGCTGCTGCGCACCT ACTCGCCGGGACCCTGAAGCCCCCCAACTA CATATAGGGGTCTTCCCGGAAAGTACGCAG GAAGTCGCGTTCGGCCCCCTCCCCCCAGCA CCACACCCAGTCCCTTCCACCCCCCGGGAT C	p000832	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000754	GATCCCAGTAGAGACAGAAACAGTGCCTTTG GTTAAGAATTCCAGGCAGGATGGTACAGGAT TGCAATCTCAGCATGGGAGACAGAGGCAGG ATTTCCAGGCCAGCCTGGGCTACAGTATAAA TGGGACCCTGTCTCAAGTAATTGAAAAAAAA ACAGAGAAAGAATTTGGAGACTGTGACTATA GCTTGGTGATGGAGTCCGTTTGCCTAGCAGA GTGAAGCAGCTGTGCTCCTGTGTTCACACCA CAAAATAA	p000833	D	--
IM000755	GATCCAGTGAATCTGGGCATTGTGAGTGTGT GACACAACTTGCTCTATGTGCTGTTAGGGAT TTGTGCATGCTCAGCCAACAACAACCGCCAA CTTAGACTGATGCTGTCCCCCTGAGAACACA GACTGACAA	p000834	B	Mm.131336
IM000756	GATCCTCCCTACCGGTCCTCGGGCAGACCT CCAGCCCTTCCCCAGACACTGTTGGAAAGCA GGCACGCCTTCCACAGTATGGTCTGAGGTTA ACCCATGACAGCACTCTGGGTGCCTGGTGG TGTTCCTGGTGGGGACGTCAGTAGCTGTAG CTCTGTCATTGGTCCTTGCAGCGTCTCATTC CAACTATTCTTCCCATCACTCCTCT	p000835	D	--
IM000757	ATATGTGTTTGTGCGTGTGTGTACATGTGCA TGCATGGCATGTATGTACCCATATAAATATGT GTATGTGTGTGAAGTGCTGATGTATTTCACA CAGCATTTTGGATTTAATGGAGAAGGTAGCT CAGATGTCAAGTGTGCCCTCCTGTCAGGAGA GGAAGCCTGATGTGCCTGCTGTCATAACTCT GGTTTTGATAAATACAGCACGAGTGATTTTTG GCTGTTGGGTTTGCCGTGTATGGATC	p000837	D	--
IM000758	GTTTGCTTGCAACATTGTCATAGCTTAGTGAA CAGTATAGCATTGTTCTGGCTCAAGAAGCCC TGGTTCTTCAAAGCTCCTACTTAGATGAAATT ATTTGCATCACAAACAAAAATTGTTTTGCATT TTTTAGATAATGAAGGATC	p000838	C	--
IM000759	GATCCTAGGCCAGTCAGGGCTACCAATAAGA ACCTGCCACACACACAAAAGGAAAGCAAATT TTTGCAAAAACTCTAGTCTCATGGTGTCACG GTCTTTAAACATCTTGAGGGGCTCGAACTGG TGAGGTGGCTCGGAGGTAAAAGGGCTTTGA TGCACAACCTGAGTTCAACCCCGTGTTTTAA AGACTTTCTGCAATGATTCTGGTCTGCAGTC CTAGCCCAAGCACAGTCAAGGAGAGATTGA GGCTGAAACGGAAGAATGGAAGTTTGCATAA CAGCTCAGTGGCAGAAATAACAGGAGAGAC CTGACCTTAAAAACAGGGTGTAAGGTGAGAA ATGATGACAAATGACATCCACTTCAACTGTG CTACGAACAGCTACCTGTTTGCACACCCCAA ACACACACACACACACA	p000839	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000760	GTAAGAGGGAATGTACTCTCTGCCATCGGGA CACCCAGTGGAACTGCTCACCTGGAGTCTTG CCTCCACGAAGACTAGGATC	p000840	D	--
IM000761	GGGACTTCAGGGCATAGAGCTTAGTTCCAGA CAAAACCAAAGTTAGCAGTCGCCTCTCTCTT AAAGACGTTCTCTCTAGCCGCAGATGACCTC AGAAGGGGCTCTGGGAGCCGACTCCCACCC TTCCTTCTCTGTTTACAGAATCTGGTTGGGCT GTGAGGAGCGACCCACGAGACGGGCTCCCT GTAGTGAGTTAGGCCAGTGGGAACCAACGA GGATC	p000842	D	--
IM000762	ACACACACTAACACACACTCACTCACACATA CTCACACACACTCACACACACTGTCACACAC ACACACACACACACACACACACACACACTTT TCCACCAGGATC	p000843	R	--
IM000763	GATCCCTGGATATGGCAGTCTCTACATGGTC CATCCTTTAGTCTCAGCTCCAAACTTTGTCTC TGTAACTCCTTCCATGGGTGTTTTGTTCCCAC TTCTAAGGAGGGGCATAGTGTCCACACTTCA GTCTTCATTTTTCTTGAGTTTCATGTGTTTAG CAAATTGTATCTTATATCTTGGGTATCCTAGG TTTTGGGCTAATATCCACTTATCAGTGAGTAC ATATTGTGTGAGTTCCTTTGTTCAAATTTCAT TTCTATCACCATTGTGTGTATATGTGTGTGTT GTGTGTGTATGTATATGACGTGTGTATGTTGT GTGTGTATATATAACGTGTGTATGTTGGGGG TCAAAGGCATGCTCATGCCACAGTGAATGAG TAGACATCAGAGGACAACTTTCAGGACTCAG TTCTCTTGTTCTACCCTGTGGTTCCAGGACA CTAACCCAGGTCATCAGGCATGGTGACAAAG GTTTTGACTCAAGGAGCCATTTTACATGCCT CATAAGAAGGGCC	p000844	R	--
IM000764	GCACTAGGAAGGAAATTGACCCGTGTTGTTG GTTTGTGTTCTGGTTTTGTTGGTGGTGCTTTT TGTTTTTTTTGTTTGTTTGTTTTTTTGTATCAG GATC	p000845	R	--
IM000765	GATCCTGCTTTCTCTTTTGACACAGAACACTT CTCCTGATTGACTCTGGTCCAGACATTTCTTT CAAAGGCAGAGGACTCTGGCTTAGCTGTGG ATGACTTCTCAGATGAAGTTCATTGGTTGCG ATTGGAAACGTAATCAGAGCAGG	p000847	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000766	GATCGCATTAGGGTTTTTTTTATGGTTTCTCA TCTTCTCTTCAAATTAGCATAGAAGCCTCTTC CTAAAGAATGGATACTTAATTCTTAACTTGAA AATATCTTTTCTCTGTGTGTTTTCCTCTCCATT GACTGTTCGCTCTATCTATCTATCTATCTATC CATCTATCTACTGAAATTAAAAATAAGGGAAC GCCTTCTTCTCTTCATTCTTGTTTGTTGTTTG TTTGTTTGTTTGTTTTTGAGACAGGGTTTCTC TGTGTAGCCCTGGCTGTCCTGGAACTCACTT TGTAGACCAGGCTGGTCTTGAACTCAGAAAT CTGCCTGCCTCTGCCTCCCAAGTGCTGGGAT TAAAGGCGTGCACCACCACCACCTGGCTCT CTTCATTCTTTTTAAAACGATTTTTGAAACCTT TTTAGTGAGGTCAACATTGTGTACTCCAGTC CCACTCATCTTCCTGTCCCTTCCCTCTTAGG CCTGCCTGTCTGGTACCTCACTCATGTTTGT GTATTCTCTGTGCTGAGCCTCTTCTGTGCTTT CCCAGCACATGGCTGCTGGCTCCAGTTTCAT TCCAGTCCCTTGTGATGTGAGCCTAGTTCAG	p000852	R	--
IM000767	CTCTCATGGCATGGGTCTCAAGGTCCTGCCA TTTCTGCTCCATCTTTACCCCAGCACATCCTG TAGACAGGACAAATTGTAGGCCGGAGGTTTT GTGGCTGGGTTAGAGACCCAGTTTCTCCACT GGAAGCCCTGCCCGGTTACAGGAGGTGACC AGTTTCTGGCTCCATGTCCCCCATTGCTAGG AGTCTTAGCTGGGGTCATTCTCACAGATTCC TGGGAGATTACTCTATTTTATCTCCTTGTTCA AAGTGTTCCATCAGATATTAATTATTCTCAAG ATTCAATATTCTCAAATATTATTCTCAAGCTAT GGACCCTTCAAATTACAGATAGATTTTATGAA TGAAAAGTTGTGTGGTTTGAATATGTAGTTGA GGGTGACTTTGAACTTCTGGTTTTCCTGTGT CTACCTTCCAAGTGCTGGGGTTACAGGTATG AGCCATCACGCCAGTTTCTGTAGCACTGAGG CTCAAACACAGGGCTTCTGTCTGCTAGGCAA GCACTCCACCTACCAAGCCAAATCCCCGGG CTTTACTGCATCTTTGTGTGTATATGTATGGT ATGTGCGTGTGTATGTAAGGATATATGTACC TGTGT	p000854	R	--
IM000768	GATCAACACCTGAAAAGTCGCGCCGCCTATA CACATCCCTAATTGAGAAGTATGTGGAAGAT TCCATCCGTGAAATTCAATTATCATGCAAGC CAAGTGGAAGCGCTTCCCTGGGGAAGGAAC CCAGCAGCCGCATCAAAACGACCCCACCTG TCTATTTTCATGTCAAAAGAGTGAGAAGTCTG GGTGATGAAATAGAGAGCATACATCAGCTTA ATGAAAATTTCCAGGGGTCCCTGCCTGTAAT GGGAGTCCCAT	p000858	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000769	GATCACCACCAGGGTGTTGAGAAAAAAAAAA AGCAAGTTAGTAGATGTTAG	p000860	D	--
IM000770	GATCTGACAAAACCTACCTGTTTTTGAACACA TGTGGGACAGCAGTCTGAGAGAATCTATGAA TAAAATTCCTTTCTGAGTCTGGCACATTGGTA CAC	p000861	D	--
IM000771	GATCATTATACCCCAAATGGTACTGTATCTAT ATATACCTCAAACATGTCATGTTAAAGAAAAT ACTCTGTTGAACTAATTCACTTGTTT	p000863	D	--
IM000772	GATCACAGGACTGAATCACATTTATGCCAT	p000864	D	--
IM000773	GATCATTTATTTACTTGTTTTGGTGTTTCATGT TTGTGGCTCCTTATGTAGTCTAGATATTAACT TGAAGTCTGAAGTGGAACTACCAAAGATTTT CTTCCATCCTCATCT	p000865	D	--
IM000774	GATCAACCGCAGATGAGGTCTATGCAGGAAA AACGATGTCTGGAATTTTATTAAAATTGCTCA GC	p000866	K	*Myc*
IM000775	GATCATCATGTCAAACCTGACACGTGACGAG ACAAATCTGTGTGCACAGAGGTGTGACATCC TAAAAGTACTAACAATACCGCTGGGCAGGGA CACACGCGGCAATTCCAGTCCTGGTATCCAT GGCTCAAGCTCTGCACGGAGAGCCCGGCAC ACGGCAGGAGGGAGAGCCACAGGCTAAGGA GAGCAATGCTAACTAACATGGCACCCGTGTT AG	p000867	D	--
IM000776	GATCTGGCTTCCAAGGGCCTGTACTCATGTC TACAATGCTCCTACACAGATATAT	p000868	D	--
IM000777	GATCAGCCTTCCTCCAAAGCTACCTGCATAG AAGAGACCTCTGCTCTCACCTACTCTCCTCT ACAGTTCAGCCCATATGGCTTCACCTGCATC CCCTACACACACACACACAGACACACACACA CACACACACAAACACGCACACAGCACACACA ACACACACAACACGCACACTCACAACACAAA CACACACAACACACACTCACAACACACTCAC ACACACACACAACACACACACACAACACACA CTCACAAACACACTAGTACACAAAGACTCCA ACACACACATTCCCATGCACTACTCCCTCAG TATCCGCCGCATTTGTGTTCACACTCATCCA CACTCTCACACATGTAGCACACACACATCAT TCCTACACAGGCATGGACACACACATGCTCC TATACAGGCATGCCCAGTACTCTCACATGCA TGTTTGCACGTTCCCAAACAGGTTCCCACAA GGGTTTGGCAAAGTACATGCATCCTCACACG CTAATGCAAGCCGTCACACCCCATACCACAA GCATGCAC	p000870	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000778	GATCAGATGTGGAAATTAGAGAGAAGTTTTT AACGGCTCATGCACATTTCTGAAAACTCTTT GCGAGGTATACTGGTAGATAAATGAACATTG GTCAGACTCCTCTAGTTTAAACCACTCTCTTC CCCGCTATGGGGGGAGGCGAGAGGCATTTC TAAAGCTTATATGTAGTTGCAAAGTGTGTGT GGTGTGTGTGCATGTATGTGCATGTGGTGTG TGTGTGTGTGCATGTGGTGTGTGTGCATGTA TGTGCATGTGGTATGTGTGTGAGTGGTGTGT GTGCATGTGTGTGCATGTATGTGCACCGTGT TGTGTGTGTATGTGTGCATGTGGTGTGTGTG CATGTATGTGCATGTGGTGT	p000871	R	--
IM000779	CTAACATCTACTAACTTGCTTTTTTTTTTTTCT CAACACCCTGGTGGTGATC	p000872	D	--
IM000780	GATCATAAGGACTGTTAGCAGGCAAAGGCG CGTGCCCAATTAAAAGATGGCTTTCGTTCCA AGAGGAATACTCTGGCAAAGTCCCAAGCGCT TCGGAAGCCCCTCCCTTCGCTCTCCCACCCC AGCTTTGATGCTCTGATTATCCTAA	p000874	D	--
IM000781	GATCAGGCTGGCCTTAAACTCAGGGAGATTC ATATGGCCCTGCCTTCAGGGTGCTGG	p000875	B	Mm.83635
IM000782	CTTTCTTTCTTTCTTTCTTTCTTTTTTTTCTGA GACAGGGTTTCTCTGTATAGCCCTGGCTGTC CTGGAATTCACTGTAGGCCAGGATGGCTCA GTCTGCTTTCTTATAGAACTCAGGACCACCA GCCCAGAGATAACACCACTCACAGTGGGCT GGTCCTCCCCACATTGATC	p000876	R	--
IM000783	GATCACACACTTCACTGTGGCTTGTCAACTG TGATTTGCTGATACAAGGGCTGTTTACAAGT CAGCTATAGCTCCGCATTGCAGCTGCAAC	p000877	D	--
IM000784	GATCACTAATTGAGAAAATGCCCCACAGCTG GATTTCGTGGAGGTACTTCCCCAACTGAAGC TCCTTTCTCTGTGATAATTCCATCCTGTGTCA AGTTGACAGAAAACCAGCCAGTACACAAGTC GACACAAAACTAGCCAGTACACAAGTCAACA CACAACGCGCACAAGCTGAAGGCAAAGAGA ACCAAGCATCTACCAGGCCTCAGTTGCTATG TCCACTTCTGCAGCCACTCCAAAACACCTGT CAGAAATTCGGTTTGATAGAGAACTCACCGA GGGATTTCCCTAACACCAGGTCAACCAGGG CACCTCAAACCTGGAGGCACGACTGGCACA ATACAACCTAA	p000878	A	*Cct5*
IM000785	GATCACTTGATAAAGATGCTCTGAGCAGAGG CTCACAGGAACCCAGCCCTGTGTGCTCCCC AGGAGCGAGATTCAGCAGTCAACAGTGCAG TGTTCACGTGACCGTGCGCAGGCCATGAGC ACTAC	p000879	B	AI615991

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000786	CTCCTTTTCAGCAAGCTCCTCACATCACAGG CCTTCTCTTGGGATGGCAGCCGCCTTCTATC TGGAAAGTATGTGACAGCTCACACAATCCTG TAAGTCTTCCATGTAATCACATTCCACTGCCT CTCTCTGAACGTGCTCCATGCCAGGGCCATG TGGAGGGAGCAGCAAGACTTGAGCTCAGCT AGTCTATGAAGATGGTGGCAGAACAGGCTCT GCTGCCTTGATC	p000881	B	MMU7675 4
IM000787	GATCAAGAGTTCAAAGTCATCTTCAGCTACA AATGAAGTTGGAGACCAATCCAGACCCTCTC TCAGAAAAAAAGGAAAAAGGAGAAAGCAAAA GGAAAGGAGGGGGAGACCGAGAAAGAGAA GAGGGAAGGAAAGGGAAGTCAACAGAACTC AAGGTCAGCCTGGGAGGGTGAATGAGGCAT TGTTGTCT	p000882	B	Mm.13880 9
IM000788	GATCACCTCCACTTTATGGTGGACAGAGGAT GGCAGTAGTAACTGCCCCAAGGAAACAGAA ACAACAACAACAACAACAACAACACCTCCAA AAAGACCAAAGCAGTAAGCTGTAGAACAAAT GCAAAGAGCCAAAC	p000883	R	--
IM000789	GTTCCACCTATAAGGTTGCAGACCCCTTTAG CTCCTTGGGTACTTTCTCTAGCTCCTCCATTG GGGGCCCTGTGATC	p000884	R	--
IM000790	GATCACATGGACCGATTGCCGCGGGACATC GCACAGGAGCGTATGCACCACGATATCGTG CGGCTTTTGGATGAGTACAACCTGGTGCGCA GCCCACAGCTGCATGGCACTGCCCTGGGTG GCACACCCACTCTGTCTCCCACACTCTGCTC GCCCAATGGCTACCTGGGCAATCTCAAGTCT GCCACACAGGGCAAGAAGGCCCGCAAGCCC AGCACCAAAGGGCTGGCTTGTGGTAGCAAG GAAGCTAAGGACCTCAAGGCACGGAGGAAG AAGTCTCAGGATGGCAAGGGCTGCCTGTTG GACAGCTCGAGCATGCTGTCGCCTGTGGAC TCCCTCGAGTCACCCCATGGCTACTTGTCAG ATGTGGNCTCGCCACCCCTTCTTCCCTCTTC ATTCCAG	p000885	K	*Notch1*
IM000791	GATCATACGCAATGATTTCTTACCTTATGATA TAATTATGTTTAGAGGGAAAACTTTTTTTTAA ATTGAAGTTCATTTATTGTATGAAATTATTTCA TAA	p000886	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000792	GATCAGCATGGTCTACAGAGTAAGTTACAGG ACAGCCAGGGCTCCGTGGAGAGACCCTTTG TCAGAAAACAAACAAACAAAAAATTAGAAAGA GACCCTCTCTCTGATTTGACCAATCACCCGT GTCAAATCTTGCCACAACCGAATCACCACCA AATTGCCAGACAAGCGGCTATGCTGGGTTTC TGAGGTTGGACTCCTCAGGTAGCCCGTGTCT AGGCAGAATGATGCCAGCAGCTACACTTTTG AGAACAAGGTCAGGTCAGGACTTGCCGCCA AACCTAGGAATGCAGC	p000887	R	--
IM000793	GATCAGTCATGTCCTTTAGACGTTTACTTTCA TCCCAACTTGGAACATTTCAAGC	p000888	D	--
IM000794	TTACAAAGGCAGAAATATCAGAAAGAGCCTG AAGTAGCAGCTGTTAACCTGTACCAGGAACT GGCCGAAGTACACACGCGTTAACTCAGCCC TAATTATTCTCGGGAGATACAGTTGATTATCA TACACATGTCAAAATGGAAAATAAATGGGTA ACTAAAAATTGAGGAAAATAAGATTAACACTT AAACAACCTAGTTCATTATGCCACGGTGATC	p000890	D	--
IM000795	GATCACAGTGGGACAGATTAAATGTTA	p000891	D	--
IM000796	AAACAAATACAAAGTGATAATTGTGTGACATC TGAACTTGTCAATGAGATAGGTAATTATCTCT GGGCAATGGGTAAATGTGCTGGCCAGCAAA CCTCACAGCCAGAGTTCAATCTCCAGGAACT TAGGTGGGGAAGGAGATAACTGACTTCCAAA TGCTCACCCCCAAATATACAATTAAAATAAAA ATCTTCCTTTTATGAGTAGCAACTGATC	p000892	D	--
IM000797	TACCCCTGGTCCTCCAACACTCCGATC	p000893	D	--
IM000798	GATCATGACATAGACTTGAGTCACTTCTCTG CAGTTTGTCAATAAAAGCCCCTAAGGGACAG TGTGGACTTTAGAGATAAC	p000894	D	--
IM000799	AATGCCAGCCATAGTGGCACACACTTTTAAT CCCAACACTCAGGAGAAGTTAAGTTTCTCTT AGCTCAAGGCCAAGTAGCTTGGTCTACTCCG TGAATTCCAGCCCAACTACATAGTAAAACTA GCCTTAAAAAAAAAGGCACAGGCAGAGGGA GATAACAAAAATGCCCAACTCCTAGCTACAG TAACTGTAGGAATTAAGATAGAATCTGTAGTT TGTTTATCATTATCGTGATGATC	p000895	A	*li*
IM000800	GATCATGGCTTGATTGTAACATTATCAAAGCT TCCTTGGCACACTGCAGGGCTGTCTTCGGG AAACTGCGTATTGTGCTCTTCAGGTACAAAG CATAGAGCCCTTACATGACAAACGCTGGGGT TAACTTCTTCTAGTTCCCTCTGCCCCACTTGT GGCGCTTCCCACTCATGACTTCTTCAGTGTG TATTCACTT	p000896	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000801	GATCATGCTGAACTCTTGAAAGTATTCTAGC AAAATGTGGCTTAAAAGAAAGAACAAACATTA ACTAGGTATGCTTTGAAAAATTACCTGTGGTA AAATTTCCACAAGCATGAGAAGTTGTTTCTTT TGTTGAACCTTCAGAC	p000897	D	--
IM000802	GATCATATATCAATTTTATTTTTAACTTTGTTT GTTTGTTTGTTTGTTTGTTTGTTCGAGACAGG GTTTCTCTGTGTAGCCCTGG	p000898	R	--
IM000803	ATTGTGTATCCAGAGTGTGACAAGGTATATA TGGTTGTGTGATC	p000899	D	--
IM000804	GATCTTCTGTCTGGAAGAGTGCTTGCTGGTT CCGACTACTTTTTTTTTTTTTTTTTTTTTTTTNG CTTGGGTTTCANATTGGCTTCAGGTTCTGGG CCCTTTCGTGGGTTGTGCTGCANAGCCCCAN ACAATGTCTTGGG	p000900	R	--
IM000805	CAGGAAACCAGGGGAAATGGGACACAGTGA CATCTGAGTCCTTAGAAGAGGTCCCACAAAG GTCTATATGACCTAGCAACGTCACTTCTGAG TTATTTCTCAGACACAGTGGATGTTTGTCACA GCACACTGTAGGACATCCCAGAACAGCACC ATGGGAGACCATGGTTGGTGCAACAGAGAA CATGCACACTGAGACAGTACAAGAGTTCCCA AGCAAGCAGACACAAACAATGGACTCAATAC ACATACAGTGGCAGATC	p000902	C	--
IM000806	GATCTGCTCACCAAAAATCTTGTCCTAGGGA AGTTGAGTTTGAACTGCGTGCTTACTGGCAA ACACGCGGTGCCCAAATTTAAA	p000903	D	--
IM000807	ACAGTTCCCCCTGGAAATGGTCCCTGTACCA GAGGAGCAGATC	p000904	D	--
IM000808	CTGGGGCCCAGACTCCAATCCCGAAATATCA TTAGCTGCTGCGCACTTCTCCGAGGAAGTTT ACACCAGTACCCTAAGTTCAAGTCTCAGAAG CCTCCAAATCCTCGTTGCACCCCTATATTTCA CTTGGTCATCCGACTGTAACTCACTCACCGA CAAGACAAAGAATATCTTAGGCTCCGTCGTA AAAGAACGAGCCCGGTTCACCGCAGCTCCT TTTATAGTCTCCTTTGTGCGAGATC	p000905	B	Mm.21798
IM000809	GATCTGAAGATATTTTGACAACAGCTAAAAAA AAAAAAACCAAAAAAAAACCCCTTATTACTAAC CAAGGGAAAATGCAAAAATAATTAAAAGTTC CTCAATTTTAAGTAAATATCCAAAAAGATTGG TTGTATAACAAAGTTGAAGAGTCAAACAGTAT TTGAATAA	p000906	D	--
IM000810	AGCTCATTGCCGTTAATTTTCCTCAGCCTAAT GAGAATCTAAGCCTTGATTTGTATGTACCATA GCATCTAGATC	p000907	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000811	CCTTGAACCTAGTTCAGGGAATAGGCCACCT GGGTGGGACTAGTGCTGGTTGGGGATGAAA AGACAGTTGGCTCAGGTGAACCCTGCTCGC ACCCTGGTCATCCTCTGAGACTGCTTTGATT GCTGACCCCAGTGCTCCAGCAAGAACTTGC GTTCTTGTTCTCTCCACTCAAGCCGGAAGAA ATCTGAGGAGAGGGTGTGAATCCTGAGCCA GGATGTCCAAAACAACGGAGTTGAGCCAGA AGGACGTCTAGTTGGGCAGAGTTAGCTCAGT CCCCTGACCCCCAGTCCGTGCAAGCTCGAG GGTGTTATATAGTGATACAGATC	p000909	D	--
IM000812	GATCTCTTCTTATCTCTACCTTTTGGGGCACA ATCTTATCTGGGGACACCACAGAGCCCAAGA ATTGTCCTGTATCAGAAATTTGGACCTTTTCT GTGGCTATCTGTAAACCCCACTGACTTAAAG TTTTAAGTAGAAAAGGATATGCCTTTTGTAGC ATGGTAAGGTCTTTATGGCACAGGAGGATGT CATCCATGT	p000912	R	--
IM000813	CTTCCTTTCCTTTTTTGAAACAGGGTTTCTCT GTGTAGCCCTGGCTGTCCTGGACCTCAATCT GTAGACCAGGCTGGCCTCGAACTCAGAGAT C	p000913	R	--
IM000814	GATCTGCTCCACTTTACACAGCTGACCATGA GACCATGTNCACATAG	p000914	D	--
IM000815	ACATGACATATCACCCTCATTCAGAGTTCAG AGTCTTCAGAAAACTGGGCGCCTGAAAAACC TGACCTTTTAAATTTTCGTCCATAGTTTCTTCT GTTGAATGAATATTCATTTAAAAGCTTCATAA ATGCCAAGATC	p000915	D	--
IM000816	GATCTTCACAGCGCACCCAGGGATC	p000916	D	--
IM000817	CTTTTTCTTGGTATTTAGGGAGTCAGGAAAA GAAAAACCATTGGGTTTTTACATTAGCTTTCA GGTAGGGTTGTGGCTTTTGAGCAACAATAAC GTATGACCTTGTGGTCGGTTCTAGATC	p000917	D	--
IM000818	GATCTTCTTATATCTGGTTTCCTGGGCGCTTC CTGGTAT	p000919	D	--
IM000819	GATCTCTGACAGGGTTTCAAAGAACTGTTAC TGATGTTTAGATTGCCTCTGAAGACATCACAT ATACTGTGCTACTCTGCCTTGTCAGAGTCCC GGGCCCTGGGCACCCCAGACGGCAGCAGA GGAAGAGCGGGGTATCACTTTCTATACTTCG GTAAAGTCATTGGGATATGTGCCCT	p000920	C	--
IM000820	GATCTCCTCTATCATTTATCTTTCTTCCTTCCT TCCATCTGTTTGTTT	p000921	D	--

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IM000821	GATCTGCTCACCAAAAATCTTGTCCTAGGGA AGTTGAGTTTGAACTGCGTGCTTACTGGCAA ACACGCGGTGCCCAAATTTAAGGAGTGCCAA CGACTTCGCGGGCCAGCAAGGTGAAACCGG AGCGCGCACGAGTGAGCAGTGGCCAGGAG GCCTGGCCAAGAGGCCAGGGTCCCTGAGCA TGACCGAGAGCTGGCGTGCTCTCTGTAACC CCCAATCAGTTCACCTAATCTCGGGTCGAAA CCTGAGCCCTGCAGGAGGCGGGGCTGAGA CTGCATCCCAGCTCCTGGCCCGCTCCAGGG GCGACCC	p000922	D	--
IM000822	CCAGGCATCTCCATTCTTAATCCAGATC	p000923	D	--
IM000823	CATAGACTCTTTCATTTAGAATAAAGTGTTCC ACCTAACATCCTGTAGGAAGTGATGAAACTA AAAAGAAAAATAAACGCATTTTCTCTTTCTCT CGTTACTTTTTCCATTCACTAAACAAAATTGA CTTTTTTTTTTCCATGAGAGTTCACACTGGGT CTGCCTCAGTAAGAGTCACACTGTTCAGCCC ACACACGCTGTGATATGTTATTTACTCATTCT CTTCTCAGGAACCACTCTCACATGTGAACCC TGAATACCAGCTCCCTCCCTCTTCAGATC	p000925	D	--
IM000824	ATAGGTTCTGTCTCAAAACAAACAAAAAACCA AAACATGTCCACAGGGTCCAACAGACACAGT CTCCGCCACTCACAACTAATGGGTACACAAA TACACACCTCAGCCTTACATGGTTACAGAGA GAAGCAGGACCACAAGGTAGGCAGGCACCT AACACTTGCTTCTTGGAAGTTGGAGCACACA CACACACACAGAAACACACACACACTTTCTC ACACTCACACACACATTCTCTCTCTCTCACAC ACACACACATGCACACATGGTCTTGTACAAG CTCCTCCTGGGATGGGCACACACAGGGGTA AGAGGACTCCAGATC	p000926	D	--
IM000825	GATCGAACACNCTNGGACTTGNTAAACGNTT CCCACACNGACAGA	p000928	D	--
IM000826	GATCGTCTGGCCCGACCGCGCCTCAGTAGA TTTGGGTCCTGGTCTGAGCAGCCGGGCTGG TGCGGGTGTCCTCACTAGGATAATGAATACA GCTCCACTACCTATACTACCCAAGACGACCC CTCACACGCTCTGCGAGGAAACCGGTCTTC GGAC	p000930	D	--
IM000827	GATCGACCGCAGATGAGGTCTATGCAGGAA AAACGATGTCTGGAATTTTATTAAAATTGCTC AGC	p000933	K	*Myc*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000828	AGTAGACTGAGATTTGTGAGCGCTAAGATAA AGATGAGCAAAGCTTTGGCAGCTCTTAGGTA TCTGAGGGCCACCGTCCTCTACAAAGCAAC GAGAGGCACGGCGGATTAGGATAGACTGGT TGCATCCAAACACTACCTTGCTGCCTCAAAG GCTTATTGGACACCACAGAAAGACCTCTGCT GGAGGCAGAAGTCACAGGACTCCTCGTCAC AGACGATC	p000934	D	--
IM000829	GATCGGCCTTCCTCCAAAGCTACCTGCATAG AAGAGACCTCTGCTCTCACCTACTCTCCTCT ACAGTTCAGCCCATATGGCTTCACCTGCATC CCCTACACACACACACACAGACACACACACA CACACACAAACACACACACAACACACACAAC ACACACAACACACACTCACAACACAAACACA CACAACACACACTCACAACACACTCACACAC ACACACACAACACACACACACACAACACACA CTCACAAACACACTAGTACACAAAGACTCCA ACACACACATTCCCATGCACTACTCCCTCAG TATCCGCCGCATTTGTGCTCACACTCATCCA CACTCTCACACTTGTAGCACACACACATCAT TCCTACACAGGCATGGACACACATGCTCCTA TACAGGCATGCCCAGTACTCTCACATGCATG TTTGCACGTTCCCAAACAGGTTCCCACAAGG GTTTGGCAAAGTACATGCATCCTCACACGCA AATGCAAGCCGTCACACCCCATACCACAAGC ATGCAC	p000937	R	--
IM000830	ACACCACATGCACATACATGCACACACACCA CATGCACACATACACACACAACACATGCACA TACATGCATACACATGCACACACACCACTCA CACACATACCACATGCACATACATGCACACA CACCACATGCACACACACACACACCACATGC ACATACATGCACACACACCACACACACTTTG CAACTACATATAAGCTTTAGAAATGCCTCTCG CCTCCCCCCCATAGCGGGGAAGAGAGTGGTT TAAACTAGAGGAGTCTGACCAATGTTCATTTA TCTACCAGTATACCTCGCAAAGAGTTTTCAG AAATGTGCATGAGCTGTTAAAAACTTCTCTCT AATTTCCACATCCGATC	p000938	B	Hs.170434
IM000831	GCTGGACCCCGGTGACAGACTGTGCAGATG GATC	p000939	K	*Pim1*
IM000832	TTAGCAAGTCCGAGCGTGTTCGATC	p000941	K	*Nmyc*
IM000833	ACTGCACACATTGCCGGTTGTCGATC	p000943	K	*Notch1*
IM000834	CAAGTGTAGACATTGCAGGAAAAAAATATGG TGACAGTGAACAAAGCCCGTGAAGGTGACA AAAGCCAGTTAAAGTAGGACAAGGCAGAGC GAGGCCCATGACCGGGACCAGGCCCAAGAA AATAAACGAAGGCCACGATC	p000944	B	AW321468

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000835	GTCGGAGGAGCTGGCTGGACCGGTACATGC CCTGGCCATCCAGGCGAAGACCCCCGCCCA GTGGAGAGAAAACCCACAGTTGGACATTAGT CCCCCCTGCCTAGGTGGGAGCAAGAAAACT CGAGGGACCTCTTAATAAATACCTGGATTGG GAGAACGATC	p000946	R	--
IM000836	GATCGCGGGGCTATCTATAGAGTCCCCGGG ATGTCTGAGAAATCAGCCCTAGAAATGACTA GAAAGAAAATCGAAGTATTCTTGGCTCCTGG AGACTTCCGCAGCGAGAAGTCACAGATTCAG GACACAGATTGACAGGAGCTGCGGGCGCTG GTAG	p000950	D	--
IM000837	GATCCCAGGATTTGGGAGGCAGAGGCAGTT GGCCCCA	p000953	R	--
IM000838	CAGGCTGGCCTCAAACCTGCAGAGATGCTC CTGTCTCTGAGTGTTAGATTTAATAAAGGGG TTCACGATC	p000954	K	*Lck*
IM000839	GTTGCTGGGCCCTAAGCGCCCACATTTCACA GCTCCGATGCTCATCAGCATGACTCTCCTGA GCACATTATCTGGTGGTGGCTGACACTCTCT TCAGTACCCCCCCCCCTCCCAAAAAAGAAAA AAGAAAAAAAAGGACTGGTTGCTAAAAGAAGT AAAAGTCAAGTCATCAAAAACAATGTAATATC CTGTGTGAAAGTCACGAAGCCTTGCGGTTTG AGTCCCTCGATC	p000955	D	--
IM000840	GATCGGCCGGCTGTCCAGCGACCGGAGAAA GGAGAGCACTCGAATCGCAGAAGCTATCAG GTGAGTCCGACCTCTCTCTGAATGAACGCTT TGGGGAGCCTGCCAACGGTGACCAAATTTA GCCAGTTAAAAGTACAGGCTGCCCAGCTGTA AACGTACATCAAACAATGTGCGATTTTATTTT TAGTGTGAA	p000956	D	--
IM000841	ATAGTAACACTTGGGAGGAGCCATTCCCAGT GAGGCTCGTATAGCATAGCCCTGTCCAATAG AGCCTCTGTTGCACTCTGTGTACACTTAGCT CCTTGCTTAGGGATTTTTTTTACATGGGTGAC TACAGCACCCCAATTTCACATTGGACAGACT CCAGGACACCCCTCGGTGTCCTGTGACGCA TACAACAGCCCCCCACGGGGCTGCACCGAA AACGCCACAGTACTGAGGCTGCACCTCACTC ACTCACACACACCTCTATGGCTCAACGTCCT GGAGAAAAGGCTGCGACAGATTCCCACATCT GGGAATGCAGTGAAAAAGCACTCACACTGG GGGTGGGGTGGGGCTGGGGGGGCACCCTG TCTTCCCGTCTTCCCATGACCCTCTTCCCTTC CAGGAGACCATAGCCAGAGCTGACAGGAGA TTCAGTCGCAGCTGCACACGCTGCTGCCTTG CCGATC	p000957	D	--

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IM000842	GATCGGGCAGGACACACATTGGGGAGGCCC ATCAAGCCCGAGCCTGCCTTGTGAGCCCCC GGATTGGCAGGGCAGAGAGGAAAGCTGCTG CGTGCTTTATAGACTTTGGGGAAGTCACAGG CTCCGCTTGCTTGGGGGAGGCAGGAAACCC CCTCCACCTAGGCGTCTGCCAGAGCACCCG CAGGCTTCCTCTTGTCTCTGTCCCCCTCCCC AGCACCTCTTCCCCTGAACAGCTTCCCTCTC CTGGCCCTGCTGTCCCTTTAAAGGAACTTGA ATCAGAGTTGAGAATGATGGTGACTCAGGGT GGAAGGGGTGGTCACTTG	p000959	D	--
IM000843	CCAGGGCTACACAGAGAAACCCTGTCTCGA ACAAACAAACAAACAAACAAACAAACAAACA AAGTTAAAAATAAAATTGATATACGATC	p000960	R	--
IM000844	GATCCAGGACATGGCAGAATATGGTCATCTT CTTTGCTTGCATGTCACACGAATGGCCTCTG GCTCCACCCCTGATTGCTTGCTCCCCTTGGA AGCCTCTTGAGCCTAGCTAACTTTTCCTGTTC ACCTTTGTATTATGTGCTCCCACCATGGCCC ACCAGGCTCTGCTTGCAGCACTGCAGCCTG CAGCTCCAGCGGCCTTTACATGGCTCCTGTA AACAAGTCCCAGAGGCCTCAGTGTCATCATT TCAGCAACCGCCTCACTTCTTGGTGCCGCCT TCCTTTATTACTTTCATATTTCTGTGACCGAA ATACCCCCAAAGAAGCTACTCAAGGAAAGCA GTATGTGTGGGCTCACCATTAGAGGTCAGTC CCCTGCAGCAGTGGAAGCATGTGCTGGTGA CGC	p000976	D	--
IM000845	GATCGCTACTTTTTCAGAGACGCCTTCATTAA GGGGAGAATGGAAAGATGCTGGTTGACTTG AAAGATTTCTCTCTGATTTGTTTTACAGGAAG TGCATTCTGTACACATGAGAGACTCCGGGTG GAGAGGCATTGTGGCGGTTGAGATGCACCT GGGAGTGCCAACTGCCCCCGCTTCTACCAC AGCTCTGCATAGCAGGCTGGAGCAAGCAGC CAGCCAACCATTGTGCCCTAGCCTCATCTCC TCCAGAAGAGGTTATCTGGGCTCTGTGTAAC CTCTGCTCTTTGGCTATGGTATTCCTTCTTGG TGCTTTCTGTGGTCAACCTCCAGGTACACTT AGGGCCTATCCTAGACAGACTGGGAAGAAA GAATGACATTCCCATTGACCTCTGTTTTTATT TCCTGGAAATCCAGACCTTGTTCCAGTTAGT GGAGCATGGGGTTAGACCAACCACACTGCT AAGAGTTTTGGCCTGTAGACATATCTGG	p000983	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000846	TAGCAAGGTAAGTACTTGTCTCAATTTCCAG GTAGTATAGAAGAAACATATATGTTACAGCTT TAACACCAGAACAATCACACAGTGTTGTATTT TAGCTAAAATATGACTCTGTGGTTTTCAAATG GCATAGTTGTGGACAACTTAATTAAGCACGC TCTTATAAGACGTGATAGAGTATGTGCCATC CAGATACTAAGAACTGTGTCCAAAGAGCTTG GGACACACACTAAGGGGCCTGCCTCTTTCAT AACGGGGATGAAAATGACTGAGGCTTCACAT TTGCACAGTACGATC	p000988	D	--
IM000847	AAGCCATCTGGGTCTCAAGTTGCTAAAACTT AATAACTCCCTCCCTGTGTTTGTCCTTTATCT AATGGTAAAATATGACCTAATGAAATAGGTTC CTAAGGCTTTCATATAAGGCATGATGTTGAA GGATGGAGGACAGAGTGGGATGGAAAATCA GAGCCTGCACAGAAAACCACAAGCAGCTAA CAAAAGTCCACAACCAAAGCCTGTGCCTGAA ATGTCACCTACAATGCAGTGGACTATTCATAT GCCAGCCTGGTCCTCATGCGATC	p000991	D	--
IM000848	ACCAAGAACAGAGCCCCAAACTAATAGGATG GTTTGTTGCACGTGTACATGTGTATGCATGC GTGCATATACGTGTGTGTGTGTGTCTGTGTG TGTACACCCACACGTGTGCATGTGTGTTGTG TGTTTTTTAAGCAAACCTCAGTGTGTCATACA TACTCTCCTATACTTCCCCTCCCTTGTTCCAT ATGAGGGTGCCTTCTTATCTCACAGGGTTGT TTTGTTTTTTTTCTATAACAGAATGCCGCTGA TGCTCTTTTTTCTATATGAACCCTACATTTAAT ACTTATCCATAAGCAAAGGAACAGTATCTTAT CTTGCGGATC	p000992	R	--
IM000849	CTGGGGGCTCTGCTACGCGTCAAACGCCTG GAGAACCCCTCGCCCCAGGCGCCGGCACG CCGCCTCCTGCCTCCCTGAGCGCTGCTGCA TCCTGCACGCCCTGGAACCCAGGAGCGCCC CAGCGACCCTGACTCCCTGCCAGCACGTCC AAGGCTGCTTACCCCAGCAACCTCCCATCCC CTGAGCCCTCAGTAAATGCCATCTGTAGCAG CTGTTTGTCTGAGCGCCCTGTACTAGGGGG CCGGTGGGCTGGGTGACAATGATAATGGAA TAGTGGCTGTCCTACTGAGGACAGCACAGTA CTGTTTGGGACCTGTACTGGTAAGGAATACA TGCCTGCTTCCTCTGGACTTTGCGGGTCTCA CCGGGTGCCTGGGCTACCCTTCTAGGCTTC ACTGAGGCGGGTTCCCTGGGAGGCTCTGAG GTTACTTTCAGCGTCTGCCAGGGGTCCACAG CACTTAGCCAAGGGGCTATGGATTCACTCGT GGTCTGCCAGGACCAGGCTTGTTGTGAGGG CCCCAGGTGGATC	p000993	A	*Saas*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000850	GTGTTTCTTTTCTTTCTTTTTTCTTTTTTCTTTT CTTTTCTTTTCTTTTTTTTTAAATCTAAGTAAG GTGCAACAATGTAATTCGAAGGGGCAGTGTC TTCCCTTCCTGTAGTCTCTGCTTAATTCCTGA AGTTTGCCAAACCAGGAGTTAGGAAAAGTTG GAAACCTGCAGAGAGAGCGTTTGAGAGGTTT GAGATGTTATACGAGAGGGTTTGGCAATGTG TGGAGTACAGGTAACTTGCGGTTATTGTTTT CTTGGCCCTCTATCTTCATCCTTTGTGCTTGC TATTTACCTTGCTGTCGGATC	p000994	R	--
IM000851	GATCCTTGAGTCTGTACTTAGCCTGAGAGCG CTATAACACTATATACAAAGTACCGACTAGAA ACTCCACACACATTTGTTGACTGACTTAATGT GTAGCCCTGCAATGGTTGACAGTTGGGGGT CAGGGGGCTCTTGCACTGAGGGTAGTGTAT AGCCTAAAGAGATAATCAAGATGATAAGTAC ATCCACACTAGGACAGGAGCTTTAACAAGAG CTTTTAGTGAAGGGAACTTTCTGGGAGCCTC AAGGAAGGCATAT	p000995	D	--
IM000852	AGCAACACCTCATGTGGGAATTCATACATTG TAGGTAATCAGTCTACTAGCTGAACTATATCT CCAACCCAGGAGGTCAGGTTTGTTTGTTTGT TTAACAATCTAGTTTTGAAACAGTCATATCCT AGGCTGGCCTCAAGTTATGTAGTCAAAGATG GCCTTAAAAGATGACTCTTGGTTATTTTCCAA GTGCTGGGATTATAGATATGCACACCACCAC ACCTCATTTGTCTCGGGGCTGGACTCAAATC CAGAGCTTCATGCATGTGAGGCAAGCACTGT ACCAACTCGACTTTTGCATACTCCATTGAAA GTCATTTTTATAACAGGATC	p000996	D	--
IM000853	CTACTTATCTATCATCTATATGTCTATCATCTA TCTATCTATCTATCTATCTATCTATCTATCTAT CTATCATCTATCATCTATCATCTATCATCAAT CATCTATCTAGCATCTATCTTCCAGAGCTCAT GTTGTGGCTTGGGCTTCTCATTTCACCATCA TCGAAGGTAGTTGCATTTTTTCTATTGGCTTC TTAGAAGCAGGAGGCACATGAAACAACTTGC TAACCCTTTCCTGGTCTTTTGTTGTTGTTGGT GGTGGTGGTGGTGATGGTGGTGCTGGTGGT GGTGGTTGATGTGCACAGGAGACCTGTCCG GTATGGAGATATGGAGAGCGTCTACGTCCTC ATGGGATC	p000997	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000854	GTGGGACGCGGAGGGTGGAGATGAATTGAG AAGCAGTTGTCGATTTCCTCCTTCTTCCAAAC ATCAAAGGCAGCGGTGGATGACAAACTGAA GGACAGAGGGTTTGATGATGCAAGAGGAGC CAGCAGCAACCAAGGCCAGCCTCTTGCGGG TGTGGGCAGGGCCTTCTTTACAATGAGTTCA CACACACACACACACACACAGAGAGAGAGA GAGAGAGAGAGAGAGAGAGAGAGAGAGAGA GAGAGAGAGACTGCTCTTTCAGAACAGCCCT AGGAGGTTAGCTTCAGACTAAGACAGGAGA CAGAGAGTCCTTGATTTTGCCAAGGTTGCAC AGCTGGGGAGAAACCCAGCTATGGCTTCAC CTTGGCCCTTGTTAGGACTCCTTCCTAGTCC GGTTGCAGTCTCCTGGATC	p000998	R	--
IM000855	GTATTAGAGGCCAGGCCATTCAGAAGATGTG GCAAGATTGTCATGTGGAAAATATTTGAAAC CATTCTAACCTAGTCATTCCATCATCAATAAT AATAATAATAATAATACTACTAAAATGAAAAA ACCTAGATATTTTGAGACTGTACTGCTGTATT TTAAGAAATACACGGAAATTTAGCACTGAAAT TTAGTGCTAGTTTTAAGAATACTTTGTACCGT TACTTGGACCCACAATTGCTTAGAGCAAGGG ATC	p000999	C	--
IM000856	GATCCTGAGACAGTACAGGAACTAAGAAGCC CTGGGCAATTTGCAGTGTGCACACCCAGCCT GAATTTGCCTGGTTCTCACCAGCCTACCAAT AGAGCATTGTAGTGGCAGGGATGTCTGCTG GTGTCTCGCAGACAACTTTTGAGGTCCTGCT TCTCCAGAAGTGTGCAGCTGGCAATTAGCAG CCTGGTCTTTTCCTGTCCCCAAGACCAGTGC TTCCACCAACCTGGTCTCTTCCCACAGCCCA GCCCTTTCTCTTCCTCTTTGACACCCACTTCC TCTAAATGGTGGTCACATGCTTTGTCTCTTGA AAAAAAGTTGTATGAGTCAGGGTATTTTCAAC GCCGGGACAGAAAAATTGACTCAACCTGGCT TTTTCAATTAACCACTAATGGGTTTCACTTAC AGTCCTGACAAATACCAGGCACAATTCATCC AGGACAATAGTGAAGAATTTCATCTCTTCCC CCCAAGCCAGTCAGTCTGGTTTTAATATGCA CGGTGGATAGCCCATAGCATGCAATGAACTG TGAGCACCCCTCTGGGAGTCAGCAGAGACA CACACACAGGCACCCATACCACACACTGTGC TTTGTATCA	p001000	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000857	GATCAAAACAATATTCAAATAATGACATCAGT CAAAGTATGATTTGATGGCCATCACTCATGT CAATAGGCAACACATAAGCCTGAGAGTAAGT TAAGGAGAAATTCAGCAATAAACAAATTGAC ATACTATGTCCACTATGAGTAAAACCTGCCT CTCTTAAAACGTTTTACTGTACTCCATGGCTC TCCCCCAATGTGCGTTCGTGAGAGTCCCCAC CCCTGTGACTCCATCTGTGTGTGGGTTCAGG AGAGACTCCTGTGTGTATTCAAAAGAGCCCC CCATGTGTGTACACACAAGAGACCCAGTGTG TGTACATGAGAGGCCCCACCCCATGTGTGTT CATGAGAGACCCAACCCCTGTGCGTGTACAT GACTCTCCCCATGTGTGTTCATAAGAGACTT GTGTGTATGGGAGACTCCACCCTGTGTGTGT ACATGAGAGACTCCTGCCTCTCCTGTGTATA TGGAATACCTTCAGAGTATCAAATATTTTCAC CCACTGAGCCATCTTAGAACTTCTCTCCCTT	p001001	C	--
IM000858	ATACATATGTACACACACACTCACAAACACA CATATATACACATACATACATACTCACACATA TATATACACACTAGTACACACATACGCAAATA CACACATGCATATACACGTACTCACACATAC ATACCCATACTCACACAAACACATATATACAC ACATACTCACATATACATTCATACATACACAC ACATATATACATACACACACTTGCATACACAC AGCACACACTCACACACAGAGACACACAGAC ACACAGACACACACACAGAGGAACCCAAAG GATTGGAAGAATAATTTCCTGTGCTCAGTGG GAAAGTTTACCAGAAAGACAAGTGGTCATGT GGGATGATC	p001005	C	--
IM000859	GATCAGGGACCCTGTACCCTCCCCCGTGCA GCCTGTGATTC	p001006	C	--
IM000860	GGACTGTAACCAACTCGGAGAGGAAAGGGC TTATTTCATTTTAGTCTTTACAGTCCATCATTG ACGGAGGTTAAAGCAGGACGCTGCTTACTG ACTTAGCTCCCCGTTGCTTTATCAGCTACTTT CTTAATACAACGCCACCCCCGCGGCCGCCA CCTCCCTAGGCAAGACCCACAGGTCAATCCA ACAGAGAGGATTCCTCAAGTGACACTCCTAT GTCAACGCTATCAATGGCAAAGGTATATTGA GCTAAGAATTGATC	p001007	D	--
IM000861	GATCTCAGGCTGCCCGTGGGCGGGGCTGAC GGAGGGAAGCAGACTAGGCCTCTACCATAT CCGTGGGAGGGACTTCCAAGGACCGAGACT GAAGAAACAGCGCGAAACAGGAGACACTGG GAGGAGAGGCGGAGACCGACACTTAGTAG	p001009	B	Mm.76753

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000862	AGAGAAAAGACTATCTTGACCTTTGGATATG CGGGTGCAAAAATGAGAAGACCACAGTGCA GCTGTGTGCCCTGCACGGGGCAGCGAGAG GAGAAAGAAGCATTTTACATGAAGCACAGAA CACGCCTGACAGTTCTCAACAGCAGCACGTC AGACCACCGCAGCACTGCTCGTTTTTCTCAG CAGACCCCCAGGAAGCACCACCCAGGATGG ACATGTAGGGGTGCATCCGAGAGAATCAAAA TCACACAGGGGCCATCCTTTTGGTTCGGCAT GAATGATGGGGGCCGCCTGCACTGGCCTCC ACCTTCTATGGTTGTTCTTCCTTGTATCAATG TTTCAAAAAAAATCCTTGGGCTCACAACTGC CTAATGACATCTTCAGGAGTCAAGTCAAGAA AGAGAAAAGTAGCCGACCTGGCACGTGGTA GATAAGACTCAAGGGTGCAATAAGCAGATGA ACTGGCTTAGTTGGGCTTTCTATTGCTGTGA TAAAACACCATGACCAAAGCAACTGGGGCG GGGGGCGGGGGGTGTCATCTTACACTTCCA TATCACAGTCTATCACTGAGGAAGTCAGGGC AGGATTCAGGCAGGAACC	p001011	R	--
IM000863	GATCGGCCAACACAGGATAGATACCACACA GGATAGGAGGTACAGTGTCTGGAAGATTATT ATCGAGCCCCTGAACGTAGTAGAAGCTGGC TGTCGTTCCAGTGCAAGCTGAGCAGATGGTC C	p001013	D	--
IM000864	GATCCACATGAAAGCCAAGCTGCACATTTGC TTCATATGTATGGAGAGGCCTAGGTCTAGCC CATGTATGTTCTTTGGTTGGTGGTTCAGACT CTAAGAGTCCCAAGGGTCCAGGTTAGTTGAC TTTGTTGGTCTTCCTGTGAAGTTCCTATTCCC TTTGGTGCCGTCAATCCTTCCTCCTATTCTTC AATAAGAGCCCGCAAGCTCCATCCACTGTTT GCTTGTGGGTATCTGTAA	p001015	R	--
IM000865	CCCTCAGCTACATAGTCAATTCCCATCTAGC CTGGGTATGCGAGATGGCAGTAAAGACACTA GCTGCAAAGCCTTACTGCCTGAGTTTGATC	p001018	D	--
IM000866	GATCCAGTCACAGGAGAGCAACTGGGGGAG GGAGCAGGACAGAAGCACACCATAGCCCTT TCAGGGGGCCGGGGGCGAGGGGTGGACAA GAGAAGACAGATAATGACTCACAGGATGAAG AAGCCTCCCACAGCCCCTCCCTGAACTGGC CATCTGTTCTGGGGCCCCAGAGCAGGCGAG TACCGTGAAGCTTGGGGACTAGCAGCCGGA CCACTGAACAAGGTCAACCAGCCAGTTGTCC CACGAGGGGAGAAGCTACCATTGAACTGTC ACTTTGGAAAGTAGCCAGAGCCCATCCCTGG TCACCACCCAAC	p001019	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000867	GATCCCTAGAGCTGCTGGTCAGCTGGCCTG GCTGAAACTACTTCTGTGCAGTGAGAGACCC TGCCTCAAAACACAGATAATGGAGACAGATA AATGACATCGTCCGCTGTGTCTGCGTGTGTA TATGTAACACAACACACAGTATACACACATAC ACACCACACTCATACCGTCACACATGCACTC TCAGTGCATGTGCAACACAACACAGTGTACA CACATACATACACACCACACACATACACATA CCACCACACACGCGCACACACACACATAA	p001020	R	--
IM000868	GATCCTTGTGCATCACTGAGCCATCTCCCCA GCCTACAGTGTAAGTATTCTATACATATTAAT TTAATCCTGCCGGGTGGTGGTGGCGCACGC CCTTAATCCCAGCACTCAGGAGGCAGAGGA AGGTAAATTTCTGAGTTTGAGGCCAGCCTGG TCTACAGAGTGAGTTCCAGGACAGCCAGAG CTACACAGAGAAACCCTGTCTCAAAAAACCA AAAAAACAAAACAAAACAAAACAAAACAAAAA TCCTATGGAGTATTCTAAAAGTAAAACCGTAT CATTAGCACTGCCAAATAACAGAAAGGAAGA CCAAAGCAAA	p001021	R	--
IM000869	GATCCTCTGAAAATGGAGTTACAGATGGTTG TGAGCTGCCATGTGAGTGCTGGGAACTGAA CTCGGGACCTTTGGAAGAGCTGCTGGTGCT CTTAACAGCTGAGGTGTCTCTCCAGCCCCTT TGGGTGTGTTTTGTTTTGTTTGTTTTGTTTTG CTTTTTCAAGACAGGGTTTCTCTGTGTAGCC CTGGCTGTCCTGGAACTCACTCTGTTAGACC AGGCTGGCCTCGAACTCAGAAATCTGCTTCC CAAGTGCTGGGATTAAAGGCGTGCGCAACC ACTGCC	p001022	R	--
IM000870	GATCCAATATATTCATATGGAGATACATGTAT ATACATAA	p001023	D	--
IM000871	GATCCAGGTCCTTTCCCCCTTATGGTCCTAT ACACCCCTGGGTACTTAGAGGCTTTCAGCTC TGACTGGTGGTGTGGGGAGAAGTGAGGGGT TACACATGTGACACAGGTCCTAAAAGCTGTC GCCATTGGCACATGACCATCCTAAGTCTGTG GCAGAAGGCTGCTCAGAGCCTCTGTCCAGG AACAACCCAACACATTGCAGAAATAACTGTG CATCTGGGCAATGGGGCAACTACTACCTGTC CATCCAGATAGCTCTTCTAGAGGCATTCGAA ATAACACGTAAAGTGGGGTGGTGATGAACAC ATATAATCTCAGCCCCTGGGAACCGGAGACA GGGGAGTCACAAG	p001024	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000872	GTCACAGTACTTGCTCACTTGCCTCTCTCAT GGTTTACTCGCCCCTCCTTCTCGTACCCCCT TTCCTCCTACAATCCTCCTCGTCTACTTTCAT GCCGTATATGTCAAACACCGTCATATATAAC AATGTATGCATGCAGCATTTCTTTTTCTTTCC CATCAGCCTCCCTTGCTCCCCATCCTCCCGC CCTTCCTCCTTCCTCCCAGGATC	p001026	D	--
IM000873	AGTTATGCTTGCAGACAGGAATGTAGCATGG CTATCCTCTGAGAGGTTCCACCCAGCAGCTG ACTCAGACAGATACAGATACCCACAAGCAAA CAGTGGATGGAGCTTGCGGGCTCTTATTGAA GAATAGGAGGAAGGATTGACGGCACCAAAG GGAATAGGAACTTCACAGGAAGACCAACAAA GTCAACTAACCTGGACCCTTGGGACTCTTAG AGTCTGAACCACCAACCAAAGAACATACATG GGCTAGACCTAGGCCTCTCCATACATATGAA GCAAATGTGCAGCTTGGTTTTCATGTGGATC	p001027	R	--
IM000874	GATCGTGGTCTCTTCTCTTTTTTCCCTCTACT TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT TCTACTGTCTTCTTCTTCTTCTTCTTCTTCTTC TTCTTCTTCTTTCTTCCTCTCTCTCTCTGTCTT TCTCTGTCTGTCTGTCTCTGNCTCTCTGTCTC TCTCTATCTCTGTCTTTCTCTGTCTCTCTGTC TCTGTCTCTCTTTCTCTGNGNCTCTCCCTGTC TGTCTGTCTCTCTCTTTCTCTCTCTGTCTCTC TCTCTCTGNCTCTCTNTCTCTGNCTCTCTCTG NCNCTCTGNCTCTGTCTCTGTCTNTGTNTNT CTCTCGCTCTCTNACACACACACAGATGTAC ATGCAC	p001028	R	--
IM000875	GATCGGCGGTATCATATTTTATGTGTTTTATT TCTGTGTCAGAAAGTTTAAAAGGCCTCAGAT TGGAAGTCTGGTTTGCATGGAATGCATATGA GCTTTTTCATCTTATTGCCCAACAGATTTAGT CTAAGAACCACCTCTATTATATAGGGTATGAT AAGTAATATAGGTAAGGGAATGCATCCCATT TGATAAGTGAAAGTTGAACACACATAGAGTT GGCTCACCCCGGGGTCTAGGCTCTAATCCC CTGGGGATACCCAGGCCAACTAAACGCTATA GCAACAGGCATTGGGGCATGAAGATACTTTT TGTTGTTTGTCTTGAATTTATATAGGGGCTTA TATCTCATTACAATTAATCATGAGTTGCAGTC AATAAATCTTCATTGCTCAACATATTTGTACC CTCAAATATTTTTTTCTTTTTTTGTGTGATAT	p001029	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000876	CTTGTAAACACGATTATTTTAAAGATATAAAT GGCTCTTTACTCTGTTTAAAAATTGTTTCTTTA CCAGTTCTTCGTGTACATTGGTCTCCATTTCA CATGAAATAAAATATTTTGTTTAATGTTAGATT TTCAATACCAGCTGAGTGTTCGATGTGTGCC TTTTGGACATATATTTGTTGTAAAGTGGTCAT TTGGGATC	p001031	D	--
IM000877	GATCAGATTCAACTCCCGCATTTCTAGCCCC AGCATCGTGGAAGGGCTACTGTGTCTTTTCA AGCACTATGGTGGATACACATAATGCCAGCT TCCCTCATTACTGGTGATGTGAGCTGTTTGC CTAAGGTCCTTTCTGCCAGGCTTCTCTGCTG CCAAGGCTCTGAATTTCCCTTTGTAGCTAAT GCGTAGCCCTATTGGCAGACTCTTCCCGTGG CTGACTTCTGCCTCCCGTCACACAGCAGTAC CTTGTTTGTTCTCACCTTGATGTTTCTTATAT GCATTGATGATGGTGAACAGCCCAGCAAGT GCGCCTGTTTCTTCCCTTCCTCCCACTTTTGT TCTCAGTTGTACATGGCAAGGAAAACCAATT CCTTCTTTCATATTTCTCCCAGAAAAAAAATC CTCTTTATAAGAGTTCACATCCTTGAGCACAC ATGATAGGAGCTGGTAGCCAG	p001032	D	--
IM000878	GATCATGATATTGTACTGCTGAAGACAAACA TATTTAAGATATAAGACTTGGAGAAATCAAGT TGGTATTGACATTGGAGATTAATCTCTTTTGG CTAGCTTTTGTAGAGCTAGAAGTTGGTATGT AAGCTATAAGGAAGAGAAGTATTCATAAGAC TTACCCAGTTGTCTCTCCTGTAAGCTAAGAC CAGCCTAAGAAGCTAAAATTATCTTTAATGTA GAACCACAGAGAAAGAAATTGTGGTATGAAT TTTGCTTGTTCGTGGACATTAACCATTAACTC AATGATAATCAAATGACAATACATAGAGACAA AGATATGCATACTAGTAAAATAGTGATAA	p001033	D	--
IM000879	GATCGTGCTAGAGAATGGTACACTTGGGTTA TATTAAGAAATCTTGGTTGAGTGGTGGTGGC ACCCTCCTTTAATTCCAGCACTCAGGAGTCA AAGGCAGGCAGACATTTGAGTTTAAGGCCTG CCTGGTCTACAAAGTGAGTTCCAGGAAAGAC AGGGCTATAAAGAGAAATCTTGTCTTGAAAA AAACAAAAAAACAAAAAACGAAACAGTAACT GAAACCGAAAAAAAAAAGAAAGAAAGAGAGA AAGAAAGAAAATCTTACAATGTGGGAGCTGG AGAGCTGGCTCAGTGGTTAAGAGCATTGGCT GCTCTTCCAGAAGACCCAGGTTCAATTTCTA GCACCCACATGGTGGGTCACACCTGCCTGT GGCTTCAGTTCTAGAGTTTCTGACACTCACA CACAAACATACATTCAAGT	p001034	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000880	GATCTTGTATTTCTTCTTGGCTTGTCTCCATA GGAACAGGCAGCACAGCAGAGGTCTGGGAG ATGGCTCCGAGGGTAAGGGACCAAGCAAGG TCACCTGCGCTCACTCCCTGGAACCCACACA GTGGACAAGAGAGAAAGACTCTATGGCCTC CACGTGCGTGCGTGCGTGCTGTGGTGTGCA CGTGCCCCTCCCCCAAATAAAGAAAACTTAA CGAAAAAAAATTAAAAGTAAAAAAACAGCACT GCAGTAGCTCCAGGAATCAACTGGTCAATCA GTGTATCACATTTGACTATCCGATGATGGTTT TATTTTACATGTATGCACGTGTTTGCATGTAT GTGGGTGCACATGTACAAACACATGTGCCAA GGCCAAAGGACAACTTTGGGTGTCCTTTCTC AGGAGTCATCGACCTTATTTTCTGAGACAGG GCCTCTCACTGGAATCTGACTGGCCAGCAG CCTCCCAAGGATGCTCCCCAACCTCAGAAG GATGCGCCTGTCTCTGCCTCCCAGCCCCGG GGGTTACACTGGTGGACCACTGGGCTCTTTT CACCTGGGTG	p001035	B	Mm.138834
IM000881	GATCTCTTCTTAAAATTACATTACAGTAGAAA ATGTTTATGAGGCCGTTTTTATCTCTAATATT ATTTATTACCACTCTCCTACCCCCAGAGTCTT ACAGGCATCAGGGAGTGGACAAAGGCCGGC GGTACTGAATGGTGATGTTATTTTTGAAATAA TGAAAAG	p001036	D	--
IM000882	TACCTGTTGCTCCAACATGGTCAGAAATCAG TTTGTTTCAATTTTAAGATACAATGAGAGTAA CACCCTAAAGACTTCACATTTTATGCATATTT GCTACTCTGTGAGCACATGAACGCTTCTCCT TGGGCACGATC	p001066	D	--
IM000883	GATCGCAGATACTGCAGGTATGTAGTAATGA AGTCTGTAAACATACAGAATGGAGAAGGCCA GAGAGGAAAGTGCAGGCATTGGGTAGTCAG TAGGTAAAATAT	p001067	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000884	GATCGCAGCTCTTCCTTGGTGCTTTTCCCCT CAGTTCAAGTGCTGTGGCGGGGAGGACTAC AGAGACTGGAGCAAAAACCAGTACCATGACT GCAGCGCCCCCGGGCCCCTGGCCTGCGGG GTGCCCTACACCTGCTGCATCAGGAACACG GTAACTGCATGGGTGCTGGATGTGAGGGTC ACCCAGTTTGCCAAACACTGCCCTCACTCTG CCCAAGTGGAGCAGGCAGTGGGAGTGGGTG GGACGTGGTGGCCGGGGCTGAGCTTGCCTT AGACCAGGGGCCCTAGCAATGGGAGATGAG TGGGCAGCTTCCTCTGGGAGTGTGTCAGTG AGCGTGTGCGTGTGTGGGCCTGGCCCAGGC GCTTTGGTTGTAGTTACTTGGTTCTTACAACA GCTTTGGAGGGTCTCAATTGGGGTAGTGTTG CTTTAGCCACTTAGGGGGACTTGCCCAAGGT TGGCAGGGCTCTTCCCAGCAACAGAGAGCC AGAGTGCCCGGCAGGTGCAGCAGGCTCTAC CCAGTCACTGGAGGCAGAGTACAGTGCAGG TGCTGTGAGCACTGGCAGCAGAGCCCTGGG CAGCGGCATGCGGTAATGTAAATG	p001069	B	Mm.28112
IM000885	CCATGTCAGGTGATTAACCTGTGAGTCTAAC TTCCAGGAATGCAATGCCTCTGGCATCTACA GGCATAAACATACTTGTGGCTTACACTCAAA CTGACACACCAACACATATGTGCACGCGCAC ACACACACACACCAAATTAAAAATAAAATAAC CCTTTTTAAAAAAAATATAGAACCTATAGATA ATTGCTTTACTGCACTCACAAACATTTTAGGA TC	p001070	D	--
IM000886	GGGGCACATAGTGAGTTCTAGGATAGCCAG GGTTATAGAAGCTATAGTGTGAGACCCTATC TCAAAAAAACAAAACAAAACAAAAAAACAAAA AAAACCTAAGCCCGTGTGGTGGTGTGTCTCA GTCTGAGCGCTTGGAAGACAGAGGGAGGTG CATCTCTGAGCTTGAGGCTAGCCTGGTCTAC ATAGAGAGCTCCAAACCAGTCAAAGTAACAA AATGAAACTGTCTCAACAATGACAACAACAA ACAAACAAGCACTAGAATAAAAAGAAGCCAG CATGGTGTCATGTGCCCGTCATCCTACCACT TGGAAGGAGAGAAGCCAGTGCAGGAAAATT AGGGATC	p001072	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000887	GATCCCAGGCTTCCTGTAGGCTAGGCAAGC CCTCTCCCCACCCTGTCCTGGTAGAATTCAT CCCGAATGTCAGCATTCCTTCAGTTAAAGGA ATGTGCTCCCTCAGGCTCTCTCCCATGGTGC ATTGCTTCAGCACGCAGGCAGACACTTGTCC AAGCTAGGCTCCCTGTCTCCCATCTGTAGGA AATGCTTGGTATGAAGGCCCTGGTGGACCT GGCTAGATGGGCAGCGCCCAGTGAAGGGCT GTGTCTGGAGCCTGGGCTGTAATTAGTGGTT TGAACTGGGTGCTCTGGGGAGAGGCAAGTA AGAATTTGCTTTCTGTTTTTAGAGCAGGAGG AGCTGGCGGCTGGCTGTGCCTTAGCCGGCT CCTCGAAGAGCATTTGAGGTGTTCGCCATCT TAATGGGTTAAGACTCTCCTGTGCTAATCTG GTGGGTTGCTTTTAGGCACGGTGGTCCCACT GTGGTTGTGTGAACAGTACCTTAATGCCAAC ACTTTGGAGGCCTAAGGTATCCCCATCTGCA GGAACTGGGGTGCACA	p001075	D	--
IM000888	GATCCTCACACAAATTGAGTAGTACTAACAA GAGTGTGATTCACATAGTCAATAAAGGTATA GGCCATCTGTGCCCTGGCTTGACCTCCGCA GACCAGAAGCTAACAAAACCAAAACAGACTC AGTTTCTGCATGCTAACTTAACCATGATTTTC CAGACTATTTCTTTTATCCTGTGAAAAATATA TTAATCTCTATTCTGCAGAGTATCCCTTCTTT AAGAGAACATGATTTCACTGTTTTTGACAATA TGCCTAGACACAGAAAAAAATCATTTAGTTT	p001078	B	AA793356
IM000889	TTTTGAGTGCTCAGTGAACTACTTAGGGCAG CCTAAGGAATACAGTGACCCACCAGGAAATG CCTTGTGTTTTGGCAGTCTGATAGCATCACT CACAGCTGTCGGTCGTGACTTCATTGGATC	p001079	A	*Edar*
IM000890	GATCCAGGGACAAAGAGCCCATTCTCCTGTT CCTTCGTAT	p001081	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000891	ACTTTCAGGCAAGCTCTTTGCTCAGTGAACC TGCTACCACACACAGACTCCTCCTCCCTGTT CCCGTCGTTAAAAAAAGTTTTATTTGAGGTTT AGAGCAATGGCTCAGTGCTCAAGACTACTTG CTGTTCTTACAAAGGACCTGGGGCTAGTTCC AACACCCACATGATGGCTTACAATTCTCCAG TCTCAGGGGTTCCAGAACTCTTTTTCTGGCA TTGAATGCACATGATGCATATATAGACAAGC AGGCACACACACACACATAAAATAAAACAAA TCTTTTGAATGTAATTTTAAAAAGATTTATTAA TTTTAATTTTATGTGTATGAATGTTTTGCCTG CATGTATGTCTATGCACTGCATGTGTGCCTG GTGCTCAAGGTGTCTGATAGCCTGGTGCTG GGCTTGGTTCACTCAACAGCTGGCCCTATGA AGGCCAGCCGTGAGGACACCTATCCATGCT GACAGACACAGATGCTCAAATGAGACAGCC CCTTCTCTATGAATGCCCTCTTGAGAATGAA CAACCTCCCTGCAGCAGACCTCCTTCTGGAT ACCCTGCCCTTCCATACTTTCTGGGTGTCTA GTTCTCTTCC	p001082	R	--
IM000892	GATCACACGCTTCACCTAATTACAAATGATTT CTTTAGAGGGGTCTGTATATAACAGAGATGA TAAAATTCAACGGCAGCCCTCCAACTGCATT GATATACAGGAAGTACTCATGAAATTGGAGA CACTGATTATCTCTTTGTGTGGTGTCCACATA TGTGCCATCATATCATATTATTATTATTACATG GCTAAAAAATGGGGTCATAGGTTTCATGACC AGAACCAAAATATTCCCCTGTAATTTACACAG GATTGATGGTAAGAAATGAAAACAGTTTACAT TTTTGATAATTTACTTACTTGACATAAAATGTG ACTTTCATTTCCTTGCATTCCTTTTCACAGGT AAGGCTACGACAATAGATTCTCAGTTCTCCA CCTCTCTCTATCTTGTCTACTCTATCAGCAGC AATAGCAACAGTTTTCCATGGTCCTTCCATCT GTAAAAGCAATAAAAAATAACAAAGAAAACCA TACAAACCATTAGAATATGAGTTGGTATTCAC AACTCTCCTCTCAATACTTCATATTTTAAAAAT TACTAGAAATATTCATCAATAATATTTCATTTG TTAGCTCTAGATAATGTTTCCAGG	p001083	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000893	GATCATGGTTATTTTTGTAGGGTTTATTTATA CATGTCTACATGAATTTATGTGCACCAGATGT GTGCAGGTGCCCATAGAGGCCTGCGAGGAT GCCAGATACAGATAGTTATGAGCCACCTAAT ATAGATGTTGGGAATTGAACCCATGTACTCT GCAAGAGCAGCAAGTACTCTTAACTACTGAG TCATCTGTTTAGCCCTCCTGTTGGGATTTAAT GGTCAGTGTGAAATACTATGAAGATAGAAGG GTTTCCTAGACTCTGGTGTGTAGGGGTGGG GTATCTGTGAGATGGGTAAGCTCTGTTGGCT TTCTAAGAAGGAGAATGAGCAGAAGGCACAC ATAGACATTCACACTTTCACACACATGCATG CCAAACACCACACATGCACACCACATACCAC ACGCGCCCTCCTGTTTCTTACTATGTAATAAT GTTCTTGTAATAACTTAGTACTCTGCTAATGA AAAGGTCACCACTAACTAGATGCTAGCCTTC AACTTTGGACCAGAACTATGAGCCCAAATAA ACCTCTTGCATTTATAATTTAGCCAGCATGTA GAACTGTGTCAATAACAATGGAATAGTGTTG	p001085	R	--
IM000894	GATCATCTGGCTAAAATTTTATAATATGACTC TTTAAATTCCTTAAGAATTCACAAGGACCTTT ATGTTGAAATTACTCATATGTAAGCTTACTGG AATGAGATGGCTCCCCAGTTGAAAACACCAT TCTTAAAATACTCAGAAAATAAGAACGAGGC CAGCCCGGTCTACAAAGTGAGTTCCAGGAC AACCAGAGCTATACAGAGAAACCCTGTCTCA AAACAAAAACAAAAACAAAAACCAAAAAAAAA ACAAAAAAGAAAAAACAAAACAAAACAAAAA GAATGTAGATATAAAGAAAGAATAGTGTTTG CTGGAAATAAATAGTAATATAAACTTAACAGC AGCCTGTCAATTGCAGGGTTTTTGCACTTGC AGCTCAGAAAGAAGTGACCCTCCTCAGGAA GTAG	p001086	R	--
IM000895	GTGGGTTGTGTGACTCAGAGAGCAAGCTTCT ACCTCCACAGGCAAGGATGCCTGTGCACAC AGAAATGAGATGAAGTCATATGTGGGGACTG GAGTTGCAGTGGCTCCCAGAAGGAGGTGTG CAGAGTTCAGGCTGGAGTCCAGATGAGGAA CATCAAATAGAGAGGCCTTTGGAGGGAGTG GGTTCTCTTGATAAGTAGGACTGCCACCCAT ATCAAGTATAAGACTGCCAATCATACTGAATC TCAGGTTATTTCCCATGTAGCATTGGGAACA TATAGCATTTGTCACACTGCTATAGCAAAGAA TCTGTGATGAGGTTGGGAGTGGAGGGGAAC GCCTTTGGTCCTAGAAAAAGAACCAAAGGTA GGCTGATC	p001087	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000896	CCTGCCCTTGCCAGACCCGACCGCAGCTCA TCGAGGAGGTACCCTCTAAAGTCGTCACCTT GAGGAGACAAGCTCTGTCATAGTGCTCGCA GCCCCGCGGCCCCTGCGCCAGGTTGCGGA CGCCATCTTCCCGCGCCGTCGCCGCCATCT CCTCCTCCTCCTCCTCCACCACCTCCCCCTC ACCTGCCACTGAACCTTTCCCCCAGCTTGGA AGCCACGCCTTAAGGAAGCAGAGTCGGTCG GACACCCGCTCCTCCTCAGAGCAGCGGCCA CCAGAGTCAGGAAGGGGGGGTCCAATCACG TGATC	p001088	R	--
IM000897	GCTCAATTAGTTTATTTAAATTCAAAACAAAG CTAAAAGCCTGATGTGTCAGTTGCCTTCAGC AGAGCTGTTTGGGGCCCATTGTTAATGTTGT GAATTAAGTTCTGATGTAAGTAACCAAGCCA CTCCCCACACTCTTACTTGCAAGAGTTCCAG GCAGATGTTAAGGTCAACCCACCTGACTCTG ATC	p001089	D	--
IM000898	GATCACAGTGTTTATCTCAGCAACAGAAAGC AAATGAGGACACACCTGGGTCTCACTGATAT ACTTGGTGATATGTGTAGTTATTATGTCTCAC AGTAATTGGACAAGGAAGAGAGTTCATTGTT TTAGAATGTTGTAACTGGCATTGTTCTTCTCT CTCTTGTTTTCATAAAATCTCACAATATCTAC AGCTGTGAGGTCCAAGGGGCTCATTGGTGA TACCCACTCTTTCTACTTTGTGTGACCAACCT CTTTTGGATGTCAAGGGT	p001091	C	--
IM000899	GATCAGTTGCTATTGCTTGATTGATTGCGAG ACTTTCTTAACAAGAGTCTTTGTCTCCTCTCA CTCCCTAGCTTCATCTTAGAACTTAAACCCAC AGCCCAAATGAGTAGTTGTATGTCATATGCC TCGGCCAAAGCACGACTGAAAGGAAAAGAA AGGCAGACACTGGAGTGCAGGAAGAAGACA CAAGGCAAAGCCCAGAATTCAAAAGTAGAAG CACAGATTGTTTTCTTTGTTT	p001092	C	--
IM000900	GTACCCTGCATCCCCGGTGTGGCCTTGGAG TCTGATGCCAGCACTACAGAGCCAAGCCATA ATACAAACCAAATAGAATTAACAAGAGCTCC ATATGATC	p001093	D	--
IM000901	GATCACCTTCCTAGGATGAACGAAGAAGGAT GGCTGGAGGTTAGGGACCCAAGGGACTTCC CCCTAGAGCTGGCTGTGTACCCTAGGCATGT GTGACTGCAGCTGTACAAGCAGGGTATTCTG GGATTCACAGTCCTCAGGATAAGATGACACT ACAGATTCTAAGCTTTATACCCAACATGGTG GAACCCCATGGTCACACTCTTTCACAGATGG TCACTCCCATTGCCCGAAGCCCAGCCTTTAT CCAAG	p001094	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000902	GATCAATAACAGCAAAAGAAAAAAAGAAGTT TACTTTTCATGTAGCAATGTGGATAATTCCCA TCCAGAGAAACAAAACCAGTTCCAG	p001095	C	--
IM000903	GATCAGGGAAGATGTCACCTCCAACCCAGC CTAGACATGGTGCTGTGACCA	p001096	D	--
IM000904	GATCAAGGAGCAACCCAATAGCTTCTATTCC CCCCCTACTAAAATATGACCCACTGATGGAT TCTGGGGATGCACAGATGTTCTCAGAAGTTA CTGATGAACACACCATGCTCTAACAAATAGT ATCAAACCCACAGTCACAGATGGCCCTAGTT AAGCACAGTGCATCACAAAGCAAAGCAAAGA GCCTTGACTGTGGGAAAGGTACTTGTGGTGA GGACTAGTGGGGTATGAAAGAAATTAGAGAG GATGAAGGTAGTGATATTCAGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTAAGACTATTAAAGAACACCCTTTTTTAA AGAAAGGCTTTCTTGAGTGTCACC	p001097	R	--
IM000905	GGTTAATAAGCTAGATTATCGTGTATATATAA AGTGTGTATGTATACGTTTGGGGATTGTACA GAATGCACAGCGTAGTATTCAGGAAAAAGGA GACTGGGAAATTAATGTATAAATTAAAATCAG CTTTTAATTAGCTTAACACACACATACGAAGG CAAAAATGTAACGTTACTTTGATC	p001098	K	*Myc*
IM000906	GTGAACGACAGCAGAATCGGGTTGTACCTCA AAGCACTTACCTTTCCCAATACACCTGATC	p001099	D	--
IM000907	GATCAGTGACAATGTAGCTTTGCCTGGAAGG ATACTTGAGTC	p001100	D	--
IM000908	GATCAGCAAAATGGGACATCGAAGTTGAACC AAAGTCATAATAAAACATCCTGAGGTACATAA ACACTCTGTAATAGACTAATACAGTTCCTCCA GGCACCAACAGAAACCTTGACTACTTCCCTT GACTACTTCAGTCAAATCTTCTGATAAAACCA GACCCAACTTGGAAACGTCCATGTATACAAT G	p001101	D	--
IM000909	GATCATCTGCTTCTACCCCCAATTAAAAGAC GGACTAAGAACATAAAAAGAATCCAGGCACC TAGGTTTGCAGAAATCTAAAGGTTGAGTTCC TTT	p001102	D	--
IM000910	GATCACAAGTTATAGTTGAATAACAAGTCCT GTGTGTGTCTATGTATCCGTATATCATATTTT CTTTATCTGTTACTCTATTCATGGAAACTAGG TGGATGTGTTAACTTGGCTATTATGAGTTTTG CTGCTAT	p001103	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000911	CTACAATGGTTCAGGCTTTGGAATATCACTCT ATAGGCTGTCTGCCGGCCACCACCCTTCAG ACTGCCACTCACAGGTGCCCGTGAAGGCTG CCGAGAGGCAGTCCCCATCAGCCTGTCTCC TACACCCACACACTCTGTGTGGAGACCACAG GCGCCCAAAGGGTATGCTAGTCTCTGCTCTA CCGCGTACCCTCTCCTGAAGGCAGGCATTTC AGAGATTCCAGTTTCACCAGGAAGCTCAGAT C	p001104	C	--
IM000912	GATCTTTTCCCCCTTTGTAGTATCAGAGAGAA AAGCCATGGCATGCATGGCACATGCTAGGC AAACACTCAAGCATCCTACTCTGTGATGCAG TTTGAAACAAACTTTTTTTTTCTTTTTCTTTCT TTTTTTCTTTTTTCTTTTCTTTTTCTTTTTCTTT TCTTTTTTTTTTTTTTTGAGT	p001105	R	--
IM000913	GATCTCTCCCCATCCTCCTGTTGCCTCTTGT CTGTCATACCTCTACTACTCCATCAGTTTGCT GCCTCTGAGTCCCTCTTCTTCCTCTCCTATC CCTCCTCCCATCTTCCTCATCTCCAGGTCTC TCCAGGTCTTCCTTCTTCCCTCTTTTCTTCCC CTTTTCCTCTTTCCACTGTCTTGTATTCCCTT CCTTTCTCTGTTGGTCCCTTCCCTCGCACCT CTTTCCTCCTGTCCCTCCTTTTCATGTACCAT ATTTCTCTTCCTCTTTCTGTGTCTCCTCTTTC CTTCCTCCTTTACTTTCCTTCTAACCTTCCTC TTTCTCCTCCTCCGGCAAGCCTTTGCTT	p001106	A	*Gata1*
IM000914	GGTTGTTCCAGTTAAATTGGCTCTCTACAGG AACATGGCTTAGTTCTCCCTTAGCCTTTCATG ACCCTACACCTCAGACACTAGTCAAAGTCTA GCTTAATAAAGTGTTCAGGATGTTGGTGGAG GGGGGGAGATTGTTAATACAGATC	p001107	D	--
IM000915	GGACCACTTTAGTATGGGTCATATGTTCTAA CTTTCTTTCATTTTCTAATTCTTTCCATCTGCA TTGATTGTGCCCAGTTATCATTAGTGACTTAT TTTAGTAACTTAAGGGAAAGTTGTCTATGCTC TACTTAGTGTCGATTTAACTTACTCTCCAGAC ATGGGAGTGCTTATTTTTGTTTGCCTTACCTC ATCCAGGAGCTTGTAGATC	p001108	D	--
IM000916	GATCCGATTATGAAACCGGTTTTGAAC	p001109	D	--
IM000917	GATCTGTGGAATGCTATCCAGCTCTTCCAAC AAATAC	p001110	D	--
IM000918	TTAGTATCTGCATCTGACTCTTTCAGCTGTTC GTTAGGCCTTTCGGAGGGCAGCCATGCTAG GCTCCTGTCTGCAAGCACACCACAACATCAG TAACAGTCTCAGGGGTCTGAGCCTCCCCTTG AGCTAGATC	p001111	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000919	GATCTGTGGTAATGATTCTGTAAATACAGATA AACAACGTACACATGGGAATTGTTCCCTGTG TGAAAGTGTTCATCATAAGGTGTTTTTATTTT ATCTACAATATCTTTGGGTTTTTAG	p001112	D	--
IM000920	ACTGCCACATTCCCTAACACCTCATCAAAGA AAACAACACCACAGGTCTCAGGCTGCCACTC TAGACCTCCGAGTTGACTCTGGCTCCTGCTC TCTGCAAGCAAACACGCATCCCTCAAGTCTT CATGCTGGTTCTCTCAAGTCTTCATGCTGGC TCTCTGTAGTTCTGTAAGCTTACCCTTTCAGT GGTGATTTGGGGAGATC	p001113	D	--
IM000921	GATCTCCTGGCTTTGTAGATAAATGAAGAGA GTTCGTTACCAACTGAACTAAAGAGCGGCAC AGGAAATTAAAAAAAAACAAACAAACTGATAGT TAACTCAATTGAGTAAGTATGGAGTTTTGGG ACCAAGACATATTAGGCAAACAGACAGTTTA AGGCCTAG	p001114	D	--
IM000922	GTTCCTGTACTTTATCATGTCTTACCCCTACC TCCCTCCATTTTAATCATCTTTACTGGGATGT AATGCATTCCTTTGTCCATTCCAGGATGCTAT AACAAGATACCTTCAGCCTGTAAGCTATAGA ACAGTGTGGTCCTCAACCTTCCTAACTTTGT GACCCTATAATATAGATC	p001117	D	--
IM000923	CCANCGTGCCANACTCANAANGGAATTTTAT TCATAGATTCTNTCANACTGCTGTCCCACAT GTGTTCAAAANCAGGTAGGTCTTGTCANAT	p001119	D	--
IM000924	GATCTCATTGCACAGAAGAGTTAGAAGAAAG AAAGAAAAGCAGACTGGGAAAAATTTTTGCA GCGAGCATTCAGAGATTGAACATCTATCTAA CTTATGCAAAATTCCTATCAAAAGAAAAAAAA AGCTTCAACAGCTGGGTAAGTTAAAATGTAA CTATAAGGCAACACAAGGCAAAGTGTTGTTC TTTTTGCTTGTTTCCGAGATGAGCTCAATTAA AATATCAATAGCGACAACAATTCTGAGCTGG ACTAACAAAGAGTAGAACAATACTACCCAAC GCTTGTGGTTAGGTAACCTTACACAATATTTT CCTAATGCTATTCGGCAATAATTGTCAAGAAA A	p001121	D	--
IM000925	GATCTTTTCCTACAAGACTTCTGGGTGACCTT GCCAAGCCCAGCCACTGGCTGTGGTACCTC ACCAGGACACTCGGTGGACATTAGGTAGTG CTCCCCAAGTGCTAGGTGACAGTTTATGCTT CAAAGTGACTCCTGCAC	p001122	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000926	GTGCTGACGCGCCCTTGCATTTGGGAGAGC AGTCAAGCTATCTGTACCTTCACCGTAAGAC TACATTGTCACTGCTGGCTTCCCTCCTGTGC AAGGGACGCATTTGGGTCAGACTATGCATGA AACAGGACAACAAAGGTAGGGCCATTGGTA GATC	p001123	D	--
IM000927	GATCTCACTGAATATAAAAAGACATCAGTCC AAGGGTGGAAATTTAACCAAAATAATACAATT GTTGTTG	p001124	D	--
IM000928	GATCCTCCAGGAACTAGAGTTACAGACAATG CCCGCCTTGTATT	p001125	D	--
IM000929	GTGGCAGTGACTGTCCGTGTGGGAAACGTTT AGCAAGTCCGAGCGTGTTCGATC	p001127	K	*Nmyc*
IM000930	CAGGAGAGTGTCTCAAAAAGCAGCAAAGCA CCCAGCACCTTAGGGTGAAGGACCACTTCT GGAATGTATCCTCCCAGTTGCAAATGTACAC TGTCTCATTCACTCCTGTGACATACTTTGTTT GTGAATGCTAATATCACATAGTTCGATC	p001129	C	--
IM000931	CCAGCAGAGACCAAGCATCCAAAACATGAG CCCATTTCAGGCTTCAACCATAGCAGCTCCC ATCTCAATCCTGTTCACCCCCCACCCCACCC CCCGCTTCTCTATTTAAATCACCACTCTCAGT GACCAAAAAGATGCTCATGGCAAATGGACTC TTGGCTCTCTTTTACCTAATACTGAAGGTAAC AAGATAATCAACTGTTTCCTCTCCTTCCCGG GGACCTCATCATACAACATTCTCCCACATGA AATTATCACCACGTCCAATACCCACATCCTC CCCGTCCTGTAGAGAAACCACATGCCTAGCA GCAGTGGTTTCCCACCTCTGTGCTCCCTTCC ACCTCGATC	p001131	D	--
IM000932	GATCGCTGTGGTTGGTGTCTGTGTATATGCA CTGTACATACTAACCAGGTACACACATAAATA TTTAATATATAAAAAATAAAGTGCTTTCTAAG AGGCCCCTAGGCAGGGACGTTATAAAACATT TCACAAAGCAGCAAAACAAAATTGATACAAT CAAAAAAACAACACTATAACCAACATAGGTG AAAACAGCCAAACACATAATGTACAATCTGG TGTTCCAGGACAAACATCTGTCATATACATG GTATATACATACATACTTTTTCACTCAATAA	p001132	B	Mm.36692
IM000933	GATCGCTAAGTGTGCGCGGCCGCCGTCTGC AGAATGAATGGAGGGAATGAATGAGGGTGC GCGCGCCCGAGGCCCGGCTTGCGTCAGCC ATGCGTGCCCGGCATGGACACGGCCTGGCC TTCCTGGGAGGATGGGACCGGATGCAGTTA GTCCAGGCGTTCAGCATCCCAGGGCCCTTC CTCTGTTGCGTGGTCTGAGTAATCTGTCTCG CAGAAGATACCCT	p001133	B	Mm.151528

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000934	GGAGGTCTCTGTAGGTGCTTAGACTCACGTT ACAGTCATTCCAGAGGAGGGAGCTGCAGCT GCTAGTTTCTGTGCACACCGATC	p001136	D	--
IM000935	GATCGGCTGTCAAGACTGGGGAAGGGTCCT CCTAG	p001138	D	--
IM000936	AAGCAAGAGGTAATAAAATACATGTGGATGG ATGACTCAGGGGTTCAGAGCATACACCGATC	p001139	D	--
IM000937	GATCGGGGACCTTGCATAAAGGGGTCCAGG GCTCTCAGTCCTTGGGAAGG	p001140	B	AA709647
IM000938	GATCGTGATGACTTCATAACCATCACGTGTG AAAAGACTTAATGGCGCTGAATTCACATGAC ACTTAAAATGCACAAAGTAACAAATTTTATGT CACATGTATTAAACTACAGCTAAGTACATGG GGAAAAAGTTAGACTTAGAATAACTCATCCA GAGTCATATGGTAG	p001141	C	--
IM000939	GATCGAGGAGTAACCCAATAGCTCCTATTCC CCCCTTACTAAAATATGACCCACTGATGGAT TCTGGGGATGCACAGATGTTCTCAGAAGTTA CTGATGAACACACCATGCTCTAACAAACAGT ATCAAACCCACAGTCACAGATGGCCCTAGTT AAGCACAGTGCATCACAAAGCAAAGCAAAGA GCCTTGACTGTGGGAAAGGTACTTGTGGTGA GGACTAGTGGGGTATGAAAGAAATTAGAGAG GATGAAGGTAGTGATATTCAGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTAAGACTATTAAAGAACACCCTTTTTT AAAGAAAGGCTTTCTTGAGTGTCACC	p001144	R	--
IM000940	GATCGGGCCACATCTCAGACACTCCTATAGC TACAGAGAGATACCGTTTCCTGTTATCTTTGC AGACAACTTTATCTGTTACTCAGAGAAAACCT CCAGGTGCCCCTAAAGAAACTGGGCCCTAC ATCACATACCCATACCACACACATGCAACAT GCAAAACATACACACATACATAGACACACAC ACCACACGCACACAGACACATACAGACACAC ACACATACTATACATACAGACACATATGCTAC ACACATACAGACACACACAAGCACACATACT TCACACACAGAGACACACACACCACACACAC ACAC	p001149	R	--
IM000941	GCCTGCCTCTGCCTCTCGAGTGCTGGGAATA AAGGCGTGCTAGAGCCTTCACTTGGCTCTCT CTCTCTCTCTCTCTCTTTTAACCTCCTTTTTC CTTTAATGAGTTATTTATTTTTATTTTATGTGC ATTTGTGTTTTGCCTGTATCCGATC	p001151	R	--
IM000942	GCTTCAATATTCGAAAAGAATTAGTAAGAAAG GCTGTTCGATC	p001152	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000943	CTACCAGGAAGTCAGGGGTTTCCAGGAACC CACACTTGGCTTCCTCTGCACAGAGGGACCT CATACCAGTGAGATGGTGATATGCTCCCTTG TTCCTGAGCCTCAGTGGAAGCGACTTTCTAT GGATACTCCCTCCCTCGTGCCTCTCCTTCTT TCCCTCTCTGCTCTCCCCCCCCCCCCTCGCC CTCACGATC	p001154	D	--
IM000944	ATACACACCATCAGATATACCTCATTCTGATA TACCTACAGGTACACCAATCACACACACACA TTTACTCACATGTACATGCACACACCACATC GGTTAGAACCAAAGACCTCACACACACCCCT CACACATGTTTCATCTCCATTATCAGTGCCGA TC	p001155	D	--
IM000945	GATCGTCAGGTTATGAATGCCAT	p001156	C	--
IM000946	AGTTCTCAGAACCAGCTACTGTTTACACAGG GCCTCATGCAGCCTTGCTGTCCTCCATTCTG CAAGCACAGGATACACACCCCTGAAGGCCA GATTGTCAGGTCAGCCCGATC	p001157	C	--
IM000947	CTTCAAACCGGTCCTGCGAGGAGTCCACAA CCTCTGCCTGCCGATC	p001158	D	--
IM000948	GATCGAGGCCAGCCTGGTCTACAAAGTGAG TCCCAGGACAGCCAGGGCGATACAGAGAAA CCCTGTCTCAAAACAAACAAACAAACAAGAT TCCATTGAGGAACACCCAGATGGAGACATG GGTGTTCTCCATAGAAGGGTTAGGGGCTTCC ACACCGTTGACAC	p001159	B	Mm.81366
IM000949	GATCGGTGTGCTTTCTGCAGTTTCAGCGAGG ACTCTGGGCCCAAAATGTTTTAAAGCAGAAA ATTGGTAACACTAGAGATATTGTCAAAATACG ATTTCCTCTGGTTCAGAAATGGCGAGAGGGA GGGCTGGAAGGGTGGAGTGGGAAGGAATTG TCATCAAAGCATTGTTGATAC	p001160	B	AA408945
IM000950	CTGTCTCAGGCATGAAAACACTAAAAGATGA CCAATTTCAATAAAGATGACCTGAATGTCTAC TCAATTCCCACCATAAGGTCTACAAGATGTA AATGGGCCGATC	p001161	D	--
IM000951	GATCGTGGAAACAGAGCCTTGAATATAATGA AGAAACAGAGGGCAGGCAGCAGCCGCAGCA CAGCAGGGGCACTGTGAGCAGGCAGCAACA GGGGG	p001162	D	--
IM000952	CTCCCTACTACCTTCCCTTCCTGGACNTCCA CTGAGATGAGGCAGGATAAAGGGTCAAAAG AGACCTGACCTTCTCTGCCAAAGCCAGGGAT TTCTGGAAGAATAGAAATGGTTCTGGAATTC ACAGATGCAGTGGTCTAGGATC	p001163	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000953	GATCCATAGGTCTCTGCTTTCCCCATTCAGG GCTGGAGTTATAGATATCTGTCTATCACCCA GCTTTTATGTAGGTTCCAGG	p001164	D	--
IM000954	TATGTATCTACAAGCCAGAAGAGGGCATTGG ATC	p001166	D	--
IM000955	GATCCGAGTTCTCTCCGGCCACGTACCTTCA CATCCCATGCACCCTGGTATGTAAGAAGAGC CCAGCTCAC	p001167	D	--
IM000956	TCCCATAATATTTCCTCAGAAGGATC	p001168	D	--
IM000957	TATAGTTCTGCCTGTGGAGTGTGAGCAGAAA TGTGTATCGTTTCTGGGTCAGAGCTTTCAGG AACTGAGCATGACTGCTCTACAGTGTCTTTC TCCTTCTGCCTGCTGAAGCCCTAGGGGACAA TAGAACCACAGGATGAAAGGACTCGGGATC	p001169	D	--
IM000958	GATCCAATGGCAGCTAGCAGAGTCAGAGAG CCCTCACTCCAGTTAACTAGGGGACCCACAT GAAGTTCAAGCTACATATCTGCTACAAATGTT TGAGGGACCTCCTAGCTCCACGCCACATGC TCTTTGGTTGGTGGTTCAGTCTCTGTGAGCC CCACTGGGCTCAGGTTAGTTGACCTACAGTC TTCTTGTGGTATCCTTGACCCCTCTGACCCC AGAGTTTAACAATAGGCCTTCTGACTCTAGA AATCTACCTACATTTTTTCCACTTTAAATTCCT CGGCTCACATAATACCAATGAACT	p001171	R	--
IM000959	GATCCATCTGCACAGTCTGTCACCGGGGTCC AGCAAGTAGCAGCCTTTCTGCTGCTGTCTGT CAGACCCTCCAGGGAGGGAGAGCTTGTCTT CTGGCCTCCCAACAGGACCCTGCGTGACGA TGCAGGGACAGCAATGACAACTCATTCCAGA CTCCAGGTCCCTGGAGGAGCCTCCCACAAG GGAAAGAGACTACTTCACTGGTCCTGGGCC CCTCTTTGCGCGCCCCGCCCCCAGACTCAG CGTCTAGTGTTGCTGGGCTCCCCT	p001172	K	*Pim1*
IM000960	AGGGTAACAGGCTTAGTTTGGGGCCTTTCTG TTACAGGAAAACCATGAAATGTCCTGAAGTG CTCAACAAACAGGGAATATAGAAAATCATAAT GGTTCCTCCCTAGCACAAGGAAGCATGTTTA AAAATTGCAGCAAAATAAAAAAGAACAGATTC TTAAGATTGAGGGATTTTACGGGGTGGTACT TTTTCTTTCTCTTATAAACATTTATTTACTTTT GTTATTCAAGACAGGATC	p001173	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000961	GATCCAGCTGTTTGCTAACATACGTAAAGGT ATGGATGCTGAGAGAGTATCTATCGAAAGCG AAGGCACCCTCCCCAAATTCAAGAAAGCAGC TGTTTCTAGAACCAAAGACACCACCGCCGCC GCCGCCACCACCACCCGCGAGCGCCCGGA CCCTGTTACAGAGTGTC	p001174	C	--
IM000962	GATCCTGAAATTATCACATTTGAATCAAATCA TGCCCTGCCGAGGATAAATAACCCAAACGAC CGAGAAAACCGAGAAAAAGAACATTTACTGA CCATCCTTC	p001175	D	--
IM000963	GATCCAGTCCAGAGCAATGTTCACGTCTGTG ATGGTAT	p001176	D	--
IM000964	AAAGGTGCTCTCAATACTTAACAATCCATAAG CTTGTGCTCTCTTAGTCGTAAAGGTGGGGTC CATCAAAATCCCATGACACCACAGCGAGACC AAACTCCTTTTCTCTTACTCCGAATCACCCAT CCCATGTGGGAGACGAATAAGAACACAAACT ACATCTTCAGTGACATAGAGTAGCATCTGCA ACAGAGGAAGTGGATGGAGACCTTGTCTCT GGTCAAAGACAAAGCATGTGACAGCTGAGC CTGGCACTTCCTACTTGGGTCACAGCTCAAA CCCACCTGAACCAACAGCAGAGCCCCACAG GGATGGGACTCACATGTTTCCCTCTTGCCCT GGAGCTTCGTGCATGTTGTTAGAAGCTAACT GGCTAACACGCACGGGAACAGGCAATGTAG TTGGAGTATGAATCGAAGTCACTGGGCATGG TCCTCAGTCAGCCAGGATC	p001177	C	--
IM000965	CTAGACTAGTATGGCAGAACCTATCTTCTTCT AATCATTTAGATGAATACTCCACATGAGAGA GCCCTGAGAATATCTGTAAAAAGTAATCCAG GTTCTGTTACTTCTAGCTAATCTTATCTAGGT AATAATAGATAAGGAATCGGGATTCACGAAC ACAAATACCTGTACAAAGCATGTTGTCTCAC ACGGGACGAACACTGTTTCTGCTGTGCTTTA TAACGCTGGGACATACAAAACTAGACTCTGC CTAAGAAGTGTTTGGAAACATTTGGGTTAAAT TATAGTCAGATAAAACAACAACCATGAGTAAA TCGAAGAATATAAAACTAGGGATC	p001178	C	--
IM000966	TTTCCTGGACAATAATGTTTTCTTCATTAAATT TACACTTAGAGCATTGTCTTAATCCATGAATA ATTCCCAGCTCCTAGCTCATTACCTGTGACA CAGCAGGGATTCATACATTTATTGAATGAAT GGATGAGTGAATGAATAAAAGAATGAGCATA TCAAGAGGATC	p001179	D	--
IM000967	GATCCCTTCTGTCTTTGGTTATCTC	p001181	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000968	GATCCACCACTGAGCCACTTCTTCAGCCTGT GACTGTCATTCTTAATCATCCACACAGACTTC TCCTTGGCAGATTTTGCCCACCTCTTAAGAC TTTCACAAAGGTTTTTTTCTTCTGCAGGGCAC ATGAGAAAACAACTCTGTCATAAAGAAACCC AGGAAGAAAACCAGCAGAGGCAGGTGAGTT AAGCCTGTGGTGGACATTCCTTCTGGGGATG ACCAGATGGGAACAGTAATTCACAGAGGCA GAGGGGTCTGCAGTCACTCTGCATGCCACA TGTGTAACCCTTAAGAAGTGAGGAATGCTCT CAACAGGAAAAACACAGCAGCAAATGCTATG ATACCAAAGCCACAACTCCATGGGTCCCTGG AGCCTCTCGAACTAAGCTGCCAGCTAGGGA GCTAACACTAGCTTTGGATGAAACACAGCTC TGGTAGAGTT	p001182	C	--
IM000969	GCTGGGATTTGAACTCAGGGCCTTCAGAAGA GCAGTCTGCTCTTACCCGCTGAACCATCTCA CCAGCCCCCTTCCGTTCTTCCTTTCTTCCTTC CTTTTTTTTTTCCACATTGTTTTCAGACTGCA CCTTGTTTAGTAGTCTAGGCTGGCTTCCAATT CCCCAATGATTGAGCTATGGGTATACTCTCT TCACCTACTTTGATTTTTTGTTTGTTTATTTGT TTTTTTGTTTTTTTGAGACAGGGTTTCTCTGT ATAGCCCTGGCTGTTCTGGAACTCACTTTGT AGACCAGGCTGGCCTTGAACTCAGAAATCTG CCTGCCTCTGCCTTCAAAGTGCTGGGATC	p001183	R	--
IM000970	GCTTCATTTAATATACATCATTTACCAGAAAC CACAGACATCTTTGTACCAACATATAGTAATA TTAATCACAATAGCCATCACTCTTATGTAAGG ATGAGAAGACTCCCAGCTAATATGCTAATGT GTAGAAGATGCCAGATGGATC	p001184	D	--
IM000971	GATCCCTGCTTCTGTAAATCCGCAACGACAA TTGTTATCTTCTCCTTTTCTTTCTTTTATTTGT TTTATTCTATTTTATTTTTCAGATGAAAA	p001185	C	--
IM000972	GATCCTCCTGCCTCTGCCTCCTTCAGCAAAT CCTACCGGCGTGCGCCACCACTACCGGCGA AAAA	p001186	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000973	GATCCCCCTTTCTCTCTGTCTACGGCCTCTG TCCTGTGTTAGCTGTAGGCCTACTCTGTATG AACAGACCTCAGCGGAGGGGTTTGGACTTG GGCTTGTGTTTCTTAAGAGAATGGGGCTTCC ATGACTGTCCCTCTGTCCCTTTCATCCTAACC CTGCCTCCCGCTAACAGGCAGCCTGTATGTT TCTTGCACTGTTCCTTCCTCCTGACGGTCTG AGTCGTTTCCCTCAGAGACTGTTGCTGCTGC TTCAGCTTTCTCTCAGCTTCTCTCAGGGCTTC CGCTCTGGAGTTTCTCCTGCTTCTCTGTTTAC TTTTCAAAGCTCAGCCTCCATCTTCTGCACCT GCGGAGTCATCACTGATTCCCAGCTGTGGC CTGTCACCCTTCCCTTTCTTTCTTCCTCCTGT GCCACCACCATGCACCCTCCCCTTCTGTCTG TTGTGTTGTCCTAACCTTTCTTCTCCCCATGC ACCCTCCCCTTCTGTCTGTTGTGTTGTCCTAA CCTTTCTTCTCCTCTCTGTGCTCTGCAGGTTT TAGGGTCTCTGTATGATTTGTACCTGCATTTA TTTGAACCTCCACTCTTCTCTTTCCCTCTCTT ATC	p001187	D	--
IM000974	GATCCTGCAATACCTCTCCTGGGCATATATC TAGAAGATGTTTCAACTGGTAATAAGAACAC ATGCTCTACTATGTTCATAGCAGCCTTATTTA TAATAGCCAGAAGCTGGAAAGAATCCAGATG TCCCTCAACAGAGGAATGGGTACAGAAAATG TGATACATTTACAA	p001188	R	--
IM000975	ATCTAAACTATAATAGTTGCAGGGCTAGTTCA TTGTCAGGTGCGTGGCGAAAGAGTGCAAAT CCCGGGGGTTCTTTCTTCAGAATCAACGAGG CAATACACTTGAACATGTATGTTTTTGTAATC TGCGGGGCATCACCCGTCCTCCAGGATC	p001190	D	--
IM000976	GATCCCCCAGAAGTGATAGTTTAACAGTGAG GTGAATGCAAGCAATAAGCTACCTAAATCAT TAAAACTTCCTATTTTATTAGCATCTATTAGTT GCACACAGCAGTGATGGGTTTCATT	p001192	K	*Irf4*
IM000977	GGACCTCTGTACAAATGTCGGGAGATAAGG GAAGAAAAAGACGACAGAGATAGCAGTCAG GATGTAATGTGTACTAGATGAGTGGTTCAAG CAATAGGATGGAAAGGGCTTAGCAGGAGAG ATTTTTAAGGATGGAGGCAGTAGATTACATC TGGGAAATGTCACTGGAACTGGATC	p001194	D	--
IM000978	GATCACCAGGCTGGGCAGGCCACCTAAGGA AGTGGCACGGGCACGGGCACTTCCCCAGAG CACCCTCTGGGCACTCTGAGAGGGGCACAG ATGTACTGCACTAGGCTGGGCCCGGAGGAG	p001196	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000979	ATATAAAATATCGAACGTCCTCTGGCTTGTAA ATATCATGTTAACCTTCAAAGCGTTCGAAAG CGCAGGAAATCTGAGTCAACAGAATAGTATG TAAGTTTATTTTTATAGAACCTGCCTGAACTG CAAGGGAGGGGCGGGGCGTGGACCCAGGC CTGCCTGCCAATCTGCGCTGCCAGTGAACTA AGCCTGATC	p001197	D	--
IM000980	GATCAAGTCCTGGTCAGTACCAAGTTAAAAA AAAAACTATATAAAAGCTATATTAGGGGACA GCTGTGGCTTTTGTAGAAAAGAAGGTCCTGG TGCTATGACCTGCAGATGCCCATGTGGAAGT CTTCAGATGAAGACTTTCTCATGGAGTAAAC ATACTCTGTTGTTTGACCATGTGGACTTGGTT CAAAATGCCCATGGATGCTCCTTTGGGTACC AGGCTTCAGTGGGAGTCCCAAGCCCATGTC TTTATTTGAGCATGAGCAGTACTGATGCTTAC CTAGTCTTATTCTTTCCTTGCCCCCTGCCTG GACCGTCTCTGGTTACAAGGATGCTGCAGTG GGAAGCGGTATGACCGTTACCTTTATGGGAC TGAGACCAACTAAGGGGAGGCTGAGGAGGC TGCAGTGAAGTTATTGTTGGGACTGTGGGCT AAGATGGAAGATAACATGTTAACAAACTCAA GTGCGGAGGTCTCAGAAGTAAAATTGCCTG GTTAGTA	p001200	D	--
IM000981	GATCAATTGGTAACCAAGCCTTGAACTGAAG AGTCGTGAGGTGGGGGACTTTATAT	p001201	D	--
IM000982	GTATCTCCCACCTGGCTCAATATAGGCTCTT TTCAAAGGCTAAATTAAGACCAAGGACACAG AAGGGTAGCTCGCTGGGCAAACGTGATCCC TGCTGATAGTGTAG	p001202	D	--
IM000983	CTCTCGTGTGGAGATATTAAAGGTGTGAACC ACTAAGCCCTGATC	p001203	A	*Scp2*
IM000984	GATCAAGCAGAGGGGTAAAATAAGGGCAAG CTCAGTGTTAGACAAGCTCATAAGCCAAAGC TGTGAACTCTCCAACGCCT	p001205	D	--
IM000985	GATCACTTCAACATCAAGAAGTTACCCAGCC CCGGGAAGAAGTACATTTCCAGGAAGCAGT GTTTTCATTTTTTGAGTCTGCTCCCATCCCGT TTCTCTGCAGCTGGGTAAACTTGAAGCTGGG CTAGCCTCTGGGTAGAAGGCAGCTAATGACA ACTACCTTGCCTGTCCCACGGAGCCCGGAC AGAACCTGAGATAACACACCTAGCTTGCTGA GTAAAGGCAGGTTACTGTGTGAATGACTCTG AGCTGTTCCAGCTCTGCAGAGCAGGAAGTCT GACTGTGGAGATAAGAGATAT	p001207	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000986	GTCATGATTTGTAATTCCCTGTCCAACTCTCA TTGCTTAGGTCAAAATGGCTTAACTCCTAGC CTACTTCAGTGTAAAAGTCATGCGTAATGAT C	p001209	D	--
IM000987	GATCAGGCTGGCCTCAAACTCAGAAATCCAC CTGCCTCTGCCTCCTGAGTGCCGGGATTAAA GGCGTGCGCCACCACTGCCTGGCTGCTTTC TTTTTTTTCTTTTTCTTTGTGTGTGTGGGGTA GTGGTGGTGGTGGTGGTGTTCGAACC	p001210	A	*Hsc70t*
IM000988	ATGTGTGTGTGTGGCATGTGTGTGCCATTGT GTGTGTGTGAGTGAGTGTGTGTGTGTCTG TGTATGTTGTGGAACAGATTCCTGTGTATGTT TCCTTCTTCACACATGTTTTCAGAAGTGAAAC CAGGCTATGAAGACCGCCAGGCAGCTCTGC AAAGCAGTACTGAGAAGGTGGGACACTGCG GGGGTGAGAACAGTATGCATGATC	p001212	R	--
IM000989	GATCACACTCCATGAAGCTTCTCTTCTGCAA CAGGAAACAAATAGCAAGCAAAACCACTGGT AATCATTATGTGGTGTCTAACAGAGAGCGGT GACAGGGGTGGAAAACTGAATGACATTTAAA AGGAGCTGGAGATGTTGGTTTAAGGCGTGT GGGGGCAGCCTACAGCATGGAATTGGTCCA TAA	p001213	D	--
IM000990	AACCATCATGGTAGCTTCTGCTTCTCTCCAC GAAGATGGTTGTTTCCACAGTTGCCCTCTCT ACAGAGTGGTCCTGTATTAAGTCACAGGTGC CATCCTGGTGATC	p001214	D	--
IM000991	GATCTAACCACCCGTTTCCTGCCCGGTCTTA GATAGACCTCTTGGCCCCCACGCACCTAGA CAATGGAGTAGACAAGACTTCGAGGGGAAA GAGGCTTCCCAAGATGACCCAGCTCATTGG CTTGACTCCCAACGCCACCCACTTACACAGT GAGTATCTCTGGTCTTTGCTGT	p001215	A	*Farp*
IM000992	GATCTATGTCATCTTCCAGGACTCAGAGTTA AGAGAGTTACCAAGTGAGAGCTCTCATCACC TTCTGAAGCAGTTGAGAATTGGAACCCAGAA AGATGCACATGCACGGGCACACACACACCC ACGGGCACACACCCACCCACCCATGCAGAG AGAGAGAGAGAG	p001216	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000993	TAGGTTGTGCCTGGCCTGTGCAGGACATGC CTATGGGGTCTTCATCCCTCTCACTTACTCTA ATGTTCACTACTGACAAGCACTAGTAAGAAA GTAGGTGCCTGTAAGAGACTGGAGCAGCCT GCTGCTGACTTCAGCACCTGGGAGGCCTCA GTAGCAAAGCTTAGGGTTAGCAATCCTTGGG GCTGTGGCTGGCTGAGCTCTGGGGTACCGT TTAAGAGGAAAGCTGGAGTCCAGGTTCTCCA GGCCCTGGGTGCATCCCACAACCTCTCTCTC TCTCCTTTACCACTCGCAGCCTTGGCTAAGG ATGAGGACCGGGACCTGGAGTTATCTGAGA TC	p001217	A	*Snn*
IM000994	GATCTCTCCCCATCCTCCTGTTGCCTCTTGT CTGTCATACCTCTACTACTCCATCAGTTTGCT GCCTCTGAGTCCCTCTTCTTCCTCTCCTATC CCTCCTCCCATCTTCCTCATCTCCAGGTCTC TCCAGGTCTTCCTTCTTCCCTCTTTTCTTCCC CTTTTCCTCTTTCCACTGTCTTGTATTCCCTT CCTTTCTCTGTTGGTCCCTTCCCTCGCACCT CTTTCCTCCTGTCCCTCCTTTTCATGTACCAT ATTTCTCTTCCTCTTTCTGTGTCTC	p001218	A	*Gata1*
IM000995	GATCTTAGATGGCCAAATGTTGTGAACGTTT CCTAGATGTGTCGTGAGCACTCAGGGTTGA GAGCCCTGGTTATTTAGCAAGTGAAGTGGAT GTATACACAAGCAGAAGGCTGAAACTAGACC CCGGTCTCTAATCCTATATAAAAACCAACTCC AAATGGACAATAGAAATAAGTGCAAGACTAA CTCCAGGGTCACTGGAGGGATACAAAGGGA GATGC	p001219	D	--
IM000996	GAATGAATATATATATGGGACTAAATGCCAT GCCATAACCAAGAGAACTTAAAGAAGAAAGT GTTTAGTTATGCTTACTCTTTCAAAGAGTCCA GCTGCCAAAGGGATGCTGTCAGGAGTAGCT GAGAGCATACATCTGGACCCATTAACAAAGA AGGGATGCTTCCCCAGCAAGATC	p001220	D	--
IM000997	GGAGGAGGGGCACCTTCTCAGAGATC	p001221	D	--
IM000998	GATCTTAAAGCTAATAGGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGGTCAGTGG TAAAATTGTCTACCAAGCTCTAGGTTCACCC CTCACAGAGCCGGAGAGAAAAGGAGAAATC AACTCAAGTCAACCCAAACAAAACAAAGGAC TCAACA	p001222	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM000999	GATCTGTTCCCAAATCCTCAGTTACTCTCTG GGAAATGGCTTCTGTATGTACACATGTTCTCT AGCTATGTAATAAAAGACCTCTCTTCCTTGG CAAAACTTAACTCTACCTTAGAAAACTCTGAT GAGTACTAGAAAGATGACATGTTCCACAAAC GTCTTAAGTGATTCAGGGTTCACAACAAAGA AGGAGATGCTATATTGTCTTTCATGACATAG CGTCTAAGTCCCATAGCATAACTTCTATAACA CACAAGTGGGT	p001223	D	--
IM001000	ACACTAGCTTCGAAACTTCTTAGTTGTCTGTC CCTGAGCCCTTTGTGGTACTTCCTCCTCAGA GCCCAGCTCCAGCAGTCCCCTTAGCGGCTG TTTTTAGCAACCACACCCTCTGACTGTGGGT TTGCTCTGCAGTGGCTTTAAGGTTTGAATAC GAAATGCCTTCCACAAACAGACACTACAGAA TCTTAGGTGTCGAGACAATGGGCATTTGAGA AGGAATTGGAACCTTCAGATC	p001224	D	--
IM001001	GATCTAAAGGGAAACCCTTGTCTTTTTGAATC TGAGCCAGCACAATATTGTATTTCCTTCAATA CGTGGTGAATGTTGTATTAGCAACAATAAAT GGAAGCAGGGAATCTCTCATCTCATGAGTGA TATTTACAATGTCTGTCTGGAAACAAACGGC TAATCAAGTTAGTCACTTACTGTTCTTTAGAA AACACAGTACTTTGAAATGCATACCTAGCAG AGAATATAAAGTATTTACTGTTGGACTAGACT GGGCCCCCGGGTGTGAGGG	p001225	D	--
IM001002	GATCTATCTCATCCTGTTATAGCCGGAAACA TGATAGCAGGATTGGGCAACTCTCCAGTCCC TTTCTCTTGGGTAAAGTCTGAAAGCAAATCG CCCGGACCCATCTCCTGTCTCTGCAGCCTGT CCCAGTTGCCTCTGCCACTCACTAACTTCAC TCCTTAATTTAAAAAGCCAGCACATTTATTGA CCGTCT	p001226	C	--
IM001003	GCATGTCTCCAGACTCTCAGCTGCTTCCTGT CTGCTCCTGCTGGATGCTTCATGAAGATGGA GTGAAGCAGTGGTCAGCTTGTCTGTCTCAGC TGTTCTATGTGCATGTGTGCACTTGCTGGAG CTTATGTGCACCACAAGCACGCAGGTGCACA CAGAAGCCAGAGATC	p001227	D	--
IM001004	GATCGAACACGCTCGGACTTGCTAAACGTTT CCCACACGGACAGTCACTGCCAA	p001229	K	*Nmyc*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001005	GATCGTGAGTTCAAGACCAGCCTAAAATACA CAGTGAGCCTCTGTCTTTAAGAAACAAACAA ACAACAACAGCAAAAACAAAAATATTGCTCAA GACCCAATGTTCCTCGGACTATTTATAGGAA TCAGAGTTGCTGTTCTTCTCAGGGCATGCCA GTTAATTTGAAAGACAAGGTGTAGAGGCAAA GGAAAAGTGATTTTACTTGGATAACCACCTC ATGGAGCAGTCAGGGGAACTCTAGCCTCAA AGCTCTTGCAGAAGTTATAT	p001230	D	--
IM001006	GTAGAAGCTTTTTAGAAATACGTTTCTTATCT ATCTATCCATCTATCCACCCATTATCATCTAT TATCTATATTTAACATCTATCTAAGTATCTGTT TATCTATCTACCTGTCTATACCTACCTATCTA CCTACCTACCTATAGCGATC	p001233	R	--
IM001007	GATCGTGCATGCATGGGTGTGTTTTGGGGA GAGGTTCTGT	p001235	D	--
IM001008	GTTACTATTCATCTGAGGTTCTCTTTTGTTGT ATTTGAACAGGAGGAAGGAACCAGGAGCTC AAGGATGTAGCTGGAAATGCTATAAAACTGG GATGCCCTAGAGAATCACACGGACAATCCTG CTAACCCATGGATTGTACACTCCAATATACAA GATAACATGTTTGTGCAGGCATGCCACCATG ATGTTCGATC	p001239	D	--
IM001009	GATCGACCGCAGATGAGGTCTATGCAGGAA AAACGATGTCTGGAATTTTATTAAAATTGCTC AGCAACTCACTGCCACGTATACTTGGAGAGC CACTTAGGGAT	p001240	K	*Myc*
IM001010	CCAAGTATACGTGGCAGTGAGTTGCTGAGCA ATTTTAATAAAATTCCAGACATCGTTTTTCCT GCATAGACCTCATCTGCGGTCGATC	p001242	K	*Myc*
IM001011	GATCGTAGAGAGATGGACCCAAATATCAGCC AGAGAATTAGACCAGAAAATGGAACCAAAGT ACCTGTCAGTCCAAGGATGTAGTGGCACTAC	p001244	D	--
IM001012	GTCCCCAAATGTAAACAAAACTATCAAAAGA AATTGGGCATGCCAGAATTTTGTTCTTCACAT TAAGGGAATTCTGAAATTGAAATCTTGCTAAG GGAAGGGTGGCTTGAGAATATTAACAGAATC CTAGGTTGAAGGAGCAGGAATAGAGGATC	p001246	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001013	CAGCTAGCCCATGGAGCTGCTGGGACACGA GGCCGCAGGCTGAGCATAATGGGGAAGAGA TGGCAGATTCATTCACCCACTTGAGGAGACC ACAATTAGTCAGAGGCATGCTGGGCCTGGT CAGAGTGCTCAAATAAACATTCACAGGACCA AAGTAATAAGCATTGGTGTTACAGAGATAAAT CCTTTAGCAGGGACACGGGACCCCAGAAAA CCGGAAGGACATCGTTCCCATCATGAGAACA AGGACAGCAAACAGTCACTGAGGGTATACTA CTGACCAGTTCCAACAGGGATGGTCAGAAGT TGAACGCTGGATATATCATGAGCTCTGACCT AAATATTCTGAGTATTCCCCATGTTTGAATGG ACTGAATACTCACATTTTCTAAATGCTGAATA CTGAATTTTCATAGCAACCATCATAAGGCAT GGTGGCAGAATAATATCTCTCACTCAGAAAG CAAACTATTCTAAGTTGGGGATC	p001247	D	--
IM001014	GATCCCGTGGGGACTGAGCCTGCAGCTCAG TGGTAAAGCAGATGTCTAACGTGGTACAGGG TCCCAGATGAGATGACACAAGTACCTGTCAG TACTCCGGGAACACTGGGTGGGACTTTTATA TGTTTATTTGTATTCTTAA	p001248	D	--
IM001015	AGTCCATTGTGTACTGAGAGAGGAGTTAGGT TTAGAAAGCCTTCCTCAGATGTCCCTCAAAG AAGCTGCTACAACTGCCCTCATCCCAAGTTG CCAAGGATC	p001249	D	--
IM001016	AGATTGCGTGAGTTCTGATGCATGCTGGCCA TGATGTGAGGCAGGGGCAGTGGTTGGATTC GGAGTCAGAAAACTTTCCCGTCTACTGCCGT AATTCCCAGCTAAATTCCTATCCTCGTTGTAG CTGTTGGTGAGGATC	p001250	D	--
IM001017	GATCCTTCCGAATCTGCCATTTATTGAATATT TAAAACACACCTCACTGCAGACTAAACACAT TGCAAGCACTGGGAGCAGAGGTGGCTAGTG AGCACCACTCTAGATGGTCCTTC	p001253	D	--
IM001018	GATCCTCCTGCGTCTACCTTCGGGTGGGATT GCAGGCATGCACCACCATGCTTGGCTTTGTG TGGTACTGGACATTGAACCCAGAACTCTTTG AGCACTAGGCAAGCACATCCTGAACACCAGT AAAACATTTTCAAAGAGAAAAGAAAATTTAAA ACATACACCTATCTACATCCATTTCCACCATG TTAGTAAACCAGGGACATTTTGAAGTGTGGT CTTTATAAAAACACCCGGGTGCTTATCTCCC ACGCTCT	p001254	R	--
IM001019	CCAGCGGTGCTCACTACTGCATGTAACCAGC TCCAGGATC	p001255	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001020	GTCTCAAAGAACAAAAATAAAAGAGGAAATT AGTAACGAGTCCTGAGAGATAGAAGAGTATT CAGCCTGGGACCAGAGCTCTGTCTTACAGTC TTGCCATTCTGTGGGGCCTGGGACACAGCAT CCTTGGTCTTTAGAATGCCATAGGCCTCCTG AGGGAGCCTTTTCTGTAGGCACTTCTCCCAC ATTCTTGGATGGATGCGATTTATTCTGTGTCA GGGGACTAGGGTGCTGGATGTGTGGGTCGA ATGACTGTTGTTCTGTCACTTGGGAATTTGG GATAGGAGAATTCTGAGTGCAAGGCTAGTCT GCACTTGAACGTACATATCGGGTTTTAAGCC AGCCTCTGAGCTACCACAGTGAGACTCTCTC TTAACTAAAATCAACATAAATAGTCTTAGTAT GGAGAGGTTAGGGGATC	p001257	C	--
IM001021	CGTTTTCCTCGGAAAATGTGAAAAGAAGAAG CACGAGACGAAACCCCCTCGAGAATGAGAA AATTAAATCTAGAACCCAAATGGCGTCCAAC AAGAACATTAGCTCTTGAAAATGAATATTGCG CCTGCGCAGCCACCGCCCGGCCAGCTGCTC AACTGCAGCTAGAGCCCGACCCCAAGCGAT C	p001260	C	--
IM001022	GTGTCACATGTATGAACAGCATCACATGGTA TGAATGGTATCATATGGTATGACGTGAATGT GTGCACCGGCACTGATC	p001262	D	--
IM001023	ATACCACCCACTCCCTTAAGAAATGATC	p001263	D	--
IM001024	GACTGATATTAGTAGGTTGTTCTCTAAGGGC CGTGAAATTTTTAGCTAGAAGTTCTTGCTTTC ATTAACAGTGCCAAGTATGAGTTCCATCTCAT GGGGTGGGTCTTGAATACAATCAGAAGGTG GTGAGTTATCGCCATAACATCTGTGCCGCTA TTGTACCAGTGGACATAGTTGCCAGGCAGG CCATTACTGTAGCTCTTAGGTCATTCCTGAA GCTCTCTGGGGTCTGTTAGGTGAGACTGATG ATAACTCTTCTCTTCCGTTAGTGTACACAGCA CCTTTTAGCACTATGAAAGCGAGGCAGTATT GATC	p001264	D	--
IM001025	GTTCCGATGTTTGTATCTCGTTTGAATTATCC ATCAGTTGATTAAGTTGATGGTCATCTAGGCT GATTCCCCTACATGGCCATCTCAATATTGCTT CTTTAATAAGACCTGGACAATTAACAGCACC AGTTGACATGCCAACTTGGATTGGGGGAGG GGTCTTAAAGGGCCCCGCCCTTAGATGAAG AGCTATACGCAATTAATGACTGTCAGAAAGG GAGAATGGCTTTCCCAGAGATGAACCCCCTA ATGGATTACCCAGTACCAAGTGATC	p001265	A	*Rad52*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001026	ATTCAACCTATGGGGCCGTTAGACCCCTGGT CTTGGGTGGGGTGGATATGTTATTCTTTTTTG CTGTGGTGGCAGCAATTTTGTTTGCTTTCTTG TTTTTTGATACAGTTTCTCGTCATGTATTCCT GGTTGCCTGGAATTCACTTCTATAGACCAGA ATGGCCTCAAATTTACAGTGAACCCCCTGCC TCTGGCTTCAGATTACTGGAATTACAGGTTT GTGCTATCTCACTAGTTGGTGTGTGATC	p001266	C	--
IM001027	GATCAAGTCCCCAGTTAAATGCTTTCTTTGAT AGGTTGCCTTGGTGATGTCTCTTCATAGTAAT AGAAAAGCAACCTAAGACAAGAGGAGAGAG TGGGTTTAAGAACGAGGAGAGAGAGGAACT CAGAGGGTCCTGGAGGTCCCGGGAA	p001267	C	--
IM001028	CTCACACATACATTCATACATACACACACATA TATACATACACACACTTGCATACACACAGCA CACACTCACACACAGAGACACACAGACACAC AGACACACACACAGAGGAACCCAAAGGATT GGAAGAATAATTTCCCGTGCTCAGCGGGAAA GTTTACCAGAAAGACAAGTGGTCATGTGGGA TGATC	p001270	C	--
IM001029	GATCATCACCAGTGTAGTGTTGGCTTTAACG GTGCACGCCTTTAATCCTAGCACTTGGGAGG TGGAAACAGGTAGGTGTGCTTACTTCAGTGA GTGAATTCCAGGCCAGGCAGGGATACAGAG TGAGAACCTGTTATCTAAATAAATAAATAAA	p001271	C	--
IM001030	CACCCACGGCTTGCTTCTTTTCTCTATGTGTA ATTGAAGCACATACCCGGTGGGAGCCATGTA AAGCCTGTGTCCATGATC	p001272	D	--
IM001031	GATCATGTGTTAATGAAACTGTCAGGGGTTG GGTAAGATGGCTCAGTAGGTAAAGGCACTTG CCTCCTAGCCTGGAGACCTGAGGTTCCTCCT GGGGCCCACAGGGAAAAGGAGATAACCAGC TCTCTGTCCTCTGACCTCCTGGGCCCCTCCC TCACAAACAAACAAACAAACACACACACAAA CGACCAGACCATTTCCCACAGTAGCTGTGGT GCGTTACACTGTAACGGGCACCATGTGAGG GTTTGGGCTTTATCACATCTCCGCTAGTCATA CTTGGTGTTTCCTGCGTCTTGCTTACAGTTGT TCTAATGGGTGGGCGGTGATATCGAATTGTG GTTTTAGCATGTATTTCCTGTGCTCTGCTAAG ACCACTTACAATTACAG	p001274	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001032	CCTTAACGCTCCCTTGATGTCCACTCCCGTT TTCTCTGCAGCGATTTATTGCTTAGTCTATCT ATAAGGTGTATGCAAGCTGCAAAGTCAAGTA TTTCCTTTGTACTTGAGCAAGTCTCCTAAGTA TTATGCTTCATAACGTTGTGATATGCTTGAGC AAATTTGAGTCTATTTCATAATTAAGCCACTG TTCTGATAAAAGACCCTAGAGTGCTATATCT GATC	p001277	D	--
IM001033	AAAAGAGTGTCAGATGTCAGAACTGACTAGC TGGGCTGACACTGAGGAATGAAGGTTGGGG ATATATGCACCTCCTGAAAACAGGAAGCCTT TTGTTGGTTGATC	p001279	D	--
IM001034	GATCAACCTTAGTACACAGCAGAGTGTTTTC TGGGAAGCTCATGGAGACCCACTTTTGTCAT CCCATAGAGGTTACTACAAATCTGAGCATGA GAATAACTACTTGCTGTTTAATACAAAGAACC ATTAGCAGTCAATGCCCCAAGTTCTAAGGGC ACAGACTTCATACGAGAAAAAAAAACAAAGC AAAACAAAAACTATCACATGCTACTATCTGTA CTGGGGAATGCATACAATTTTGTAGGTAT	p001281	D	--
IM001035	GATCAGTAGAGAGCAGAGGGGTCTATGAGG GAGGTAGAGCAGCCTGGGAGGCCTGAGGAA GGAGGGACAAGGGCAGAGTCTTGGTCACTC TTTGGTCTAATTGCCTTCAGAAGGCTTGCAG ACTCTGGTTTGGAGTTCCAGGTGGGTGGCT G	p001282	C	--
IM001036	CAAGTAGGGTTTGTGTGTGTGTGTGTGTGTG TAGCCAGTGTCTTTCTCAATCACTCTCCACCT TAATATTTTTTTTTGAGACAGAATCTCTCACT GAACCTGTATGCTGTCAATTTGTCATGGCTG ACTGGCCAAGGAGCCCGAAGAATTTATCTCT ATGCTCAATCCAACCCCCAGATC	p001285	R	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001037	GATCACATGGACCGATTGCCGCGGGACATC GCACAGGAGCGTATGCACCACGATATCGTG CGGCTTTTGGATGAGTACAACCTGGTGCGCA GCCCACAGCTGCATGGCACTGCCCTGGGTG GCACACCCACTCTGTCTCCCACACTCTGCTC GCCCAATGGCTACCTGGGCAATCTCAAGTCC GCCACACAGGGCAAGAAGGCCCGCAAGCCC AGCACCAAAGGGCTGGCTTGTGGTAGCAAG GAAGCTAAGGACCTCAAGGCACGGAGGAAG AAGTCCCAGGATGGCAAGGGCTGCCTGTTG GACAGCTCGAGCATGCTGTCGCCTGTGGAC TCCCTCGAGTCACCCCATGGCTACTTGTCAG ATGTGGCCTCGCCACCCCTCCTCCCCTCCC CATTCCAGCAGTCTCCATCCATGCCTCTCAG CCACCTGCCTGGTATGCCTGACACTCACCTG GGCATCAGCCACTTGAATGTGGCAGCCAAG CCTGAGATGGCAGCACTGGCTGGAGGTAGC CGGTTGGCCTTTGAGCCACCCCCGCCACGC CTCTCCCACCTGCCTGTAGCCTCCAGTGCCA GCACAGTGCTGAGTACCAATGGC	p001289	K	*Notch1*
IM001038	GATCTAACTCAGGCTGTTCAGCTTGGCCAAC AAGCTCAAATATCCATTCCGCTGTCACATCG GGCCCCATGTGATGCTTTATATACTAAATAG AACAAGCAAATTGATACTAGATGGGACAGTC TGCTTACCCAGTTTGGTGTTTGGTGGGGGAG GTGAGACATATCCCACAGTCCCAGAGCAACT GTCACTGCAGGGTCCCAGGGGAGGAGCCAG GTGTGAAGCTGGCAGTGTGTGAGGTACCCT GGGGAAAATGAATGGTTACT	p001292	D	--
IM001039	AGGCCTGGTAGTGACCAGCAAGTACTGAAC GCTCGCTCTATGCCAGACACAGACCCTCTTC TTCCTTCGTCTTATCCTATTATCCATACTGAA CAGACAAGGAAATGAAGGCTTAGATGAGTCA CCCGACTTGCTGAGATC	p001293	D	--
IM001040	AGTGGGGCCTGAAAATCACATCTGGGCAAA CCCTGAGGCCTGCCAAGTCCTCATCAGAGG GATGCCCTCTTCATCCCAGGTGCTTTCTGAC TATAAAATAAGGTGAATACTACCTCCCCTGA GGTTACACCTCCAGGGTTAAGCTGGTTAGAG AACCCAGGGACACACTGGGAAACAGCCCAC AACAGCAGGAGCTGGAGCACTCACCCACGG ATGTCCATGGGGTCCAGCTCCCTGCGCTGG CGCCCACCACTGGTACCAGGAAGCAGTGAA GAGGTGGCCCAACCCACTGTAGAGCGCTTG ATTGGGTGCTTGCGCAGCTCTTCCTCGTGGC CATAGTACGGGAAGATC	p001297	K	*Notch1*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001041	AGTGGAACCAGATTCCTCCTACGCTTTGCAC TCCACTTTCGTTTTCTCTTCTGTACCATTCTA ATGGAGGCCAGAGTAGCAACTGTATAGACAA ATCAAATCGTTTACTCTTCCAGTCTTGCCCCT TAACAGTCTTTCCTTTGTTCTTCCTCTTAGCC TCATTTTCTCCTTTCTCAGATC	p001298	B	AI604147
IM001042	GATCTTCTGCTTCATCTGAGTAGGCTTAGAC TGGTTTGTATTATTATTATTATTACTTGTTGTT GTTGTTATTTTGGTGGGAGTAGTAGTAGCAG TAGGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTAGATGTCACAGCATGTATATGGAGG CCAGAGAACAGCTTCTAGCGGTTGCTTCTCT CCTTCCTTCCACTGTGGTCCAGGGAATAGAA CTCAGGTCATCAGGCTGGGCAGCTGTCACC TTTAATGCTCTGAGTTATCTCACCAACGTTAA TAAAAGGCTTTTCAAACAGCAGTTTGGGCTG GGCCTGGTTGTGCAGACCTGGAATTGCAGC TTCTTAGGATGCTGAGGCAGGAGGACTGGA AGCTCAAGTTGTGTCGGGGAAACTTAGTAAG TCCCTATTCTCGTCCCGCACGCCCCCAAAAA GCCAAGACCAAGACCAAGCAGTTTGGTACA GCAGAAAAAGCACGAGAGTCTCCTCCTCCTC CTGCTCCTCTTTAATGATGCAGAACCC	p001300	R	--
IM001043	GATCTGTGCATTATTCTGTTGGAAATGTGACA AGATTCTGTTGAGAATCTCATACTCTATGAAC TCTTAAAAAAAAAAAGGTTTCTGCTGTTTTGAG ACAAAATTACTTATAAAGGTTTATGATGTAGT TAAGGCCCTGAATGTCCCCCAAAGACATGTG TGTTGAGGGTTTGGTCTCCACTCCGTGGTCT TTTGGGAGGTGTTTTATGTTAGCTGGTGAGG CATAGTGGCAGGGGAGGAGAGTTGGGTCAT AGTCCTTTTGAAGAGGCTATTCAGGCTCTGG TGCCTAA	p001303	D	--
IM001044	GATCTGACTGTGATAGGAGGGTCCTGGGGC CACCCTGACATAGGCCTGGTCTATGAATGCT CTCATGGACTGGGCCTGTTTGTCA	p001305	D	--
IM001045	CTGCCTCTCTCCCTGGTCCCTCTCTGAGGTT CTGGACCCTCAAAAGGCCCTTTCCCACCCCA GCCTTCAGGCCTGTAACCCAGCCTCGGTTTC TCTCCCATTGCCAAAGCACAATGGCTGTTAT AATTAACGGATTATCTCAGCGCGACAGCTGC GCCCCTTTGAAAATTAGGTTGAATAACAAGA TC	p001306	C	--
IM001046	GATCTTGGACCACCACGTCAAGCCTCTTGTA CATTTCTTTGAAAAACAAAGCTTGGTTCCCCC TAGTCACCACGGTGAAAAAAACCCAGGACAG TAAAGGTCCCAA	p001307	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001047	TTAGTACCTCTGGTGGAATCACCATGCCTGA CCTAAAGCTTTACTACAGAGCAATTGTGATAA AAACTGCATGGTACTGGTATAGTGACAGACA AGTAGACCAATGGAATAGAATTGAAGACCCA GAAATGAACCCACATACCTATGGTCATCGAT C	p001308	R	--
IM001048	GATCGCACCGATTGCCAGTATAGTACCTAGA GTGTCAAGTTGGCCTCTCAGGGAAGAGAGA ACATGTATTAGGGTAAGACGCAAGCCCCAGT AAAAACATGTGAG	p001311	D	--
IM001049	GATCGCTTCACCAAGTGTGAACTGTTGGTAG GGACAGAGCAGACCACAAGCCCCTCTTTGC ATTTACATGGGGGCGTCCTAGTGTAGGTGGC TAGGGATGGTGGACAGGAGAGGAGGGAAGA CAGTATCACATAAGAACAATAGTGGAGGGCA GGGGAGGAAGCCTTCTCATGGCTGGGGTGA AGTCACTTCCGTAGCCAGAGCTGACTGAGAA TATCACTGCTTTCCTAGTAAGGAAACACCGG AAGTCGGAAGATGATAAACGCGAAACTCACT ACATCATAGACACCATTCTGTCTTCATCAACA GAGAAATTTATAA	p001313	D	--
IM001050	GATCGTCCACTTCTGTGTTTGCTAGGCCCCG GCATAGTCTCACAGGAGAGAGCTATATCTGG GTCCTTTCAGCAAAATCTTGCTAGTGTATGCA ATGGTG	p001316	R	--
IM001051	AGGGTACAGCGAAGCTTGAAAAAAGCAAGG AGTGCTCTGGGACCGGGAGTGATGGAGAAA GTCTGAAGCCCCTTTGCACACCCCTACAATG GGTTTGCGCCAAGAGAGGCGCCGGCAACTC TACGCGGCGTGGGGCTCTCCCCAGCGCTCT AGGTTCTACTGTGCTGAGCCACACTAGTTTC TCTCCCTAGACCTGAAGAGACCCCAGAAGTC TGAGAGTCCCTTTGGTTCTCCATCTCTCACC ACCCCCCACTCTCGTGCTTTAACTCTGAGGA GGGCCACTCAAGTTCATTCATAAGAACAAGG GCTTTGCTCTTAAAGGAGCCGCATACCGAAA GCGTTTGTGTGACTGAGGGTTCACATGCACA GAGCTCCGCGTGTCTCGACATCCTCTCTCTC CGATC	p001317	D	--
IM001052	ATCTCAGGAAACTCCTAGCAGCTTTAGTACG CATCGTGCTGTTTCCAGCTGTCGGTATTTTA CACAGGTTTTGAGCGATC	p001318	D	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001053	CCTTCAGGATTACTTTGGATGATTCATTAGAG AATCTTGTCTTTAGACTATAAAGCACTTGTTG AACAAGGTTACAATGTAGCAAGCAACCTTGT TTTGGAATGTATTTTGCTACATTGTGCTCTTC CCTGGTCTGGTGCTTTCATTTCACATATTTTG CTCTTAATAGAAGTAGGGTTCAGTGCTGGGG ATTTCATTTGCTGTTTTCTCCATTGACCTCTT GAGCTGAAGTTATTCTTATTAGAAAGTCAGG GTAGGCGATC	p001319	D	--
IM001054	CCAGCAGGCAGCGAGACGCATTTTCGCGTG GCGGTGGTGAGCTCTCGTTTCGAGGGGATG AGCCCCTTGCAACGGCACCGGTTGGTCCAC GAGGCACTGTCGGAGGAGCTGGCTGGACCG GTACATGCCCTGGCCATCCAGGCGAAGACC CCCGCCCAGTGGAGAGAAAACCCACAGTTG GACATTAGTCCCCCCTGCCTAGGTGGGAGC AAGAAAACTCGAGGGACCTCTTAATAAATAC CTGGATTGGGAGAACGATC	p001321	B	Mm.104531
IM001055	GTTTTTCCTGCATAGACCTCATCTGCGGTCG ATC	p001322	K	*Myc*
IM001056	AAACTAGGAAAGGGTATAGCATTTGAAATGT AAATAAAGAAAATATCTAATTTAAAAACAAAA AAGAAAGACAAAGGAAAATTAAAAAAAAAAAA AAAAGAAACAAAAGCCACTGCAGGACTGCCC AACAGTCTACTGAAAACTGTGAGCCTTATTC CTAGATGAGCCTCTGATGCCTCCACTTACAA GCTACCTTCACTCCTCCATCTATCTCCTTTTG TTATGTCCCGCGATC	p001324	R	--
IM001057	GATCGGACTCGAAGAGCAGAAGAAACAAAA CTCAAAGCAGGGATTAGGTCAAAATTAAAAA GGGTTTGCACACAAAAGGAAACCATCCGAAG AGACAACCTACAAAGTGAGAGAAACTTGTTT TGAAC	p001325	D	--
IM001058	GTCTGAGAAATTGTCTTTAATGTAGTGACTGT GGAGCCTTGCAGGGATACCCACGATGGGGG TGTCATTCATATGTCACTGCACCTGGAAGAC CGATC	p001326	D	--
IM001059	GATCGCACAGCCTGCTTTCTCAACAGTAGGT AGGACCAACAGCCTAGGTGGCACCACCCAC AGTGAGCTGGGCCTTCCACATCAATCATCAA TCAAGAAAAATAGCACAAAACCCTTTCCCGA AGGCCAATCTGCTGGAGGCATTTTCTCAGTT GAGATTCCCTCTTCCCAAATGACTGCATAAA ACTTGTGTCATGTTGACATGAAACTAGCCAG CACAGGGTGT	p001327	K	*Pvt1*

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001060	GATCGGGTAATTTAGTAATAGTTCATGATATT CATTACTCGGCGTAAATCAGGAAAAACATTT CTAGATGAATGTGGTATTCTCAGTGCACAGT TTGTTTAGTTTAGAAAACAAAT	p001328	D	--
IM001061	GATCGAGGAGGGGAAGTCCTTCCTTCCTTCC TTCCTTCCTTC	p001329	R	--
IM001062	GATCGGGGGTTCAAGGTCCTCCTCGGGGTA CCTATTAGGAGGGCAGCCCAGGCTACGTGA GACTCTGTCTCAATAAAAATAAAAATAAAAAG CTGGGTGGTGGTGGCGCACGC	p001330	R	--
IM001063	GATCGACCTGCCTCTGTCTTAAGCAAGAAGG GAGATAGATATGCATAGTATTTAGTGTAATGA AAGTTACGTTGTATTACGCTGAGGTTTATCAC A	p001331	D	--
IM001064	ATCTAAGTAGTATAATGTTTAAGACGATC	p001332	D	--
IM001065	GATCGTCGTCTAACTTAGCTGGCTTTATAGT GATATAACAAAATATTAGAGGATGCTTTGGTT GAAAAAGAAGTTTATTTGCATCACAGTTC	p001333	D	--
IM001066	GATCGAACACGCTCGGACTTGCTAAACGTTT CC	p001334	K	*Nmyc*
IM001067	GATCGTCATCATTTTTATAACAGTAGTGAGGA GATGTCCCCTGGGGCCGCCCTGGCTCTGGA GAGGGAAGCCACATGCTCCAAGGGGCTATG GTGAGGACCACAGCCTTTACATTTGGCTT	p001338	D	--
IM001068	GATCATGCACTGTCTGGGATAGTGATGGGCT GTGTCCTTTGTTGGCCAAGAGGAAGTGGCAA AAGGCAAAGTTGCTGTTGGCTCCAGGAGTCA GTCTGGGGACGGGGCTGAGATGCTGTGGGA CAGACTCTGGAAAGGGCAG	p001339	D	--
IM001069	GATCGTGGCCACTGAGAGACCTTCTTCTGGC CACCAGATGCACACAGCTGCATGAACATCTG CATACACATTTAACACATACAAAGTTGAAGAG AAGCACGTGTGTCTTGTGGTCTGACCACTTC CTGGGCACCACCAAGCTGCTCTGACAACGG ATTCCCACTGGGTTCGGCCATCTTGCTTCCT CCCCTCAGAGTTTGCCCATGTCCTCTGTCTT TTCATAGCCACAGCCTTGCCCAAGATAAGAT ACATCCAACTGTACAGTGCTCCAT	p001341	D	--
IM001070	GATCGTACCAGGAGCTCCAAGCGTACCCCT GATGCTACAACCTCATTCCTGAGCCTTGATT CTGTGGACTCTAG	p001342	C	--

MUTATION	SEQUENCE	CLONE	CLASS.	GENE
IM001071	GAACAAGGAAGGAAATAAAGAATAAAGGACA TCTGACACTACCAAAGTTAGGTCAGGATGTG TCTTACAGATGGCCACTCAACAGCCTATAGA AAGCACCGCACAGACCAGCACGGTCTTTTTC TCCCAGGTGTCTCTGAGGTACTGCTTTCTTT CCAGGGATC	p001344	D	--
IM001072	GATCCCGAGTCCTTTCATCCTGTGGTTCTATT GTCCCCTAGGGCTTCAGCAGGCAGAAGGAG AAAGACACTGTAGAGCAGCCCCCAAA	p001345	D	--
IM001073	GATCCTGGGATTTTCTGGGCAATTGGAGGCC ACAATTTAGATAGTTTCCGGAATCGATGTCC CTTAAAGACCAGCGCCTGGACTCTACTGAGT AAACTCCCATTTCAACTTCCTCCTCTTCCTCT ATTTGAACAACGTGTATCATTAAATTATAAAA TTGTTGTTGTTGTTGTTGTTTCAAAAATTA ACTTTATTGGGGGAGGGGCAGTTGCCCGAG GACAACTTGTGAGAACCAGGTTTTGCCTTCC ACACTTAGGGGTCCCTGGAATGGAACTTATG T	p001346	R	--
IM001074	AGAGGAGAAATGGGGGTGCGAGAGGACAAA GTCTGTGCCCCACAGCGCTGGGGCCAGAGC CCAGGAGGGCCTCATGGGAGAGGTTGCCTG AAGGCAGTAAGAGAGGCAGAGGATGCTTGG GCCAGAGAGGTTCCCCACAATTGCTTGGATC	p001348	D	--
IM001075	GATCCCAAACAACTGGAACAGGGGTTATCCC AAAAGCTGTTGCCTG	p001349	D	--
IM001076	GATCCAACTCCTCTTCACAAAGAGACTATGT GCAGGATGGAGAAGAAGATGTATCCAAGCAT ATCCTGTGAAATTTATGTCAATGCTGTGAAAT TTGTCCCAGCACTCACAATCCAGATTTCTGC TTTTTAGGTGGCTTTTTCTATTTCATTTCTTCT GGCTTCATAGAAGTTTGAGGTGACATTTTTAA GACCTGTGCCACTAAAATTTCAGACCCTATTT G	p001350	B	Mm.123802
IM001077	GATCGGTTAGTTTGACCAGCCATACTATAAC TTTAGTGCAACCCTTTACTTGGTGGGTGGTA CTAGGAATTAAACCCAGGACCTTCACATATA CTACTATCATTGAGTTACATTTCTAGCCCTTT TAACCAATTTCCCTTTAACCCTTTTTATCCTTT G	p001351	D	--
IM001078	CTCAAGATTCTGTTGTCTGAGAATCTCTCCCT CTGCTTGGGGACCCATTTATAATGAGGTGAT ACTTCATCTGAAGTAATGGCCAGGCCACGGT GTGAGACTCTTGAATGTCACATGCTGGATC	p001352	D	--

Breast

TABLE 2

SAGRES #	SEQUENCE	SEQ ID #	CLASS.	GENE
IM000127	CATGTGAGACTTGTTAATTTAGATTTATT CTGTAGTGTTTTTGATATGAGTATAAATA AGACAATTAAATTCTATATTAGAAAGTGG CTTTTTACATTGAATATGCTTTCAGGATA TGCGTGAGAATTTGGCGATGTGTAATC	1	D	--
IM000128	CCTTACTGCAGAGATGACTCGGCCAACGG CTNCGAGCTCCTGACCACTTCCTCAGGTT TGGTTTTGTTAGTTTTTTCTCACAGCAAT GGGAAGCATAATCAATACAACTTCCCAGA ATGCGACCTGTGACAAGACCAATGAGCAG ACTCAAGGCTGGGCACATAAAAGCACCAA AAAAAAAAAAAAATTCCCTTGCAATTATT GTTCATG	2	D	--
IM000129	GCTGCTCATCACCAAAGGAAGTCAGGACT GGAACTCAAGCAGGTCAGGAAGCAGGAGT TGATGCAGAGGCCATG	3	R	--
IM000130	CATGGCAAGATGGAGACTTTGTCTACCAG GGCCACTCCAAGCACCCAGCTG	4	K	*Fgf3/Fgf4*
IM000131	GTGAAAGGGCAGAAATAATTCCTGAAGGT TGTCCTCTGCCTTCTACATG	5	C	--
IM000132	CATGACTATGTTTCTTTTAGGTATATCTG AATAGTATGGATCTAAATGATGAAGTTAC ACCATTTTCTACAAATGGGCACAGAACAC AGGGCATAGATACAAATGGCAAGGTGAAC CCAGATCTCTGTGCTTATCTGCAATATAA CAACACTAAGAAATATTAGGTCTCTCTGT GGTTTTCCTTAAATCTA	6	D	--
IM000133	GTATTTCCTGTCAGAGGAAAAGAGTTTTC AAAAAACTTTTAAAATTTTTATTTGTTAG CCTGGACCAGTTTCATAGCAACCTGTCAT CCATATCCTCAGATTCACTTATGAGTTTG TCTGCCCATTAAGATCTTTAAAATGGTTC TAACAGCTTACTTCATTGTTCATTAGTAA AGGGTTTATATCTACACTTTGATATTTGC TTACTCCATACATG	7	D	--
IM000134	CATGAGATGAAAAAGAACCTTTTGGACTT GAATTTTGTTGCTTCAAATGCGTACTGCA GTTGATGGAAATT	8	D	--
IM000135	AGGGTCCCTTCAACTTCCTCAGAGCCAAG GCTGACTTACTACCGTTCCCCAAGATCTC ATG	9	D	--
IM000136	CATGCCTCTGGAAAGTACCTTAAACATAG AATCCCCTCCCTAGTG	10	K	*Myb*

IM000137	CCAGATCCCATTAACAGATGGTTGTGAGT CACCATG	11	K	*Wnt1*
IM000138	CATGACTTCTTTCATTTCTTCTGTGTGTC TGTCTTCCTGTGTTTGCCTGCCCCTCTCT TTCTCTTCTAACAGCCCCCTTGAACCAAC TGATGCGCTGTCTTCGGAAATACCAATCC CGGACTCCCAGCCCCCTCCTCCATTCTGT CCCCAGT	12	K	*Braf*
IM000139	CATGGGAATGTAATGTATTAATGAATATT ATATAAAAGAGGCTAAATAGCTTGGCTTT AATTTCTCACTTTGCCTACTCAATTGAGA AGTTTATGGATCACCAAAAGT	13	D	--
IM000140	CATGTCCTTATTCTAGGAAGCCCCCTTTT TTACCCCTGCCTCTGAGAGAAACAG	14	D	--
IM000141	CATGAACACCCAAATCCATATGAATACAC ACATAAAATATTTTATTTTCTCTATAATT TATGCCCACC	15	D	--
IM000142	GAAAGCATTGAAATATACTGGCCTTATTA ATGGCACATG	16	D	--
IM000143	CATGTGCACACACCCCACAAATGACCTCA GATGTCAGTGGTACTGAAACTGAGAAACT GATGATAGAGCCAGTAAAAATACTGAAAG TGCCTGTTTTGAGAGTTTATATTTTACAA TACTTTAATATCTAACTACACACACATAC ACCTGAAAAGGGCTCAGAATACACAGGCC TGAGATGGCTCTCAAGAACCAGCCTC	17	D	--
IM000144	GGCCTTCCACTGCTCAAAGCTCAGACTGC AGAAAAGGTTGATAGCCTCCCAGGGGCAA TGACACCCTTTCTGCTTGAGCTTCCCCCC CCCCCCTCTCAGGATGTAGTCATG	18	K	*Wnt1*
IM000145	CATGCCAGTCCACATCTGCTTCTATGACA AATGCCACATCCCAACGACAAACTCACTC ATTCTTCCTGTATCAATTTACGCATACAC ATAATACTTTTGCTCAAGGTACATTCATA TTTCCGGCAAACAGACAGCTATAG	19	D	--
IM000146	CATGTCACTCACTTGGAGAAAGAGTTCTA ATTATTTATCACGGCATTTTTCACAACTA TAGAAATAAAGTTAATTTCTTTGGAAATA AAGTTGAAGTTGTAATTTCCAGATGGGCT CAGGTTGCTGTT	20	B	Mm.6055 2
IM000147	CTCCTCCTAAAAGAAAAAAGGAAAAGAAA AGTTAAACCTGCAACAGCATCAGCAGAGC TCACCCCTCCTCACCTGCAGCCCTGGTTG CCTCTCTTCCTTTCATG	21	D	--

IM000148	GAAAACACTGTTCTGGGTTCAGGGGTTAC TTAGCCTTGGAATCAGAGTCTACCCAGAG TCTACCTGCTTCTACCCAAAGCAGGTGGA AGAAGCTGCCCAGGACGGGGCTCAGAGTC TACATTTGAACTCCCTGTGCCAAGAAGTC TGGATAGAGTATAGTGTCTGTATATTCTA AACTTTCTGGAACAACCCCTGCTTACAAT ACTCTTTCCAACTCTCAGGCCATG	22	D	--
IM000149	ACCTCTGTGCCAGCTTCTCGGACATTTAA CAACTCTGGATCATG	23	K	*Fgf3/Fgf4*
IM000150	CTGGCAGTAACACACTTAAACTGCTAGCA CCTGGGAAGTGGAAATAAGATCAGGAGCT CAATCAAGGTCATCCTCAGCTAAACAAGA CCCCCCCCCAAAAAAAAAGAAGAAGATGGC CTAGAAAGAGAACTCAGCAGCTGCTGATC TTACAGATGACTAGAGTTTGGTTACCAGC ACCCACATG	24	D	--
IM000151	CATGCCTGGTCCCTGCTGAGTGCAGAAGA GGGTGTCAGATTCCTTGGAACTGGAGTTA TATACAGTCGTGTGTCACTGTGGGTGCTG GGAACTGAACCTGTGTCCTCTGCAAAAAC AAGAGGTCTTGGTTGTTGTTGTTTTGTTT GAAACAGGGTTTCTCTATGTGGCCCTG	25	C	--
IM000152	GCAGGAGCCCTTGTGCAGGCCACAACCTG CACAGCTGTACAAGGCCTGCCTGACTGCC TGAACAGATGTGTGGGATCTTGCCCCCCT TGTGCAGGCGTACAGATGCAGACTGCTCA GAGACACACATG	26	K	*Fgf3/Fgf4*
IM000153	CATGGGCTAGACCTACACTGAGTTGTGCT AAAGAAGTGAC	27	D	--
IM000154	CATGTCCTCCACAGCTGAGCACCCTCAAC TGTCTCCCAGGGCCTCTGTTCTATCCAGG GTCTGCAGGGTCTCTGCCCCACGCCTAGC CCCTGAGAAATCTTAAGCAGTCTGAAAAC TACGCCACTGAACTGCTAAAACCCTGGAG TCACTGATGGAA	28	K	*Fgf3/Fgf4*
IM000155	TAGTGCTAGACTCTGCCTTTTCACCTGGC ATAGATTCACCTTTTTCCAGATATCCAGG GCACTTGCAAAGAAGCCAGGCATCATCAG GGGTTTGGACTTCCAGCCAGAGTCTGAGT TGTCACTTGAATGTGCTGCATTTTGTTGG ATTCAGCCCCAGTCTCCCGACTCTTTGTG AGTTTAGGATAATAATCACAACAGCACCC CTTCTTATTTGATGGCTAATAAGCTCTAG GCCAGTGTCTTAGCTCCATTCATG	29	D	--

IM000156	CATGTATTCTGAGAGTAGAATTTATACCC AGAGAATACCTAAGAAGTGAACTGACGCC GGGCGTGGTGCCGCACGCCTTTAATCCCA GCAGTTGGGAGGCAGAGGCAGGTGAATTT CTGAGTTTGAGGCCAGCCTGGTCTACAAA GTGAGTTCCAGGACAGCCAGG	30	D	--
IM000157	GCCTGGTGTGGTAGCTCACACCTTTAATC CCAGCACTCATCTCTGTGATTTGCTAGGC CAGCCTGGTATACACAGTGAGTTACACAT CAGCCATG	31	K	*Fgf3/Fgf4*
IM000158	CGACATCCAACTTCTGGAAGGAGAGATGG GAAGGGGCATTTGGGGTGCTAGGAAGGGA TGGGAGGTGTCCCTAGAGCAGTGCTCATG	32	K	*Wnt3*
IM000159	CATGAAATAATGCCTTCAGAACTGCATTA GAAATCACAAATAGCCCTGAATGCCCTCT AGATGCTTTTCTTGAGAACAATTATGTGT TAAAGTCCTAAGGCCCTTGTCAGCCCACC ATATGGAAAGGGAGAACTAACTGAAATGG GAGTT	33	D	--
IM000160	ACTGACAAGAATAGAGAGAAGTTCAGTCA TG	34	D	--
IM000161	GTGTCCTGCTCCTGTCTGGGTCAAGGTCA TAAAAGATGAGCCAAGGCTGACTTCAGTG CCCACCTGGGGAGACTGATGTCTTCACAG GAATGCTCACCTGGAAGGTGTCCTCTGGG TGCATCTGTGTCACATTCGGTATAGAAGG AAGAATGCCAACAATACTCTAAAAATATT AGAGGCCTTGAGAGTCCTCAGTGGTATTC CACCAACATCAAAGCTGCATCGTAATATG CCAGCCTGGTCCTCACCTTTCCTGCCCTT CCCAGGAAAACATCAGCCTTTAACCTCAG CCCATAGGGGACATG	35	D	--
IM000162	AGGATCTTATAAAAATAACAGTGACCCAA AACATAATTTTTGCCATCAAGAATCTCAA AATCAAGTCTCATCCAAGTCTACTCTTCT TTATTGTATCTTAAACACACACACACGCA CACATCACACAAGCACACACACAAGAATT CACACACATACATG	36	K	*Wnt1*
IM000163	CATGGTATTCTGATGATAGTACCAACATA CTGCTGCAGCTAGCTGTATCTGGAAATCC CAACCTCAGCCAAGTATTTGTGGTTGAAA TAACCTATACTTCTCACATCAAACAC	37	D	--
IM000164	ACTGTGACCTGAGCACTTCTTGTCTTATC AATAGCTCACGTGCCCAGGCCGGGTGACC AGTCTCTAGGATGTTCTCCATG	38	K	*Fgf3/Fgf4*

IM000165	CATGCACACAAACTGGCCCTGAACTTTTG ACTTCCAGGCCTCTGCCTCTCTGCGCGCA CACACACACTCGCACTCCTGTATATGAAG CGTATATGTGTTTCTCTGGGAACTGTTTT TATCAGGTGAAGCACTTCCTTTGTTCTTG CTACCCACCTCCAGGGCTCCAGGATCTCC AGACAGCCAACCCTAAGACAGGCCCAGCT TCCTCTGTATCTCTGTGATGAGAACCTTG GCATAGAGCTGCCCTCACCCTCGGGATAG GGCTTATGTTCCCCGGAACGAGCCAGGCA CCTCAACAGCTCCTGGGGAGGAATAGGGG ACT	39	K	*Fgf3/Fgf4*
IM000166	CATGGCACTATGAAGGAAATGAAGATACA AAAGATTTCCCATACAAAGGGTCAACTGT TCAATTTGGCATTTATT	40	D	--
IM000167	CATGATAGAAGACCACGTCTGGGATGGGG TAAGGGTTTCTCAGAGTACCTTGCCCTGG GGCCACATCCTAAATCTACAACAAAGCT	41	D	--
IM000168	CATGCAAAAGAATTCCAAATGATTTTACA GATCTTAGCCCTCTAAGAGATAGATATAG CACAAGTCCTGACTCCTGAGGTAGGTACA CACTGACTTCCTTCCACAAGCACTGCCTC AGCCCGGAGATGAAGGTCACATCAATAGA GACAAGTCAGGTTAACCGTGAGCAACCTC AAGACAAGGAGGAGCACAGCATAGGTCGG TGGAAGTGTTTGCATAAGCCTAAGGCCTG GGCCCAGTCACCAGCATTGCAGAGGAAAA GGAAAAACAGATAGTAGGTGCCTTGGTGT GT	42	C	--
IM000169	CATGCAGTTTACCAATCTTTTTCCACTCT TTAAAAAGACAAAAAATATTAGAATACTG GGCTGAGGAATGGCTCATCAGTTAAGAGC GCTGCTCTTTTGAAGGACTCCCGTTCTGT TCCAAATGCCCACCTGGAGGCTATCCTGT AGCTAGAGGT	43	D	--
IM000170	AGGAAGTGCTGAATAGAGAGGTTTGGGGA GAGCCCAACAATCTGACCTATTTATACCC TGCCAGGCCCTGCCCATG	44	K	*S100a4*
IM000171	CATGGTGCTGGAGGATCATCCATCCTGAC ATTCTGGGA	45	R	--
IM000172	CTTTAACCCATTTATGGTGTGACCAGAAA CCACAGATCTTACCTAGGCTTCAGACACA TCACCCGAGGAAAGCTCCATTAAAATCCT CATTCATG	46	D	--
IM000173	CATGTATTCATAAGTGGATATTAGCAAGA AAGTACAGGCTAAT	47	D	--

IM000174	CCTCTGGAAGTCAAGTGCAGCTTTGCTTA TTTGTTTAAGCCATCCACCATCCAGTTAT TAGATCTGAATTCATCTTTTAGGGTCAGC TTTGTTGTAGATTTAGGATGTGGCCCCAG GGCAAGGTACTCTGAGAAACCCTTACCCC ATCCCAGACGTGGTCTTCTATCATG	48	D	--
IM000175	GTTTTCTTTCTTTTTTTTTTAAAAGAAAC AGTCTCAAGTAGCCCAGGCAGTCCCTAAA CTTATTATATAGCCCAGGACAGTCTTGAA TTCCTGAACCTCCCTCCTCTACCTCGTAG TCCTGAGACCGATTGCATG	49	D	--
IM000176	AGAGACCCAGAAATACCAAGGTGATTTCC AACTGCCTGACCTGGGAGGCAAGCATG	50	D	--
IM000177	CATGTAAGATCTTCACTTTTCCAGTGTCT GTTTGTGCTGCCTTCAAACTGTTGACCTG ATGTAAAAATGTTTGCATCAGCTCAGGTG TATAGAATTGGACTGATTCCAGGAGAGTC AAATATACAGAATATCTAGTGTCCAAGAT	51	D	--
IM000178	CATGCTAATGGAGTTTATTCTTAGGACTG CCTCCTGCATCCATTGATTGACTTAAATA TGTGCACACT	52	D	--
IM000179	ACTAGGTGACTGTCTCAGGGTCTCACTGT GTAGTCCTGGCCTAGAACTCTCTATGGAG ACCAGCCAGACCTCACACTCAGATCCAGA TGCCTCAGCCTCCTAAGTGCTGGGATTAA AGGCCAGTCCCACCATACCCTGCCCCTGT TTCTGACATTTGAACCCCTCCTTTAGACA GTAGGGAAACTGAGGCCCTGAGATATGAC ACTTTTAGGGGCATG	53	R	--
IM000180	AAACTTCAGAAAGCGGGGGCTACCAAGGA GACTCAATTAAGATCTCTCCTCGATCTTG AAACCATCCCCAGCCCTTCGCAAAGCACA TTTGACGGACAGGGTTCTCTTGTCTTGGG CAACACATCCCGGCTACGCTCTGCAGGGT GAAGCTGTTAAGAACGTTCCATG	54	D	--
IM000181	GATAAGCCTCTACAAAGCTGGAGAGGGCA GTCCAAAGAAACTTGAAAAGATTAAAAGA CAGTGCCTAAGGACACAAACGTTTTTCCA TAAAGAGCCTATGACATATTTTACTGCTG CTAATGAAACTGACCTTGAAGGAACAAGT GTTTAGGGTTAGCCTAAACTTTGGAATTG GTGAAGGCAATGTGTCAGCTAGACAAATT AGAGAAAGAACTCAACAGATGAGTCAATG AATTGTTCTAAACTAGCTTGACTTAGGAT TTTCAGCACAGGAACAAAAGCACATACTG TCCCTCTGGTTGGCATG	55	D	--

IM000182	CATGGAAAATGATAAAAACCACACTCTAG AACATATTAGAGGAGTGAGTTACCCTGAA GAACACATTCGTTGGAAACGGATATTGTG TAA	56	R	--
IM000183	CATGCCCGGCTCTATTACTATTTCTTTCT TTCTTTTTTGTTTCAGGATCCAGTTTCCT TGATAAATTTTTCTTGAATGTTGTTGTTG TTTTTTCTTTTGCTGAGTTTTTCTTCAAT ACTGCTGCTTTTTCTCTCCAGGTTCAGGA TGAGA	57	D	--
IM000184	CATGCTGTCACTAAGCTGTGCTCTTCCAA GGAGATGAAGAGACTAGCTGGTACCCTTG CTATGCCAGGCTTTCTTCTTGTTTATACA CACCTAATG	58	D	--
IM000185	CATGATCTAATCTGAACTTGTATCCCAAC CCTTTATAAACAAGTGAATGTGTAATCTA AACTAGTATAAGCTCTTGAATAATAGCTG AGTGAATTGCCTTTGATACACGTTTCCAA ATTAGTAGCC	59	D	--
IM000186	GTCAACCACAGCAGTACTGTTACTTTCTG TGGGGGAGACGTCTCCCCTCCTCATG	60	D	--
IM000187	GGCAGTGAGCTTGCCCACTCTGCTACAGGACCTCGG TGACCCACTATATACAGCCCTCTTCACTACGGCTCA CAATCGGAGTTTAAGACCCAGTGAAGTAAACCCAGC AGGACCCTTTACAAAGCCAGGACATG	61	D	--
IM000188	CTTGTCCAAACCAGCTTAGTCAACAGCCT CCTATCTGGGCTCCATCTTACCCTCCTCA TCTAGCTGATGAATGTACCTGCCTTCTGT TCCCTTCCTCCTGGTCTGAGCTGAGCCTT CTTGGGACTGAGAGCCTTCATCCACCACA GGCAGACTATCTTTAGATCATCATAGCCC CAGGTCTTCATTGCAGTGCAAAAGTGCAG ACCTTACATTTCCATTTTTATGCTCCCTT TGTAACGGCTCCTTACCGGACTGCAGCAT AAGTGGCTGAGTATCCAATCACAATAGAA CACTTAGTTGTTTGCTTGTCTAACTCTCT CAGTTACACCATTGAGTATGTTACACAGG GCTGCTTTGTAGCTGTCACTGAGGCCACA AGGCAAGGGGACTAAGGCAGGACTCAGAT GAGCCTGTTTTTACTTCCCGTTGTCCCTT TCACTTTGGGTTGAGCATG	62	D	--
IM000189	ATATAGACTCAATCAAGGTATTATTCTGG AACAAACAACTAGTAACAAAAATAGTGCA ATTGCAAGTATGATAACACAAGGCAGCCT TTACCAGCTTTGTCGGAAGGAAATTGTTC TTTGAAATCTGAATTCCAGAGAAAAAGTC AAATGTAAACTAGAAGTGTTTGCATG	63	D	--

IM000190	CATGTATGTGCGTGTGTGAGTGCATCAAC ACAAGTGCATAGATGCGTGTGTGTTTGTG TGTCTGACTGTTTAAGTAGGTGGCATCTG TCCTAGTCCTGACTTTTGATAAGTCTACA CGTTTGATAAGAGGATCTCTCTCACCACT CAGGTTCCTCCCCCCACCTCCACCCCAGT ACACAGCCATAACTATAAACTCCCCACGC AGATGAAGCCCCTCTGATCCCATTTTAGG GACATAACACCCCCCTCCCAGACTGAGCT AATGCCTTGGACCCTCCAAAACTGATCTG AACCCTCTCTGACCCTGCCCTCCTCCCAG CACAGGGCAA	64	B	BF163810
IM000191	CATGATTTTCAGTTTTCTTGCCATATTCC ACGTCCTACAGTGGACATTTCTAAATTTT CCACCTTTTTCAGTTTTCGTCGCCATATT TCACGTCCTAAAGTG	65	R	--
IM000192	AAGTATGTCTGCTATGAGTCAAAAGTCTT ATTTTTGCATCACATG	66	D	--
IM000193	CATGCCGCAGTGGCCAGCAGCCCTGGTTC CAGCATTCTCAGAGATAACAAGGAGCCAG TGACCCTTTCTTCAAGCACCAAAGAAAAG CTAACCGACCCCACAAAGACCTGAGTATG AATGGTTTCTGCAGCTAAGGCACTTCCTT TGAGGTCAGCGCAGTTCGGGGCTGAGAAA AGAGCTTGCCCTGGCTTAGAGCCTTTCTC TGGCTCACTGTCCCAGCCAGGACCCATCC ATCAGCCCACAGTGGGGTGGCATAGTGCA ATCCTAGAGAGATGTTCAAAGGGACATAT C	67	K	*Fgf3/Fgf4*
IM000194	ATTCTCTGGGTTTTCCTGTGGTGCTCTGG ACCCCTCTCGCTCCTACAATCCTTCCTCC CCATCTTCCACTGCTCTGCCTAGTATTTG GCTGTGAGTCTCTGCATCTGTTTCCATG	68	R	--
IM000195	CATGCCCCTCTCGACCCTGGGAGCATTCA CCATCTTTATAAACTGATTCTTTCTGGGA AGATGATG	69	D	--
IM000196	CATGAAACACACTTTTAACTTTCCACATA CTTTTTAAAAGTGTACCTTCCCATTTTTT CGCCCCTAGACCCAAATTGGATGTTTCTG GCTCCCTCTCGTTCGTAGCTTTCCTGTGA TGTAGAAACCTCTTAGAAACCACACC	70	D	--
IM000197	GTTTCCCACGGTGGAAGAGGCAAACAAGA TCCCTTGGGCCTGCCTTCTTGTGGCACTA ATCTTACTCATG	71	D	--

IM000198	ATGTGGTGTTTAAATGAGAATGTGGCCCA TAGGCTCATATGTTGAATACNTATTTTCC AGTACTTGGAAGTATTTGGGGAGGACTAG AGGTGTGACTTTTTGAAGGGGGTGTATTA TGTGGATGTACTAAGAACCTTTAAATCCC TCTGACCATG	72	D	--
IM000199	GCATCATAGTTGTACCATG	73	D	--
IM000200	CATGGGTTAACAGTGGGCCCTAAACTTGA ACTAGAAAACTTAAAGATG	74	K	*Wnt1*
IM000201	CAAGTCTGTCTGTCTCCTTACTAGCCTTT TGCTGTTCTGACTCTCAAATGGTTCCTTA ATTGGCCATTTGTCCCCTAAATTAGGGGC GATTAGGATCAACACTCAAGCAATGTTCC AGATGGGGTCTGACGTTCCTCACTGGGGT CCCAGGGCTCCTCTGACTTGGTCACAGAA AGGTCAGCCCTCTGACCTGGCATAGATGT CTGGATGACCTCTGACCTCAGCTCATAAA CCTGACTGTGGAGATTGAGACTGGAGGGA CTCAGGGCAGTGGCTCACTGGACAGTGCC AGGGTGTGCAGTGGTAGGCAGACTTCTAT GTCAGGTCCTCCTGTGCCTCCATG	75	K	*Fgf3/Fgf4*
IM000202	GCACATATCTGAGCATCTCAAGAAGCTGA AGCAGCAGAATCATCCGCTCGAAGCAAGT GTAAGCCAATAAGAAGACTCTGTCTCAGA AGAAACTGAAACGAAGAGAGACAAAAACA ACTTCTGGGGCTGAAGAGATGGCTCAGCA ATTAAAAGCCCATTCTGCTCACTCAGAGG CCCTCTGTGAGCTGTCTCCAGATGTTTAA CAAGCACAGCTAACATTTGGCATG	76	R	--
IM000203	CACATTCATTAAAGAGACTTTATTAAAGC TCAAAGCACATATTGCACCTCACACAATA ATTGTGGGAGACTTCAACACACCACTTTC ATCAATGGACAGATCATG	77	R	--
IM000204	GGGGAGAGGCTTCAATGAGCCCCCTCACA TTTGCATTTAAATAGCAGCATCAAGCGCT TCGCGTGCCACACACCAGTGGGCTCCCAG ATGTCAAGCCGGAGTCAGTCAGATGGCCA GTGCCCAGCTGTCCTCCCTATGTCGTGCC GGAGCAGGCAGTGACCTTAAAGAGACAGC GCTCACCGCTCCTGGAGCCCGACTCTGGG TCCCTCATG	78	D	--
IM000205	CTTGTCCGCCACCCCGCCTGCCTCATTAC CTGGCTCACTCACTAACGTGAAAGCCTTA CAGAAATCTCCAGGTCCTCAGCGGGAAAG GAAGTCATCTTCTTCCTCATCCTCGGAGG ACAGAAGTCGGATGGTAAGCATCTGTGCT GTGCTCCTCTAACTGTGACGCCGGGTTCC CATCACATG	79	K	*Braf*

IM000206	ATATAGTATGACTGCCTCAAAACAAAACA ACAACAACAAAACCCCAAGATATCTAAAG GAGGAACATTCCAAAAGACAGAAATGTCC ATAGACCTTGACAAAGGAACATG	80	C	--
IM000207	GTCAAGTGGATGTTTCTCATTTTCAATGA TTTTCAGTTTTCTTGACATATTTCACGTC CTACAGTGGACATTTCTAAATATTCCACA TTTTTCAGTTTTCCTCGCCATATTTCACG TCCTAAAGTGTGTATTTCTCATTTTCCGT GATTTTCAGTTTTCTCGCCATATTCCAGG TCCTTTAGTGTGCATTTCGCATTTTTCAC GTTTTTTAGTGATTTTGTCATTTTTCAAG TTGTCAAGTGGATGTTTCTCATTTTCCAT G	81	R	--
IM000208	CATGAAGTTAGAATAATTGGGATAAAGCT TTTATCATTATCAATTGGTTTTGAAATTA TTGTATTGATATCTTGTAAACTGAATATT TATTGGTACATAAGTCTGGTTATGGTTGA CTACTTTAAGTTTTAAGAGTTTTGATTCT TCCAGGTAAATGGGTGTTGTAATG	82	R	--
IM000209	CATGCAGCCGGGGTGGGATTTGAAGATTA TGCCTAGTGAATATTTAATATTAAACACG GTGTGATCGAATTGATAGCTGTTGAAAAC TAGAGCGAAACC	83	D	--
IM000210	GGACAGGGTCTCTCTCTCTTGTTGTTCAT TGTTTCATATATCATCGTCGGCCTGCTTA CAGACTGCATTGTGTTCCCCTGTCTCTGC CTCCCATCTCACTGTAGAAGTAATGGGAT TACAGATAGATGCTACTGTGTCTGAAAGT TAAATTCCTAGGCCCCATG	84	D	--
IM000211	AGTGGGAGGGAGCGCCACTCTTGGAGCTA GGCAGGAACTGTTGTTACTTCAAAAACTA ACAAGACAATCTCACATTCCTGAGCTGAA GACCAGATGCAGCCAGGGACAGGGTTCTG CCCTGGCCACTAGATGGGCTCTCTGGCCC TGCTAAAGCACTGCACAAAACTGGACGAG GTGCACCAAGAGTCCCGTGTTTGGCCCTC AGGGCAGACTAGAGAGCAGGACTTTCTCC TGGGAGCAGAAACTGAGCCTGGGGTCTTC ATG	85	K	*Fgf3/Fgf4*
IM000212	CATGCTCATAATTCTGCAGTGCCTTCTCA TAACACAGGATAAAACACTCTAACCTTTA ACATTATACTTGAAAACTTATGTGGTTTT TTCCTACCAGAGTCATATCAAACCAGTCT CCCTCTCCACTCACAAGGATCCAGTCACA ATGGCCTTTTA	86	D	--

IM000213	CTGTAGGACCTGGAATATGGTGAGAAAAC TGAAAATCACGGAAAATGAGAAATACACA CTTTAGGACGTGAAATATGGCGAGGAAAA CTGAAAAAAGTGGAAAATATAGAAATGTT CACTGTAGGACATG	87	R	--
IM000214	CATGGCGAGATTCTGTGTCCAAGCTGCCT CTACTCGTGACATTCCAAGATGCCTCTGA GGTGGGAACTGTGAAATAGGACAGAGCCC CACAGTCCCCTCTT	88	K	*Wnt3*
IM000215	CATGGGGGGGGGTACCAAGAAGGGACTGC TGTGATTGGGATGTAAATAAATAAATAAA TAGAATAAACAAAACCCAAAAACAAACAG AAACCTAAACTCAATAACTGCAGAAATGA CTCTTGCTCTTTTCTGGTAAGGTTAGAAG CAGGTTACAAATCTATATTAGAGATGGAG GCATTTCACACCAGCATAGGTATAGGAAG TAGATGAAATGAGGACTACACTAGAGTCT GTTTGTCACAACCAATTCTGAGTGATTTC ACTGAGATAT	89	D	--
IM000216	CTCTGAGAAACCTACCCCATTCTCCCTCC TTTCTCCCATAAGCAACCACCTCCACAGC ATTATCAAAAGACTGCTGACAGATTGGTG GCTCAGCAGGGAGAGTCAGAGCTGTTTCT TAGGTCTAAGTTGTAGCTCCACAGTAGTA TGTTCTCCATG	90	D	--
IM000217	CATGGAACACTCAAAGCTGGCCAGGGCCC ATTTACCAGGTATCCTTTGCCTTCTCAGC TGATGGGCATCAACACATTAATTCACATA TGACTCGTTTGTGTCATATCAATAGTAT	91	D	--
IM000218	GTGGTTTTTGTGGTAGAGAGACACAGAAG AAACTGAAGTCCTTGGAACATAATTATCA CTGTGGTTGAATGTTTGTGTTCCTATAAC ATCCTATGTAGGAACTGAACCTATAAAAG TAGTGGCTCCGAAGGTGGTGTCCTTAAAT GTGAACTGGGCTACAAGATTTTGCCCTTG TGAATGGCTTTATGGAAGAGGCTGTCACT TTTCTGTCTCTTCCTCCATTATCTTGGAA GACACAACAGTTCAAGGTCTCATCTGGGA AACAGAGACCTTTACCAGACCCTAAATCT GCCAGTGGTGTCTTGATCCTGGTCTTTCT GTCCTTAGGAGCTATAATGCATG	92	D	--
IM000219	GGCCACAGCCAGTCCACCTGTATGCAGCT GGGTGCTTGGAGTGGCCCTGGTAGACAAA GTCTCCATCTTGCCATG	93	K	*Fgf3/Fgf4*
IM000220	CCTTAGGGCCCAAAATCCTTCCTCCCATT CTTCCATAAGAGTCCCCAATCTCCATCCA CTGTTCACCTGTGGGTGTGTGTATCTGTC TAAGTCAGCTGCTAGGTGGAGATGCTCAA AGGACAACATG	94	R	--

IM000221	GACAGTAAAGAAGACAAAGAAGTGAGTAG AGCTGGATGAAAACTAGGAAGTTCAGACA AAGACTGCGGGAATGANGTGTAGAGTCTA GAGCCCAAACAGTTAAACATG	95	D	--
IM000222	CTGCTACATTCTTAGCTCTAGCTAACTAG CATCAATTGTCCCAACCCCTTCTATGTAT GACTCCAAAGCCAGTGTCACATG	96	R	--
IM000223	CATGGTCTCTAGAGCTAAGAGATACCAAT GCTGCGGCAGGCAGTTTTTATTACAATCA TTACAGTTTTGACAGTGTCTGGCCGTGTG CCAAGGCTGGCCTTCATCCCTGAGCTCGG TGATGCTTCTGTCCTGGTCTTCTGGCTCG TCACAGCTTAAGAAAGTAGCTGCTTCTC	97	D	--
IM000224	CATGGAAAATGATAAAAACCACACTGTAG AACATATTAGATGAGTGAGTTACACTGAA AAACACATTCGTTGGAAACGGGATTTGTG TATATCAATGAGTAGTTA	98	R	--
IM000225	CATGGAAAGATAATGTGTAAATTTGGGTT TGCCGTGGAAAACTTTGGTTTCTCCATCA ATGGTAATTGAGAGTTTGGCTGGGTATAG TAGCCTGGGCTGGCATTTTTGTTCTCTTA AGGTCTGTATGAAGTCTGTCCAGGATCTT CTGACTCTCATAATGTCTGGTGTAAAGTC TGGTGTAATTCTGACAGGCCTGCCTTTAT ATGTTACTTGACCTTTTTCCCTTACTGCT TTTAATATTCTA	99	R	--
IM000226	GGTAAGAGTGGGAGAAAATGGGGGTGGGG GGTGGGGACACTGCAGAAACCTGGGAGAA AAAAAATCCAACTAAAATCAGGAAACACA TG	100	D	--
IM000227	CACCCCCATCCCGCAGTTCCCAGAGGGAA CAGTCCCAGCAAAAATACATG	101	D	--
IM000228	CATGGAGATGCAATGAAAGCACACAATAT TGCTGAACCAAACAGAAAGCTCAAAACTA GGCACAGAAAAGAGATACAAACACAAATC TGAACAAATTGACCTTCTCCCTATAGCAT AACTAATATCTCAGAGATAAAAGTGGTCT TTATATACCAGGGCGAAAGAGGTCTAAAA AGAGAGGAATAAAAAATATGGCATATTTC CTGTCATATGCAGAACCTATATGAGTCTT TTTGTTTGTTTCTTTCAATACAGCCTATG TAGCTCTAGCTGTCCTAGAACTTACTTTG TAGACCAGGCT	102	R	--
IM000229	CTGTTCTACAATGCCGGTTTCCAACGTAT GTGTTTTTCAGTGTAACTCACTCATCTAA TATGTTCTACAGTGTGGTTTTTATCATTT TCCATG	103	R	--

IM000230	GACAGGCTCCAATCAGATATACCAAGGGC AGGAAGCACGTGACAAAATCAGATGCCTG GAGACAAGTGTAATAAAAGAAGCAACAGA AAACAAGGTTACTTGGCATTGTCACAACC CAACTCTCCCACCATAGCAAGTGATGGAT ACACCATCACACCAGAAAAGCAAGATATG GATCTAAAGTCACTTCTCATG	104	R	--
IM000231	CATGGGTCCCTGAAGGGTCTCTCCTTTAG CAAACCCCTGTACAGTTGAAGTGANTTTT CAGGTACCCATTGGTCTTAGC	105	D	--
IM000232	CCCCACTCCTCACAGGGCTCCCCACATCT GCCCTGGGACACCCCACTCCTCACAGGGC TCCCCACATCTGCCCTGGCACCCCTCCAT TTTTCAGGCACCTGAAGTCCCTACTTTCT AAAGGCCATTCTTCTACCTCAGGTCTTGC TCTAGGACTGTCAACATG	106	K	*Fgf3/Fgf4*
IM000233	CAGGACAGCCAGGGCTACACAGAGAAACC CTGTCTCAAAAAACAAACAAACAAAAAAA AGACCATTATGCATTCCTGCGGCTCTGAC ATG	107	R	--
IM000234	CATGGGCAGCACCTCGTGGAACACTATTA TAAGTGTCCTCCAGTCAGGTCAACAGCGT AAGAT	108	D	--
IM000235	CCTGTACATTCTGTGTTAAGGACAGAGGG CCTCCTGCATG	109	K	*Fgf3/Fgf4*
IM000236	CATGGAGGCGCAGGAGTTATTGTCTAAAG TTGTGAAGATGAAGCCTAGATTGTATTGG AGATCCGGGTAT	110	D	--
IM000237	GCAGATATTTCCACCTCTGCCTTCCACAG TCCTTCCTCCCATG	111	C	--
IM000238	CATACGCTTACAATGTGTTGTTATTTCTG GTTCTCGTCTGCCTTCTTTATAAAAACAA ATCCACTAAGGTGGAGTAGCCAGCCTTTA CTCAGGGACTGTCACCATG	112	D	--
IM000239	TTCTGTATATATTGTGTGGTCAGAAAACC GTGGTTTTCCTGGTGTCAAGAGTTAACAC TTTCAGTAATCACTCATTCTAAACCAGAC AAACCTTTAATCTTTCATCTGGAAAGGTA CTCATTCAAACCAATGCTCTCTTAAAACC AGAGTATTTAAACAGCCAACTGCATCTTC AGGGTTTCATAGAAAATCAGCTTGATCTA AAATAGTCACTGAATTCTGATATCATAGA CATG	113	D	--

IM000240	TCCACCCACCCACCCACCTGCCCACCCAG ACAAATGTTCACTGAGCATTCATATACTC CATTCACTTCTAAGTACAGAGCCTAAGAA TATGAGAAAATCCTCATAGCAAAGAAATG CCTCTTGCAACTCGAGTAAAAACTCGAGT ATGGGATGGAAGAGTTGAGAAAACAGATG ATAGTATGAGAGCCTATG	114	D	--
IM000241	AGGAGCCTAGCAGAATTGCCCTCTGAGAA GCTCCACCCAGCAGAAACAAATGCAGAGA CCCATCGATAAACACTGGACAGAGCACAG AGTCTTGTGGAAGAGTTGGGGGAAGAATT GAGGAACCCAAATGGGATAGGGACTCCAC AAGAAGAAAAAGAGAGTCAACTAACATG	115	R	--
IM000242	CATGTCCTACAGTGGATATTTCTAAATTT TCCTCCTTTTTCAGTTTTCCTCGCCATAT TTGAAGTCCNAAAGTGTGTATTTCTCATA TTCTGTGATTTTCAGTTTTCTCGCCATAT TCCAGGTCCTACAGTGTGC	116	R	--
IM000243	CATGTGGAGGCCAGAAGTCAACATATAGT CTCCTTCCCAATTACTTGTCACTGGAGAG C	117	D	--
IM000244	GTTCAGTAGCCAGCAGGGGGGATAGGACC AGCCCAAATTCTCCCTTTGCTTGGCCTTG ACTACTAGTCTGGGAAGGGATAAGTGGGC TAACCAGAAGTCTTCCACATCTCTAAGTG ATTAAAAATGGAAGACGTGATCTCTGGTC ATTCATAAACAGGCATTTCTCAAAGTTGG TCTGTGCAGTTTGTGGGAAAAAATGAAAT GTACTCATG	118	D	--
IM000245	CTACAGAGTGAGGTCAAGCTCGAGGATAG CCAGGCAGGGATGCACAGGGAAACCCTGT CTCAAAAATCAAAACCAACCCAACAAACA AAAACAAAAATGGAAGGATAGAAGAGAGA TAATCCATG	119	D	--
IM000246	CATGTACTGAATCCCTGAAGTTGATGCTG AGCACCATCTTGTGCTGTTCTACCGCATT TACTGGGG	120	D	--
IM000247	CATGTGTCACTCAAAGGCTGCTGAGAATC AGGCTGTACCTGTATTCCTAAGCCATCCA CAGCCATCCTGACCCACAGCAAATGCTGG CAGTCGCCCCACAGCTGGACTCCGTTCCT CCCTCCACTCCTATAGCCGAGGCTATCCA CACAGGCTATTTCAGTGCCCTAAGCCTTG CTACCCTTATGTATACATTGAGGACAATG AT	121	D	--

IM000248	AGAAACCACTGCCAAATCAATACATTTTA ATTGGAAGTGTTTATGAAGCCCAGGAGAG ATCCCTAAATGTATTAATTGCTTCCTGAG GAAATATAAAACTCACAGTTACTAAAGCC ATG	122	C	--
IM000249	ATCTTCTACACAGATGAAACTGACAAAGT ACAAATAAAGATTATATACCAAAATGAAA AAAAGTAAACAGCACACATTTATAGATGC ATCTAGCATCCCCCAAAGCTCAACACCAT CCATACTTGAAGACTGCAGTGGTCCCTCT AGACAGTATGCTCCAGGTCAGCCCTCAGC ACTTGAGAATAAACAGCTTCATTTACTCA GCCTGTTGTCAGGATCCATG	123	K	*Fgf3/Fgf4*
IM000250	ACTGCCTCAAAACAAAACAACAACAACAA AACCCCAAGATATCTAAAGGAGGAACATT CCAAAAGACAGAAATGTCCATG	124	C	--
IM000251	CATGAGCTGTCGATAGTGACCTGCAGTCAAGGAAAT CTGAGGGCTTCCTAATTAACAGAGGAGCTCTAAATG AGAGTAACGCGCTCCACAAACCCCCTCACACTCGGT AAGTGTCACGGTGCAGATAAT	125	C	--
IM000252	GCCGCGTATGTGTTTCTTTTTCATAGAAGAATTAGC ACATAATGGAATGTGCGTATCTGAAGTGCACAACTG AGGAGTATTTATTATTACATACCTTTACAAGATATC TTTTCTCAGGGAGCAACCTGAAAACATAAGGAGAAA AACATAAGAACTGCCACTCTAAGGGTTGGTGAAATG GCACAGCCTGGCGGTAGGACACACACATG	126	D	--
IM000253	CATGGAGAAACCTGGGCTTATTCAAGCAGTTTCCTT TGTTTACCCTGCCCAGGGTTGCCAGTGAAGGGGCTC CTCCATCACTAACTAAAGGTCTTATCCTATGCTGGT TCCTCTCCACCCCACCAT	127	D	--
IM000254	TATAGGAATAGAAATTCAGAACTTATCAGTTTGTTT TGCTTCAAATGTCAACACATAATTTAAATTTACAAA CCCCTTGCACATTTGCATG	128	C	--
IM000255	GAAGACAAAAGATGTGTCAAATACCTGGGCAAAAGG GGGTGGTGGTGCTCTCTTTCCAACTCCTGAAAGACA CCTCTGCTCAGCACACTAGTTTCCAGGTTCCTGGGT TAGGATTTGGGTGAGATTGGTCGGCGATGGTTTGGT TCCTCCATTCTGCTGCTTCTCCCTGATACATTGAGT TACAGCAGCCCACGCGTACACACTCTCGCACATG	129	K	*Wnt1*
IM000256	GAAGAGGAAATAAGGCAATAGCTAGACTGGAAAAAC GAGCCAGCCTAAGAAGCTGCAGAGTAGTCTGTGGGG TTCTGCTTTGGTTAGCTGCCTTTAGTGCTCATG	130	D	--
IM000257	CATGGATAGAGGATGGAAGTTGAAAACCT GCTATTAAGAACATAGCCCTGTCCATTAG TGAGAGTG	131	D	--

IM000258	CATGTGGCCCAGGGGCACTTGGAGCCTTAGATAGCT GCCTTTATGGCTCCTGGTGGCCTTGGATGTGGGTGG GTGACAGGAAACAGGAAGAGCTGGATAGTGGGGGGT CCCCAGGAGGAGCTAGCTGTGCTCTCTATCACTTTT GCTCTCCTGGGGCTACCCCCGTCTCAGGGGAAGGCC TGTGACTGGCTAAGCAACAAGTGTGGGCTGAGACCT TTCTCTGTGACACTCTGGTGCTACTCTGGCCATAGC ACAGATCTCTAGGAACGCACTCT	132	K	*Fgf3/Fgf4*
IM000259	TATATGGATATGTTTATGTGAGGGTAGGCACTCCTG GAGGGTGGAGGCATTAATTAGATCCTCTGCAGGTGA GCCACCTGACATG	133	D	--
IM000260	ATATGTGGACTGTAGTCATCTTGAACATCTGTAACA AAATATATAGATTAGGAGGTTTAGACAGCAGACATG	134	D	--
IM000261	GTGCCTCTTGTCTGCCAAGCTGGTATTGTAGCATG	135	D	--
IM000262	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCTTCGA GACACAGGGCTGTCCCCTGTAAAGCAGGTTCCATCA GTGACTCCAGGGTTTTAGCAGTTCAGTGGCGTAGTT TTCAGACTGCTTAAGATTTCTCAGGGGCTAGGCGTG GGGCAGAGACCCTGCAGACCCTGGCTAGAACAGAGG CCCTGGGAGACAGTTGAGGGTGCTCAGCTGTGGAGG ACATG	136	K	*Fgf3/Fgf4*
IM000263	CATGACGACTTGAAAAATGACGAAATCACTAAAAAA CAA	137	R	
IM000264	CCTAAGTCTGACCGTGCCACTTCCCAGTCTTCCCTA CACTTCAATGCTTTTAGGCACAACAAATTTGTACCC CTCATG	138	B	Mm.102899
IM000265	CCCCCCAGCCTGCTCCCTCCCCGGAGGGAGTCCCCA GTGTGACATG	139	D	--
IM000266	GTTTAGGTGATAGGGTACTTGCCCAGCAGTAGGTGG TGCCCAGGATTCTATCCTCAAAATTGCACAAACAGA ACATG	140	D	--
IM000267	CATGTTGTGTAGATACCTACATAATTATAATTCATA ACTGTAATTTGCTAC	141	D	--
IM000268	CATGGGTTTGAGCCTTGTCCTGAGCTGGAGGAAGAG AGTGACCCAAAGGGACCTTGGTAGCAGCCAGGGATG TGTTGGGGAGCAGAGAAACTTTTATGAACTTCAGTT TCAGTACTGAAACTTCCCTTTCCCTAGACTTCCTTT G	142	D	--
IM000269	CATGGGACAACTCCTTTTTCCTTCTGGGTCAGGGGA GAGAGACCTCCTATCTAAACTGTATAGGCCATTGCT GTAGCCCTTAGCTCACTTCCGGGGCGGGGAGGAGGA GGTTAAGACCCTAT	143	D	--
IM000270	CATGAAATGAAAGAACAGAGTAGCAATTTGGGGAGA AAAGCCTGCCGAGCGGACTTAATCTTTCCCAAGTGC TATCAGT	144	D	--

IM000271	ATGCTTGTCTTTCCCGCCCATTACCTGCTTTTGTTT GAGATAATAGTTTTGTTACTTTATCAACTAGTAGCG ACTAGTTTACATTTGGTTTCATAAATAAGATCCATT TTAATCTGAGTTTTCCATCCTTGATTTATTTTGATT CATATTTTAATTGTCTAGTTCCCATCCCTGGGCAGG ACTTTTTGGGAAAGTCTTGCAGGTGACTATGTTGAG AATGATTTATGTTGTATTAGCACAGGTACATTCGAC AGTGCTGGTTCCTTCTGGAGCGCCTCGGGTGTGGGT CCTTTTCCTCAGC	145	D	--
IM000272	CATGAGTTTGATTATTTCCTGAATTCTACCTCTCTT GGGTCTATTTTCTTCTTTTTGTTCTAGAG	146	R	--
IM000273	GGGATAAGACTGGATAGTAAGCCGGGCGTGGTGGTG CATG	147	D	--
IM000274	CAGAAGGTAGTGTTTCACAACAGTCCTCCCGATGAT CAATTGTTTTACACTAAACCATATAGGAATTCACCC TGAGAGGAGTTCGAAAGCCTTTCAAAACCTGTACTG ATATAAAGCAAATCTCTTTTGGATTCCCAATCAAAA TGATTTGGCAGAACTTTAAGGCCACAAAAATTGTGT CTGAACAACCCCTCTGAGCCCAGTTTTGTTAGCTTA AATTAAGGGCCATG	148	D	--
IM000275	CCTCAAACTAAGAAGCATCCATTTCGAAGCTGCTGG GATTAAGGGAGTATGCCACCACCACCAGCTATGGCA TTTTTTTCTTTAATTTTACTATTTTTTTGCTTGTAT ATTATGGTTTCCAGTTTTGTGGGTTTTATAAGCTTT GAGTGTGTTTCTGCATG	149	D	--
IM000276	GTCCACTTTAGGACGTGGAATATGGTAAGAAAACTG AAAATCATG	150	R	--
IM000277	CATGGTCAGCTCTCACTGCCCCATCCCCTGTCTCCA GTTCACGCACTGTATCCTGTGTCTTTCTCTGTGGCT AGACTCTTCTCTTGGGGGAGGGGAGTCTTGTATATC GATGTGTGCTCACGCACATAGAGGCTAAAGATTAAT CTAGGTGTATTCATTCATCGTCTCATTGC	151	D	--
IM000278	CATGTGTTTCCTGATTTTAGTTGGATTTTTTTTCTC CCAGGTTTCTGCAGTGTCCCCACCCCCCAC	152	D	--
IM000279	ATGGTGTCTGTTCATAGCAGTAAAACCTTAACTAAG ACACTGATATAACTCACCTTTCCCAGCCTCAAAGTC TCTACCATCTCAGGATCCACTCACTCATTCACCAAA CTTCATCAAATGCCCACTGTGCTATCATCAGTACAG AATAAATCATG	153	R	--
IM000280	CATGAGACTGTCACAAGCTCCTGGGATGGGGACCTT ACCAGAAAGCCACCAAATCAGAGGCATCCCTGTTTG GTGAGGGTACATTTGTTTTTCCCCAGGCCCTGAGTG CCAGGCAGGAGCAGGCAAAGTTCACCTGGGAGGATG CCCTGGAT	154	K	*Fgf3/Fgf4*
IM000281	GTTTTGGTTCTTTTCAAAGAAAAACAAAGGTCATTG CAGCTTTTTGTACCATTGAGGTGATGGTAGGAATTG AGATATATAATCTACTTGAAGATATATATTATGGCA TG	155	D	--

IM000282	CCGCTGCTCTCTCACCAACCCAGTGTGTCTGCTTTTAGCCCAGACGGGGGAGGGGGTAAGGGGGTGGTCTGTCTCATG	156	K	*Wnt1*
IM000283	GTGTCCCTCCTGTCGTTAGGCAGTACTTCCAAATCAAACCATG	157	C	--
IM000284	AGCTGGTACAATGCTTAGAGCAGAGCTGCAGAAGCAATACAAGAGATCCTGGCTCAGCTAGGTGCAAGCTGGAATAGACTCCTGACAGTTGTCCTATGAACTCCATACACAGGCATG	158	D	--
IM000285	ATGGATCCCTGGGGGGCAGTCTCTGGATGGTCCTTCCTTCTGTCTCAGCACCAAACATTGTCTCTGTAACTCCTTCCATG	159	R	--
IM000286	CATGATGCACTTAGCAATTCCTCAATTGAGACTCAAGTGAGCCTAGGCTGTGACAAAATGACTGTTAAAACT	160	K	*Fgf3/Fgf4*
IM000287	CATGTAAAGCTAGTTCAAAACATACTAAATAATTCAGTTGTAGAAGAGGTGAGGTTATCTCACTGCCAGGATAAGCTATTGAACAAGCAAGGGTTCTCACTTACTGTTTAAGTGGAAGTGTTTTCTTACTTCAAAAAGTCATTAATGAATTTTAAGCTGCATAAATATTTAGTTATT	161	C	--
IM000288	TAAGCTTTTCTCTTACACAATCCCCCGGAAACCCACAGTTTAGGTCACAAAGACCCAGGCACCTATTCCTAGGCCTGGTAAGTGGGCACCCACCATTTACAAAGAGCTCAGCATTTGGCTCACACATG	162	D	--
IM000289	CATGAAGATGAACCGGGCTTGTTTCTCTGGCAACTAGGCTCAGAAAGGATAGGACCACCAGCCGAGTAGCTGTCAGATGGAGCTGAAGACCTGAGGGAAAGAATGCTTGTGGGAAGAAGCTGGCTCCTTTTGGTTTTGTTGTTGCTGGTTTTGTGACCGGATCTTGCTGTGTGACCCTACCTAACAT	163	K	*Wnt1*
IM000290	CATGGACTTAATTTTACTGCATTTGAATTATGGAAAATATATATGAAAAGTCTTTAGAAAAAGGCAGAGGACGAAAAAAACCAAAGAACTTTAATTATCTGAGACCAAGAAAACTCTTTAAGAAAAAGCAGTAGATTTAAACTACGTGTTGTTAAAATAGTCCTGTATAGATATAAAGTCCCTCAGAGGGAAGAGATTTGTTGAATAAATTCAGACACTCAAGAGAA	164	D	--
IM000291	ATTAAACAGCCCAGTGCACTCAGAAGTGAATGTTGAGAAGTGGGTAATCTGGGGACAAACAGAGGGAAGAATAGTGCCCTTGGCACGTGCAAAGGAGTTTGGGAACAAACATG	165	K	*Fgf3/Fgf4*
IM000292	CATGTATGACAGTGAGGTCAGGAGTGCCCAGGGAGCTTGCATTGGCAGAACAGCCTTTCCTGGCCAAGCCTAGTGTCATCAAGTATATATTGGACCAGACCTTATAAAACTTGGGTTCCACTCTGGCTGGACCAGCCTCAAGGCGTCGCCTCTCCAGGCCTACCTCCCAGACGCAGAGGCAGCATTTGGAGGATTGAA	166	D	--

IM000293	CATGGGAACTTGTTCCAAGCAAGGGACTCTGCTACA CCTTCAAGGGACGCTGCTAATACTGGGTTCAACCTT GGGCAGCGTGCACAGCAGGAGTGGGAGGGCTCTGAT GAGGAGAGCCACCCACACTGTGAGATCTAGGAGATA AGGTCACATCCAC	167	D	--
IM000294	CCCTCCAGCAAATTGAAATACGAAAGACTCAAACAC ATTAGAACCATTCCAATAAAAACTTGCATTGCCCCA GGCCCCTCCCACCACCATG	168	D	--
IM000295	CAAGAGTATATATCCAAGAAAAATACAGCTGAGTTG ACTGTTAGTTCTGTTTTGGCCTTCATG	169	D	--
IM000296	GGTAAAAACTCTACCAGTTAAACTACATT CCCAGCCTGCCTCCAATGAATTTAATTTG TGTTTTTAGGGTTTCTGTTATTGTTGTTT TTGAGACAGGGATTCACAAAGATCTGCCT GCCTCTGCTTCCTGAGTGCTAAAATTAAA GGTATGCATG	170	R	--
IM000297	GTTTAGTAACTGTTTTCTGTATTACTTTTGTTGAAA ATTAGATTGTTCCTGGTGACTTTGTGTGCTATATTC TCTGCATG	171	D	--
IM000298	CATGTTTCTGCTTCTACTTTATCCACCCTGCACACA CTGACTGCTATGTTCCTGTACCTTTTCCATCTCTCC ATTGAATATTCACTCCAACAGTGGCATTGGAAATTG CAGTGGAGATACC	172	D	--
IM000299	ACGATGGTCTTGCCCTTTCTCACACCATCAATAGTC ACTCAGAGCTGTGGTTGTTATCTGAAGTGTGTTGCA GTCCAACTTTGCCCCATG	173	D	--
IM000300	GGAGTGTAAGCGTCGGTGTGTCACCCGTGAGATTAA GTCAAAGTGTACATG	174	K	*Wnt1*
IM000301	TAGACCCAGTCTTGCACTGGCCTGGGACT CGCTTATTAGGTTTGACTGTTATCTGGCC AACAAACACCAGGAAATGGGGTGACAGGT GGTTGTGAGCCCTCTGAAATGGGCATTGG GACCTGAACCTGGGTCCTCTGTAAGAGAC ATG	175	D	--
IM000302	TCACCCCAGCTGGGGCTGTGCTGAAGACTCTGAAGG GGAAGATAGGCCTATGGTNACATG	176	K	*Fgf3/Fgf4*
IM000303	GTTGGGCTGAGCCACAAGTACACCTCCACTCACTGA GCCATCTAGCAGGTCCCAAACAAGGTGACTTTTGTC ATCCAGCAAGACATAGCCATCTATGCCAGTCATCCT TGTCATG	177	K	*Fgf3/Fgf4*
IM000304	TAACATATTTGCTTGTTATGAAGGAAAATGTTGGAT GTGTGTGCCTGTGGTTGAGTACTGCAAGTAGTGTCA GGGAAGAGAAACCTAGCTTGAACAGTCCCCTCATCT CCTTCATATCCTCACTCCTTGTCAGGCCCTGTATTA GGTAGTGCTTCCCTACCTCCCTAATGCTGTGACCCT TTCTTTAATAGAGTTCCTCATG	178	C	--

IM000305	CATGTGAGCACAGGTACCTATGGAAACCA AAAGTGTAGGATCCCTTAGAACTGGAATT ATAGGCAGCTGTACGCTATTGATGTGGGT GCTGGAAACTGAACTCCAGGCTTCTTGAA GAGCATCAACTGCTCTTAGCTGG	179	D	--
IM000306	CATGTAGAGACTGCCATATCCAGGGATCCACCCCAT AATCAGCATCCAAACGCTGACACCATTGCATACACT AGCAAGATTTTATTGAAAGGACCCAGATGTAGCTGT CTCTTGTGAGACTATGCCGGGGCCTAGCAAACACAG AAGTGGATGCTCACAGTCAGCAAATGGATGGATCAT AGGGCTCCCAATGGAGGAGCTAGAGAAAGTAGCCAA GGAGCTAAAGGGATCTGCAACCCTATAGGTGAAACA A	180	R	--
IM000307	CATGTCCTAGAGTTGTTCCAGCACAGAAGCTTTTGG GAGAGACCACCATTACTGAAACGCAGCAGATGCTGC AGCT	181	D	--
IM000308	CTGCTTGTTGTGGGGACCAGCCAGACACCCTCCACA GGTGCAGTGGTGCAACATG	182	K	*Fgf3/Fgf4*
IM000309	CATGATGTTTGTGCAGGAATAGAAACCCTGACTAAG ACAGAGGATATTCAAGATCCAAACTAGCAGGTTAGC TGTGGTTCC	183	R	--
IM000310	CATGAAGCACACATTACCCTGTGACTTGCTTTTTTA TTAAT	184	D	--
IM000311	CATGTGTCCTCTTGTCTTGTAGTCTCTATTCTTTGT GATTCCGCAGCTCTCCATAGAGTGCAGTTCTATGTC CTGCCTGCAAGGTCCATTGGCTTACTAGGGTCTGCC CCTCCCAGAAGAGTAGCTCATTTAGAATGCATTACT GGTGTGCTGTCTTGCATCTTTTTTACCCAT	185	D	--
IM000312	ATCTATGTTTATGCACTACTAATTACTGTTTAGTTT ATATATGCCCTAATAATTACCCCATTGAAAACTTAA ATTTTGTTTCAAAAGTGTGGTCTCATTGGAGGTGTT AATGTACAATGTCTTTCTCATG	186	D	--
IM000313	CATGGCCAGCTGAGCGGGCTGGAACCTGCCCTTCTG CTTCCTGTCCCTGCACCTCAGCACCGCTGTGCACTT GGTACTAGACCTCAATCACCGCAG	187	D	--
IM000314	CATGTGCGTCCCCCCCAAACACGCAAGCGCACACCC ACAAAGAGAAGAGACAGGG	188	D	--
IM000315	CATGGCCACTTGGAGAGAAGGGGGAAGGGAATGCGG AGAGAGCGGGAGCAAGAG	189	C	--
IM000316	CTTAAGCACTGATCAATGGCCAAGGTTTGCCGACTT GGGATCTGGGGTATAGACATCCACCCACTGAGACCC TCTAACAAAACCAGATGTGGAGGTACGAAGCCTGGC TCAGGGGCCTGTCCTTTGTCATCAGAATTCACCAGC TGCAGCTCCTGGGTCAGCTTTGTTTGGCATG	190	K	*Fgf3/Fgf4*
IM000317	GTGTATTGATATGCAAATGTGTTAAAATATGATTTA AAATTCCCCATG	191	D	--

IM000318	GCAAAGTGTCCACACTTTGGTCTTCGTTCTTCTTGAGTTTCATG	192	R	--
IM000319	ATAGCAGGTCCTGGATACCCCAACATACCAGAAAAGCAAGATTCAGATCTAAAATCACTTCTCATG	193	C	--
IM000320	CATGTCCTGGCTTTGTAAAGGGTCCTGCTGGGTTTACTTCACTGGGTCTTAAACTCCGATTGTGAGCCGTAGTGAAGAGGGCTGTATATAGTGGGTCACCGAGGTCCTGTAGCAGAGTGGGCAAGCTCACTGCCTGCTACCAGCAGTTCACTATGTTTTATGGTCTGCTGCCTGCTGGTGGTTTATAGATGCTGTGTCGTAAGAGAAAAGTTCAGGGTAGCCTGGAGTGAATGGAGTTGGGGTATCAGGGAGGTCTTTGTACACTGGGGTGAGCTAGGCCTCTGGAAAGCTTCTGGGGGTTCCCC	194	D	--
IM000321	CATGCTCCCAGGCACCAGGCTTGCTTTGCATAGGTGGGACAGGGTCCCAATACTCAGCCTGGGGTGCCAATGAGGCTCAGGCCACACACCCTCTTGGTAGGAGTCACTGTAGTGGGGTCTGTGAGAGCCAGTAACTTGTGAGGGTGTGAACTTAGCTCAGGACAGAGGCCAGCAGGAAGCTTTCCCTACAGAGAGTGTTTTCGTCTTTTCCTTTTTCTGGTTTGTTTCTTGGGAAGGGAACAATTTTCGCTTTTAGTTGGCTTGTATTATTCGCTACTGAAACCTTAAG	195	D	--
IM000322	CATGTATTAAGTCCCTCGTGAGGAAGGGT	196	D	--
IM000323	CATGAGTCAGAGGCTTCTACTCCAGTTAAAACTGATCTGGGTATAGAATTGTGTTCTCAAGAAATAGTAAGTTATAATCAACTAAGTCATCTCCTGTCTCATTTTTTTCTTCCAAATCGGGTCCTCGAATTGTTATAAGAAGATTCAATCAATCAACAGTATCCCTTTCCCAATTTGTGTGCTAAGTGGAAACAGGTCTTAGCACATCAATCACATAAAGTTCAATTAAGAAGGAATTTAAAGATCAG	197	D	--
IM000324	GCTATGAGTCTCCACTTGTAAACAATTATACTCAAACATATTCAGGACACACTTGGGCTTCCTCCATCAAGCCAGGCAGGTTTGTTTTCTTGTTTGTTTTGAGATAGATGGATGGGCCAGCTTCATG	198	C	--
IM000325	CCCACCCCTAGCAACCAGTTCCTCCTCTGAATGGAAGACATCTGATACCAACTTTGAGCTTTCACATG	199	D	--
IM000326	ATCNNCGAATCATTCTAGGCTTGTGGGACCATG	200	D	--
IM000327	ACTATTCTCAACAATAAATGAACTTCTGGGGGAATCACCAATCCTGATTTCAAACGGTACTGTAGAGCAATCATG	201	R	--
IM000328	CCTAGGCACCCACCACAATAGTTAATCCATCTTTGAATTTTTGACCCAGTGTTGCCAAGTATTCATTGCAACAGCTTTTCAAATGTTTTATTCTTTCCCAAATAAATTCCATG	202	D	--

IM000329	AGAGGCTACCCCTTCAAGTGGCTTGCCTAGTATAGC TATTACAGACAGAGAACTTCCAGTAATTTCCTCAAG CCACATG	203	D	--
IM000330	ACTCTGAACTTTGCTTTGCCTGGTATTTTTGCCTCT CTTATCCCATTGACCCTGTACAGAAAAGCTGAGGAA GCAGGTGCAACCAGGCATCTCAGGCACCCAGTTAAG AAGTAGATGAAATACTGTAATGTACATG	204	D	--
IM000331	CATGATTTTCAGTTTTCTTGCCATATTCCACGTCCT ACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGT TTTCCTCGCCATATTTCACGTCCTAAAGTGTGT	205	R	--
IM000332	CATGAGACAGTCCCAGATCCCTCACCATAAAGAGCT ACCATATAC	206	D	--
IM000333	CATGCGACCATCCATCAGGAGTTGGAGGTGCCATCG GCTCTGCCTTACAGAAAAGGAATCTGAGATTTAGAA ACCCCAGGTGACCCACTCAGGGCCACCGGGGCAGTA AAAAGAATCTAAGATCTAAAGTCAGTGGAAACTCCT CCCAACCAGCAGAGACTCCTCCCAGCCAGCTCTTGA T	207	K	*Fgf3/Fgf4*
IM000334	GGGAAGCAAGAGGCAGTAAGAAAGGGGAAACTGGGG AGGTAACCAAAGTCACATG	208	D	--
IM000335	CATGCTAACAAAGAATGGGGAAAGCTCTCTAGGCTT CCACCTTAAACAATGAGGAAGGGAAGAAGGAAAG	209	D	--
IM000336	CATGTTGGTGGGACTTTATGGGTATTGCTTCTGATA TTACTAGGAGGCACAATCTCACAGAAAACTCCCTGA TCTTACAATCCTTCTGCCCCCTCTTTTGCAATGTTC CCTGAGCCTCAAGTATGGAGTTATTTTATAGCTGTA TTCATTGAGACCAGAATCCACAGGTATGC	210	R	--
IM000337	CTCACACAGATATGCATG	211	D	--
IM000338	AGAAGTGATCTTTCTTCTGTGTGTCCCTGTCACCCT GGGAGGCAATCAGACGGTCCCTCATG	212	D	--
IM000339	CTTTCCTTTTGTTTTGGACGAATATTATTGAAATAT GTAGTGTGCATG	213	D	--
IM000340	CATGAGATATGATTTTAGATCTGAATCTTGCTTTTC AGGTGTCTTGGCATATTCAGAACTCGCTGTGGTGGG TGAACTGGGTTCTGATGATGCCCATTGGTGCTGGTT TC	214	B	AI597062
IM000341	CATGGAAAGGTATTTGGAAATAGGCTGTTTTGTGTG TAACTC	215	D	--
IM000342	CCCTAGGACTCACCTGGTAGGAAAGAAGTAATTCTT CCAAGTTGTCCCCTGACATCCACAAGCACATAGTGT CAGGCATG	216	D	--
IM000343	CATGCCATTCATACATACTGGCAATGGATATATAGA AAATGAGACTCCTTCTAATATTGTGTGATGACAGAT	217	D	--
IM000344	AGAAACCATTTACACTGCCAGGTTTGGGGCCTGCCT ATGCATG	218	D	--

IM000345	GATCCCTTTAACTTCTTGGATAGTTTCTCTAGCTCC TCCATTGGGGGCCCTGTGATCCATCCAATAGCTGAC TGTGAGCATCCACTTATGTGTTTGCTAGGCCCTGGC ATAGTCTCATAAGAGACAGCTATATCAGGGTCCTTT CAGCAAACTCTTGCTAGTGAATGCAATGGTGTCATC ATTTGGAGGCTGATTATGGGATGGATCCCTGGATAT GGCAGTCTCTAGATGGTCCATCCTTTTGTCTCAGCT CCAAACTTTGTCTCTGTAACTCCTTCCATG	219	R	--
IM000346	AGGGTGGTCTCTGCAACCCAGGCTGGAACCCAGCAC AATAAATAGTTTTATTTACATAACCGAACGCGTGGC TCTGCGGCCACATTTCGGTGCAAATTATTTACACAG TGATGAGGAGGCAGGACAGGAAGGGGTGGGAGGAGG CTGAGGGAGGCATG	220	K	*Wnt1*
IM000347	CATGTGTGTTCTTTTGTGATTGGGTTACCTCACTCA GGATGATATTTTCT	221	R	--
IM000348	CATGAGGCCAAGGGAGAGGCAAATTCCTGTGTGAAT CAATTATCATCTCACAGAGAACATACC	222	D	--
IM000349	AGTAGTATGCCACAGGGAGAAAGGGTATTTATCAAA GGGACAGGAGCTAGTTGTGGTGACCTTACCTATCTG CTTGCCTCTGCCTCCACGGTGCTGGGATTGAAGGTG TGCACCACCACACCCAGCTTCAGATTTTTGTTTTTA TTTATTGNGTATTCCTGTTTCACCTGCATG	223	R	--
IM000350	CATGCATATACAGGATATAACCTTTGTAAGTAAGAA TAAAGCACATAAAAAATACTTTCAGTAATATTGTCC AAACCACTT	224	D	--
IM000351	CATGTGTGTGTTTGTGTTTGCGGAGTGTGGGGGCGG CAGGGAAAGGTGGCCAGGCTGTCACTCAGAGATCAG GATGACAGGCGCTCCCTCATCTAGGCGCGGGAGCTC TGATTGCAGATTCGAGGAAACAAAATAGCAATTG	225	K	**Fgf8**
IM000352	CATGAAGATGAACCGGGCTTGTTTCTCTGGCAACTA GGCTCAGAAAGGATAGGTCCACCAGCCGAGTAGCTG TCAGATGGAGCTGAAGACCTGAGGGAAAGAATGCTT GTGGGAAGA	226	K	*Wnt1*
IM000353	TCAGTTCCAAGAGATGACACAGCCGCAGT CATG	227	R	--
IM000354	CAGAGACTGAAGGAAAGACCATCCAGTGACTGGCCC AACTTGGGATCCATCCCATTTGAAAGCATCAAATCC AGACACTATTACTGATACCATG	228	R	--
IM000355	CCCTACAGTGACACTTACTCCAATAAGGCCACACAT CCTAGTAGTGCCAGTCCCCATG	229	R	--
IM000356	GGCCTCTATTCTCGGTTCAGATTAAGTACCTGGCTT CACTGAGAGCGGCTCTTTCATTCCTAAAATGGTTCT CATG	230	D	--
IM000357	AGTAGATGGCAGAGAATAATCAAACTCAGGGCTGAA ATTAACCATG	231	R	--

IM000358	CCAACCCAACAGCTGGGAAGGGTTGGAAGTAGCCCC GAGGCTGGTTAGTCCCCTTCCAGATGGGGAGGTTAG ACTGGGGCTAGCCAGGCTGCTCCACATAGACTTCCG ATTCGCATTAGAAATGAAAAGAGGAGAGGAAAGGGA AAAGGAAGAAAGGCTACAAGCATG	232	C	--
IM000359	CATGGGGTCTGGAGCCAGCTATCAAACCCAGGATTG TCTTAACTGTGGTGGCTTGGATGAGAATGGCCGCCA TAGGCGCATAGATTTGAATTCTTGGTCCCTAGTT	233	R	--
IM000360	ACGGTGGGCTGATATTTTCTAGATCTCCTAGTGCCT ATCCCCTATTATCATG	234	C	--
IM000361	CATGAATTTTGAGATATTCTCTGAACCAA ACAATATT	235	D	--
IM000362	GGAGAAATTATGCCTTAAATTAAAAAGCAAATATTG AAAAATTAAATATAATTTCCATTAAATCATAATGGA CCAACAACAGAACACATCTATCTATGTATCTATCTA TGTATCTATGTATTTATCTACCTATCTATCTGAAAA GCAAAAACTACATG	236	D	--
IM000363	GCAAGGACAACTGACAGTTTGAAGCAACTATTTTCA TCTTGACTCTCACTCGGCTTTTAACGTCCATTCAGG AAACAGGCATG	237	D	--
IM000364	CATGAGAAGTCACAATTCCACCACTTAAA ATCAGTGCTTGGAAGGATACTGTAGGCCA AGAGGTAAGTAGAGGGGACAGCAGTGCAC GTTTTTCAAAGTGTGGGTGTGTGTTTGTG GGTGTGTGTCTGTCTGCCTGTGCGTGTAT GTGGGTCAGTACAGGAAAAGC	238	D	--
IM000365	CAAGATAAACTCTTAATGGGATTCTAGGGAGTCATT CTGTAGAGAGCACTTGACTAGAAGGTTAAGTCTTAG ATCCAGATCCCAGCACAAACATAATACATCCTATAC TCACACACACACACACACACACACACACGCAGTCCT CATG	239	D	--
IM000366	CATGTCTCAAAAAAAAAAAAGAATCACTTGGATTGT ACATAGTAGTTAATAATATGTAATTAGTCTAACTGT GAAGGGGCACTTATTAGTTTCTACTATGTAGTGTAA ATGAACTATGTTGCTATTAGAAATTC	240	D	--
IM000367	GAAGGTTGAAATCTGTAATCTATCTTCTATGGCATC ATTCACCTCTCTAATACAGCTGTAGAGAAAAATGTC TGAAGATTCGGTTCTACTCTCGTTCTTTGAGGTCTC CCAACCCATG	241	D	--
IM000368	CATGGCTGGACTATAGAGCTCTAGCTTCAGTTGCTG GGATGTTCAGTGCATCACCACAGAGAGGGTTCTTAA GTGGTGATGGTGGTAGTGGAAAGGTGGACCCTCCAG ACAAAGGAAGCACTCACCACGACCCTGCTCACCTGT GAACCTTTCCTTTCAGACTGATTCCTGAGATCAGCC AGGCAGGGCTACCAACCAGGGACTCGTAATGAAAAT TTAGGCATATGG	242	D	--

IM000369	CATGGTCTGGTGAGTATGGCACCAGATAGGATGTTA TGCCCGTTTCTTATCTCAAGAAACAAGGAATCTTGT TTCTTATCATTAATAGGAAGAATAGAGCAGTCCTGG CTAAATGAAAGGTGGNAAAGTTGGTTTGAGTATCTC TTTCC	243	D	--
IM000370	AAAATCCAATACACATTCATG	244	D	--
IM000371	CCCTTTGTTGTGCATTTCAGCTAATCTCATCCCTGT TTGGGTCCTGGAACCCTCTTGCTTCCCTGGCATCTA GGACTTGCTAGTGGCTACCCCCAGCTCCCCATTCCC CATTGCTACACACCTCTGTTCAAATTCCTGACCCTC TGTATATCATCCCAGTCTCTTCTAATACCTGACCTG AACCCCCTTTTTCCCCTCCCTCTATTCTCTTCCTTG CAAGTCCCTCCCACCTTCTACCTTCCATG	245	R	--
IM000372	CATGGGTCATTTCTGATCTTTACCAAGCAACAGTGA TGAATCTATAAATAGAACCATCAGTTCAAGAAACAC AACTTTAGATTCCTTTCCATACCTTGCTTTTGTTTC TTACATCTTCCCCCTGCCCTGTGGTTTTTCTTTTAA TCTTGTTTTTACAATCCAAATTGTATCCCCTTCTCT GTC	246	D	--
IM000373	TTGGGCCTTTGCATACCCTGTTCTGGCTAAGACAAT TGTCACCTGACTGGGCATG	247	D	--
IM000374	AAGTGGATGTTTCTCATTTTCCATG	248	R	--
IM000375	TATAAGCAATCCCAAAAATTCTACCTGGGAACTCCT AGAGCTGATAACACCTTCAGTGAGCCAAGTATCTGG GTATAGGATTAATTTTAAAAAAATAGAAAATCAGTA TCTCTCTTACATACAAATAACAAAAGGGCTGAAAAA GAAATTAAGGAAATAAAACCCTTCACAATAGCCATA AATAATATAAACTATCTTGGGATAACTCTAACCAGG CAAGCAAAAGACCTGTATGATCAAATCTTTGAAGAA GAAAATTGAAAAAGGTATCAGAGGAGGTAAAGATCT CCCATG	249	R	--
IM000376	CATGGGCTCTGCTTAAGAAACCCCGGAG	250	C	--
IM000377	CATGCTTTTAGGCCTTTTCACGATCTTANNGGGGAC CGNGAGAGNTNGCTGCTGGATGATCTCTGAGAGAGC TTATCGTCCTCAAACTGCTGATATTCAAGCTGTTTC GCAGCTGCAGCAGCAAAGTCCCGGTCTTTGTCACCG ATCTGTGAACAGCAACAATGAGCACCTTTCATAACA GACAGGAAATGGATGCT	251	A	*mDal1*
IM000378	GGCGTACCTGTGTATATGCATGCATG	252	D	--

IM000379	GTGCTAGGCTCACTCAAGATAAAATTTGC TATTTCAGCTCCCTGGATAATAAAATCTA TCCTCTCACAGCTGTGACTCTCACAGGGG TGCAGGCAGGACGACATCAAGAGAGTGAT GGCCTCTAACAAGTGTTCTGCCCACTTCC TCTTCCGGGTCAAAGACTAGATCTAGACT GGTGGGGCTGTTGATTCACTATGAATGTG CCTGACACCATCCCACACTTAGCATCATA GACACTTGGGGGACTGGTGATACACTATG ATGCCTGACACCATCCCACACTTAACATC ATG	253	D	--
IM000380	CTATCCCGAGGGTGAGGGCAGTTCTATGC CAAGGTTCTCATCACAGAGATACAGAGGA AGCTGGGCCTGTCTTAGGGTTGGCTGTCT GGAGATCCTGGAGCCCTGGAGGTGGGTAG CAAGAACAAAGGAAGTACTTCACCTGATA AAAACAGTTCCCAGAGAAACACATATACG CTTCATATACAGGAGTGCGAGTGTGTGTG TGCGCGCAGAGAGGCAGAGGCCTGGAAGT CAAAAGTTCAGGGCCAGTTTGTGTGCATG	254	K	*Fgf3/Fgf4*
IM000381	GGGGTTGACTAGAAGAAGGAGGCGATTAGGGTGTAT CATATGAGAGAAGAATAAATAAAGGAAAAAATAAAT TTACAAGGATTAAAAAGTAATTACATACATACATAC ATACATACATCCATACATACATACATACAAGTTAAA CTGTTATGGTAGCATG	255	D	--
IM000382	AGGATGATATTTTCTAGTTCCATCCATTTGCCTAAG AATTTCTTGAATTCATTGCTTTTAATAGCTGAGTAG TACTCCATTTTGTAAGTATACCATATTGTCTGTATC CATTCCTCTGTTGAAGGACATCTGGGTTCTTTCCAG CTTCTGGCTATTATAAATGAAGTTGCTATGAACATA GTGAAGCATG	256	R	--
IM000383	CATGCCTGCAGGTCACAGCCTTGCGCGCCTCCAGTG CCCAGCGTTCAAAGTGACACAGACTCTGTCAGGATG GTTCAAATGCAAATCTCTGCAACTGCGTTAGCCGCT TCTAACCAAGACAGAAAGCTGCCGTCCTGTCCTTCG TGTCTGTCCCCATACCCCATATCGGGTAGCTTTTCT TTCAGCATTGTCCAGACACCATCATATGCCTACATC GCACAAGTTCTCTGAGGCCAGATAATTGGCAGCACT CCTGTTGTGTGCCGAGAGTGCAGAAAAGGGCTATCC CGAAAAGGTGTGATCTGGAAAGAAGGAAAAAAC	257	D	--
IM000384	ATCTTTTGGCCAGAGCAAGCAGGGACTGAGTGAGCA GAGGTGACAGGAGCGAGCAAGGCTGACAAAGTCTTC CATATTCCTACTAGGATGACCCATTAAGCCCCATTT AAAGCATTCCATTGCTTTCCAAATACAAAGTCCCAA AATCCACATTCTTTCAAATAAAAGCATG	258	C	--

IM000385	TTAACATATGGTTTTTAAAAATCCATAATGAGCATA TGATAGAGAAGTCATCAGAGCTCTTCAGCTCCACAT CATCTGTCCCCAGAAGTATTACTACTCCTAACTTGC TGAGCCAAGGCACAGATATTCTTTGTGTAAGCATCT CTTCTTTATCCTGTGTTGCCACGCAGGAGCACGCAC ACTGCTTCCTGTCTGAGGTTGTTCCATATCAGCATG	259	D	--
IM000386	CATGCCAGGGCTTGAATTAACACAAGTGCCCCAGAT	260	D	--
IM000387	CCTGTCTGTATATGCACATG	261	D	--
IM000388	CATGGAAAATGAGAAACATCCACTTGACGACTTGAA GAATGACGAAATCACTGGAAATCGTGAAAAATGAGA AATGCACACTGTAGGACCTGGAATATGGCGAGAAAA CTGAAAATCACGGAAAATGAGAAATACACACTTTAG TACGTGAAATATGGCGAGGAAAACTGAAAAAGGTGG	262	R	--
IM000389	CATGAAGGTAAATTATGACCATCAGGGTTCAGACCT CAGCTCGACCGGAGACCAGCCTGCAANTCCCCACAG CCCTCCCTAAAGTGGGTTAAAAGACAGAAAAGAATT AAATATCTGA	263	R	--
IM000390	CATGCACTAGCAAGATTTTGCTGAAAGGACCCAGAT	264	R	--
IM000391	GACACATACACACACATG	265	D	--
IM000392	GTAAATGTATTAGGTTCAGAACTGGCACTGCTCACT TATGTTCACAGTTGTTTGGGTAAAACTAGAACCAAA CACAAAAGCAAAAGAGCCAAGCAGCAGAGCAGGGAG CAAGGGGCTTGGGGAAAACACTCACCTCTGTTGTGT CTTCTTCTAGCTGTCAGGGCATTGAGTGGCAAGGAG TGGAAAGGAACTTTGGGCATTCCGAGTCAGGAAAAG TGTACCAAAATAACACTATGGAGGTTAGCAAGTGTT CTAGAGGGCAGAATAAATACATG	266	D	--
IM000393	GTTTAGGTCATTGGTGGTACACTCTCCAAGGACAGT ATAAATTGATTTTTTTCTGTATCCTTCTTTGTTCTT GGCCATAAGGCACTTGGAGTGCATTAATATGTACTT ATTATTACTATGTCTTTTCTTGTCTTTGGCTTAAAA GAAACAGGGTCAAGTGACCATG	267	C	--
IM000394	AGTTTTCTTTAAAAAAATAAAGTAGGAATGAAACTG GAACAAAAATGCAATAAATTTTAAACCATCACCGCT AAAACATG	268	D	--
IM000395	CATGATTTTCAGTTTTCTTGCCATATTCCAC	269	R	--
IM000396	GAGAGGAGCCTGGGGAAATGAAGGTCCAG CAACAGGCCCAAAGTGGGATCCAGCTTAA GGGGAGGCCCCAAGGCCTGACACTATTAC TGAGGCTATGGAGCACTCATAAAAATGGA CCCAGCATG	270	R	--
IM000397	CATGGCAGCCTTGGAGTATCAGGCTGCTG TTCCCAATGTGGGATGCAGAGGGCACTGC CAGCCTGGTTATCACGCACCACTGTCACA CAGGGAAGCGCCCCCTTCCC	271	D	--

IM000398	GGAGTTCTTCTCTTCAATAACAGAGTAAATTCTCCC TCAGCAGTTCTCCCAGGAAACCCATAACCTAGCCAT G	272	D	--
IM000399	CCTTAGATGTTTGTCTAATCGACAAAATACTTTATA TGTGAAAAGGAAAGCATG	273	D	--
IM000400	AATAATCAGATTTCCAGAGCTCCCAGGAA CTAAACCAACAACCAACGAATACACATG	274	R	--
IM000401	ATCCAGTAATCATTCATCTTATTGTTTCCACACAGG AAAACCTGTAATAGATGGTTCATCAGCTTTATTTAT AACTTTCTATCTTGAAAGCAACTGGAATGCCCTTCA GTAGGTAAGCAGATACACTAGGCTCACCTCAACTAT AGGCACAATGAAAGGAATGAAATGTCAACTCACGAA AGGTAAGTACACATG	275	D	--
IM000402	CCTCGCCATATTTCACGTCCTAAAGTGTGTATTACT CATTTTCCGTGATTTTCAGTTTTCTCGCCATATTCC AGGTCCTTCAGTGTTCATTTCTCATTTTTCAAGTTT TTTAGTGATTTCGTCGTTTTTCAAGTCGTCAAGTGG ATGTTTCTCATTTTCCATG	276	R	--
IM000403	CATGCAAGAACAGGACAAATGTCTGTGAAGAAAATG AGTGAGCGTGAACAGGAGGTCAAGGATCCGGTCCCA GGCAGCTCTCAGTCTGGGCAAGCATTTCTAAACTTT GCCTTCCTTCCTGTTGGGGGTGAAGGTCTG	277	K	*Fgf3/Fgf4*
IM000404	AATAGGAGTAGATGAGAATGAAGATTTTTCAATTTA AAGGACCAGCAAATAGCTTCAGCAAAATTATAGAAG AAAACTTCCCATACCTAAAGAAAGATGCCCATG	278	R	--
IM000405	CATGCAGCCCCATTAGTGATTGATCCTGTTCCATAT AA	279	D	--
IM000406	CATGGGCTCTCTGCTGATAATGCTGAGGC TGTTTGTGCTGTAGTCTGCGCTTTTTGCC CCCTCTCAGAAAAACTGTATGTCATAGGA GTTGCTGGCTATTGGGTACATAAGCAAAG CCACCCTATTGTGCCAGTGCCTTAGACAG TGAGACAAGAAAGGCCCCTGGTTAGAAAT CTTATCAGGACTGGGAATGTAACTCAGTT GATAAGAGTGCTTGCTTAGCGTGCACACA GCCCTGGGTTCAACCGCCTAGTACTACAG AAACTGAGTGTGGCTTCACACACCTGTAA TCCCAGCACTTGGAGAGATAGATGCAGGA GGATTAGAAGTTCAAGGTTATCTTTAGTC ACATAGTATTGGTAGCCAGCCAGCCTGGA ATACTTGAGATACTTACAGGAAGGAAGGA AGGAAGGAAAGAAGGAGGGAGAGAGGACA GGAGGAAGGAGATAGATATACACAGAAAG AGACAGAGAAACAGAGATTCAGGAGACAC AAAGACATACGGAGACACAGTGAGA	280	R	--

IM000407	CATGTGGTTGCTGGGGATTGAACTCAGGACCTCTGG AAGAGCAGTCAATGCTCTTAACCGCTGAGCCATCTC TCCAGCTCCCTTTTAGACTTCTTAGTAGCAGCATTA ATTCTTGCTTGGTTTCAGTTCTGACAACCACAGCAG TCAGGAGTTTGAGTAAGAGG	281	R	--
IM000408	CCTCATAATGTTTGTTTGAGCATTTTTTT AAAACCTAACTTGTCTTTTGCTTATCTAT TGTGGTTTCTTAGTGTGTGTGTGTGTGTG TGTGTATGCGCGCGTGTGCTCTGGTCTTC GTGCACATG	282	D	--
IM000409	ATTTGTGACATCTTAGGAGCTTAGGTTGGTCTTCGA GACACAGGGCTGTCCCTGTAAAGCAGGTTCCATCAG TGACTCCAGGGTTTTAGCAGTTCAGTGGCGTAGTTT TCAGACTGCTTAAGATTTCTCAAGGGCTAGGCGTGG GGCAGAGACCCTGCAGACCCTGGCTAGAACAGANGC CCTGGGAGACAGTTGAGGGTGCTCAACTGTGGAGGA CATG	283	K	*Fgf3/Fgf4*
IM000410	CATGTATGCACAACCAAAACTTATAAATATGAGAAT TCACTTATAGTCCTAGTCCTTTAATACAGAATTTAG CATTCCGATATAAAACAACAGATTAAACCCCAACAG TTAGAATAGAGCAG	284	D	--
IM000411	AATAGGAGTAGATGAGAATGAAGATTTTCAACTTAA AGGGCCAGCAAATATCTTCAACAAAATAATAGAAGA AAACTTCCCCAACCTAAAGAAAGAGATGCCCATG	285	R	--
IM000412	CATGCACACCCTACTCCTGGGTGATCGTACCAGCTC CAGCCTCTGTTCTGCACGCTGTGCCTTCAACCTGGC AACCTCC	286	K	*Wnt1*
IM000413	CATGAAAACCTGTCTCAGAAAACAAAAACACGTTGA GAGCCAGCATAGAAGCCATAGGAGGTAATGTGTGTG TGTCTGTATATATGACAAGAGCAGACCTGTGCTGAA CCAGTTAACTACTTTTG	287	D	--
IM000414	CATGCTACTAACCAGTTGAGGCAGTACCAGTTGTTG AAGATGCTGTCTTTTATCCAATGGATGGTTTTAGCT CCTTTGTCAAAGATCAGGTGATCATAGGGTGTGAGT TTATTTCTGGGTCTTCAGTTATATTCCATTGATCTA CTGGCCTGTAATTGTACCAATAC	288	R	--
IM000415	GGTTAGGAATTCTGGACAGTTGGTACTTGGTTTGAA TATAGTAGGTGACAAGCTGTGCCTTGAGTGGGGTGG CAAGCAGGGTTCTCTGCAGCAGGATGCAGTGTACAT G	289	C	--
IM000416	CATGAAAATGTTAAGTCCTGACAGACAGGGTGCCAT CTGCCAAGAATTTGAGTAATCTAGAAACAGAAAT	290	D	--
IM000417	CATGGGGTTTTGTGGATCTG	291	D	--

IM000418	CAGAACAAATAAGCTGGAAAGGATGAAGCAGCCACA ACATAACTGCTGTTGGCTTCTTTGTGTACATTTTAA ACCTTCCTCTGAAAGAGTGACCAATGCTTTTAACTG CTGAGTTATCTCACCCGACTTACTTTCTCTCTCTCT CTCTCTTTTCCTTCTTCCTAAAATTAATTGTGTGTG TATGTGTGTGTGTGTGTATGATTCAGAAACCTTTTA TGTGGTGGTAGAAGACCATCTGCAGGATTCATG	292	D	--
IM000419	CATGGTCCCACAAGCCTAGAATGATTCGT GGAT	293	D	--
IM000420	GGGGTCCAGGAGAGAAACTTGAGTCATG	294	D	--
IM000421	GGAAAGAGATACTCAAGACCAACTTTACCACCTTTC ATTTAGCCAGGACTGCTCTATTCTTCCTATTACTGC TAAGAAACAAGATTCCTTGTTTCTTGAGATAAGAAA CGGGCATAACATCCTATCTGGTGCCATACTCACCAG ACCATG	295	D	--
IM000422	GTCCTTCCCAAAGAATAGTGTTAACTGAGCTCTTTG GGTGGCAATAAATGAATTGCTCTGGTGGGACAGGCA GTGCACATATGGGGAGGGGGAGACACATG	296	D	--
IM000423	CATGTTCTTACTTCTTGTTG	297	D	--
IM000424	GGGTATATGAATTATATATATATGTGTGTATATATG TATACAGGCATG	298	D	--
IM000425	CATGCGCCCTAAGACTCATCTCCACGAATGACGTGA CGACCTAATTGCATTCCTTCTAACCCACTGATTAGG CAAACCACCCTCCAAAGGGCTCGCTGAGTTCCTCTT CGGGAAGAGGTGTGTTGAGTACGCTGGAATGGATAT TCGAGGGCTGAGG	299	R	--
IM000426	CATCTCTCGAGCCCTTGCCCAGCCTTTTTTCTTAAA ATTGTATTTTTAAAATTTATTTTCTGTACACAGGTG TGTGAGTGTGAACATG	300	D	--
IM000427	CATGTGGACCTGGGGGCTAAGTCAGGGTGAAGCTTC CACAGCTAAGTGGCTGGAGGCTGCCCTAAAAGCTCA GGAGGCACCGCAAGCAAGCCTTGAAAAACCTTACCC ACCAGCTTGACCTTAGACTTCTGGCCTTCAGGCTGT GACAATACATTCCTGCTGTTTAAAGAACCATATGGT TGGTGATGTTTTGTTTGTTTCTGGTTCTTTTGTGTT GGTGTTTTTTGTTTGCGGGGTGTGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTTGCAGTGCTAGAG ATAAGATCTGA	301	K	*Fgf3/Fgf4*
IM000428	GTCTAAAGTTTTCAAATGATGGATAAGTTGTTAAAC CTCCTTTAAGATCTCAAGCACAAAAAGAAAGACATC AAATACGAATAGTAGAAAGGAAAGGAGATTTGGAAC TAGAGGCCCCAAGAGTCATAAAGAGAAGAATTTAAA CAACTGTACCCACAAATTCATTAGCATAGATCAAGT AGTCCATTTCTTCATG	302	C	--
IM000429	CATGTATGTTCTCGATGCCTTGGCCTG	303	D	--

IM000430	AAAGACATTAACTCTTGAGAACCAAGGGGTAGGACA GTATAGACTGAATTTTGCCTCCCCTCTTCATAAGTT GTCACTGCTAACCTCATTTCAGAACTTAAGCATATA ACCTTCATG	304	D	--
IM000431	CATGGAGAACTAGCAAGAGCAGGATGGCGTTTCTCT AGAATGCCGTATAG	305	D	--
IM000432	CATGGTGACTTTCCATCTTTAGAACCATAATCANGT TTAAT	306	D	--
IM000433	CATGCTTATATCCCTCAAAAATTTTACAGTTAAACT GAAAATGCTTACTTACTTTTTTTTCTTACTTATATC TAGTATCGATAAGAACTGTCCCAAAGGACAC	307	D	--
IM000434	CTGGGTCTTAGTCCTCTGAGGTCCCTAGCACATCAG AGGTTCATCAGTTCCAAGAGATGACACAGCCGCAGT CATG	308	K	*Fgf3/Fgf4*
IM000435	CATGGAGAATGCACAGTCAAAACGCTTGCATCCT	309	D	--
IM000436	CACCCCCTCCCGCCTTACATCAATCCTGG GTGCACAATGGGACTGTGGATGACTGATG TCTGCGCAAACAACTTGCGGGGAAGTCTA GCTGACAAACGCTCATG	310	K	*Fgf3/Fgf4*
IM000437	ATGTATCCAATGGCAAAGCACGGGGGAGGCTTCATC TTGAAGAGAAGAGTGCTCTTGGTAGGCTATCCTTTT TTTGAGACAACTAGAAATAGGAGCATTTCAACAATC TGGACATATGTCCTCCCACAAGAACTTGTTGAGAAT GGGTCTGAATTAACTGGAAATAAAAGTGAACACATT CTCCTATACACATG	311	D	--
IM000438	TCACTCCATTTTAGTTCAAATGCTACAAC TCCTTTGAGCACCACTGTCATTTCAAGAC CTTATTCTGTGAATACCATG	312	C	--
IM000439	CATGCTTAGCCCAGGGAATGACACTATTCGAGGTGT GGCCTTATTGGAGCAGGTGTGGCCTTGTTGGAAGAA GTGTGTCACTCACTGTTGGGGTGGGATTTGAGAGCT TCCTCCTAGCTGCTTGAGGATGCCGGTCTT	313	R	--
IM000440	CATGAGCTGGGTGAACGACAGCAAAGGTTTGTTTCT CTTTTAAGGAAGACAATGGTGTGAAATTGGTTGATC CTTTGGGGGAAATGTTGGCCCCTT	314	B	Mm.20245
IM000441	CATGATCTCACTGTGAGGGCTGGCTACCTTGGAGCT CACTGTACTGAAATATTCTGGCCGATTGCCTCTTCG CTGGGTTTATGGGCACACACAGTACTTGTCTATGAG TCTTTGTTAGGCTGAGCCTAGTGGTGCAGGCCTGTC ATCTCCCCTACTTTACTTTAGGCTCTGAGGCAGGAG GAT	315	D	--
IM000442	TCTGGTAACTTGGGGGTCTGATAAAACAG TTGGGGGATTTCTTTTCTTTTCGCGTCTG AAGCCAATGTTATTACAGGTGTGTGCTTG TCTCTCCCACACCCTGCCCCTGTTGCCTA ACACACGCGGCACACACATG	316	D	--

IM000443	CATGACTCTTCCTCCAGAGTTAGAGGTGGAGCCAGG ACAAACTCTAAAGAAAAGAAACCCCAATCAAAAAGG GAAGCTGGTATCATCCAACCTTTAAATTACTCCACA TCCCTCCAGAG	317	D	--
IM000444	CATGTCTGTCCCAAAAGGAAGTTCCTTCCTCTGTCC TCCACATCTGACCAGCACCATCATTCAATCTGCAAC CCAAACCAGACATTTACATCATCTATGCCTCCTTTC CTGCTTGTCTCCCCTCAACCAGCACCCAGCAAGCTT TCAGGTATCCCCTTAGTGTTGTCAGGATCTCTCCAG TTCTCCAGACCCCAATTCTGTTCTCACTCTACACTG CTAGC	318	D	--
IM000445	AAAGCTAACTTCTCATCACCTACCTAATAGCCTGAG AGCCCTGTGTAGAAAAATTAAGGAGTTTAGTTCCTT CATG	319	C	--
IM000446	CATGCAGACAAAGTAAATAAGAAAACAAATTAAATG TAGGCTGGACGGATAGATGGT	320	D	--
IM000447	CTCAGCTCCTAGGCAACACTTGTAGACCCACAGCCC CTTCACACACACACACACACACACACACACACACAC ACACACGGCTGGGGATCCAACCCATCTCGTCCTTAC ACGTGCTCTACCATCACACCACACATTTCCAGCACT TTTATCTGAAGTGTTTCCTTTTATTTGTGCATG	321	K	*Wnt1*
IM000448	CATAACCACTATAACCAGCCTGCTTACTTGGCTTTG TTTCGAGGGCTTTTGTTTTAGAGCTCTTTCTTTTTA CCCTTCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTGTGTGTGTCTGTCTGTCTGTCTGTCTGTCTG TCTTAGTGTTTGTACATG	322	C	--
IM000449	CATGTGGTCCACGGTTTTACTTTACTAGGGAGCAAC CTGTACCACAGGGAGAGAGGCCTAAGGACAGGAAAG GAGCTGACCCAGAACTGAAAAGGCACACACCATTCT GCCAGCACTTCCC	323	C	--
IM000450	CATGTCCTACAGTGGACATTTCTAAATTTCCCTTCT TTTTCAGTTTTCCTCGCCATATTTCACGTCCTAAAG TGTGTATCTCTCATTTTCCGTTATTTTCAGGTATCT CGCCATATTCCAGTTCCTACAGTGTGCATTTCTCAT TCTTCACGTTTTTCAGTGATTTCGTCATTTATCAAG TCGTCAAGTGAATTTTTTTCATTTTCTCTGATTTTC AGTTTTCTCGCC	324	R	--
IM000451	CATGTTGCCTCAAGACAGATCTCCACTTTAAAGACA TACCTAAAGGCCTGGAAGCTTAGTCAATTAAGCTTT CCTGCCCAGACACTCCTCCCTGAAAAAGGTATTTAA CCTCAGGCCCACCCTGAGAAGTGGGGTATGATTTTA CTCATCCACTTTC	325	R	--
IM000452	CATGGTTTCTATTACTGTGTTGAAGCACCCTGACCA AAGCCAATTGGGGGACGAAAGGGTTTATTTGGCTTA AACTTCCAAATCAGTGTTTATCATTAAAGGAAGTCA GGGTAG	326	R	--
IM000453	GCAAGTGTCAGACGGCTCTCAGGGAGATACACATAG CTTTATTGGATAACTGCAGCTTGAAGACATG	327	D	--

IM000454	CATGTACCTATGTGTGTGTAACATTTGCCTATTTTC ACACAGTTAAGAAAGCATCGTTATGAAAATCATTAC AACTTTCCAGATAAACAGATCCACTCAGCCACAGAT	328	D	--
IM000455	GCCCTTCTCTCTGAACTTTTCAGTTCCTGGATAAAG TCAGTGTTCCACCTCTATACCTGACTAGTTTTCCTA AATTCTGAGTCAAGCATATTTCATG	329	D	--
IM000456	GACCTCGTGGGCGGGCCTGAGGAGACAGTGCAGATG AGGTGTCAGTAAGGAGGATGCAAGCAAGAAAGATGC AGGAGATGATGGAGAAGCTGAAGAAGGCACTGAAGA AGGCACAGGGAAGAAGAGTGCATG	330	D	--
IM000457	CTTGCCGTTGAGAGCGTCCAGATCCCCTGACTTGAG TGGGTCCACCTTGTTTGGTTTGGTTCGCAGTGTCGG CTGTGGAGCCCCAGGCCTTGCATG	331	C	--
IM000458	TTCTTATCCACTGAGCCACACTGCTAATACTGTGAT GTCTTTTTTAAGACTCACCATG	332	D	--
IM000459	GGGTTCAACACATTTTTGGAGATTGATCAAAATTAA AACATG	333	D	--
IM000460	CATGAAGGAGAGTCTGAGGCTACATCCACCAGGCTC TATGATCTCCCTCTGCTGCATCCAGGACATTCTCCT TCTGGATGAAGATGATGCTGGCGCTGGCGCTGGCGC TGACGCTGATGCTGCTCGCTTCTGCGTCCT	334	C	--
IM000461	CCTTGTCCTCAAATTACAAAACTCCCTAG GGTCTTTTCTCTGGGCTACAAAATTCTGC AAATGGACTCAGGAGGAATCAATGTGGAA ATTTCACTTTGCCTTCCCAATCAGCAAAA TAATGTTTGCCAAAATCGTTAGATTTCTT TCCCCTAAGTAGGCTACTGCCGACTTGAA AGCAGTGGTTCCAGAACCCGAGCCCAGGG GCTGCCACTTCCTATGCATG	335	B	AI426908
IM000462	CCCTTGTCCTCAAATTACAAACTTCCTTA GGGTTTTTTTTTTGGCTNCAAAATTTTNC AAAGGGCTTCAGGAGGAATAATGGTGGGA AATTTACTTTTGCTTTCCAATCAACAAAA AAATGGTTGGCCAAATCGGTAGAATTCTT TCCCTAAATAAGCTACTGCCGACTTGAAA GCAGTGGGTTCAGAACCCGACCCAAGGGC TGCCCTTTCTATGCATG	336	D	--
IM000463	CATGTATCTTAAGAACAGAGCCAGTGCTCTCCCTCT CCCACTTGAT	337	D	--
IM000464	CATGCAGANTAAAGTACATATATGTAAAAAATAAAA ATAAATCTTT	338	D	--

IM000465	GTGCTCTCCCTTGCCTCTCCTCTCCTGAG TTTCTCTGTAGGTGTAAGGGCTGGAGGTG GGCCCAAGAACCAGAGATCAGAGGAGGGA ACTTCCGGAGCAGAGGCCCTGGGAGCAGT GTTAAGCAGGCTTTGGCCAGGTCTGGAGG TGTCCAGGCAGGGAGGTGGAGCTGGAAGA GACCAATTAGTCAAACGGCTGCAATTGGC CATTTGGAAGCAATTAACAGGGTCTCCAT TACCATATTATGCCCCTCCACCCCCTCCA CACTCTACTAGGCTCTGCTCTGTATGGAA GGGGGAAGGTGGAGGCTCANCTCAAGCCA GGGAGACTACAATGGAGGCCCAGTGCTCG CCAGGATGCACACACTCAGGCACCCTCCG TGTGAGGAGGGGAGGGCAGGGCAGCATCT GAAGCAACCTGTCATTCACAGCCTGANAG ANGGTGGGAACAANGGCTTNCAAAGCCAA GAANGCANGTGGNTAGAAATGCANGAAAA CCTCTCTGGTAAGAAAGGCTGAANGAAGC AGCTAGGGTTGTAAAACAAGANCAT	339	K	*Fgf3/Fgf4*
IM000466	CTCCCTCTCCCTCTAGCTGGCCTAGCAGGGGCCAAT ACAACTGCAGGGAATCAAGGAAGAGCCTTTTCCTGA ACTGTCCTGGATGCCCCAGTCCAACAGCAACTCCCA CTTGCCCTGGCTTGGTTTGCTCCACTGTCCTGAAGG CACAGTGTGATATCCCAGACCTCCAGCGAGACAGCC CAACCTGCAAGCCCTGATGGGAGGGGTGGCCTGAGA CAACAGTACCTACATG	340	B	AI550057
IM000467	CATGGACTCCAGGGTCAGGGTGTAAGAAAAAGGTGG AGCCTGCTAGGTGTGGTGACACACACCTTTAACCCC AGAACTCAGAAAGCTGAGGCAGGTGACTAGCCAGGA GTTCAAGGTCATCTAGTTCATCAGATCTATAGAGTG AAACAGCCAGGCTACATTTGAGATC	341	K	*Fgf3/Fgf4*
IM000468	GCTCAACACTTAAAAGCGCCTGCAGAGGGGTGGGGG TTTAATTCCCAGCACACACATAGTGGCTCAGGGAAT CTGAAGCCCTCTTCTGGCCACTGCGTGAACTGCATG	342	D	--
IM000469	GTGGGAAGCTATACGAAAGTAAAACACACTCTAAGA AAGAGAACAGGCTGCCTGGGAGAGGGAGGTGCCAGG GGCTTAGACAGGAAGGTAGTTTTCAAAAACTGAAAA CTTAAGCTATCTGAATGAATGATACAAAATAAAAGA AGACACAAGAATTTCCAGTCACCTGAGATATCTCAC ACTCCTGTTCTTTCAACCTTCTAGCTGAAAGGAGAA AGAGCCATG	343	D	--
IM000470	CATGGAAGGAGTTACAGAGACAATGTTTGGAGCTGA GACGAAAGGATGGACCATCTAGAGACTGCCATATCC AGGGATCCATCTTATAATCAGCCTCCAAACCCTGAC ACCATTGCATACACCAGCAAGATTTTGCTGAAAGGA CCCTGATATAGCTGTCTCTTGTGAGGCTATGCTGGG GCCTAGCAAACACAGT	344	R	--

IM000471	CATGCTTAGATTGACCGCAATATGTGTGGTACTCTT CAGACTTTTAAAGATTTGCTGAATATCCTATTCCCC TTAAATTGTGATCACCCTAGCTAGATCTAATCTTAG ATCTCGAAAGTTCTACAATTTGCCTCAATTTGATTA CTGTTTTCCTCCTTGAAGAC	345	D	--
IM000472	CTTGCCTTGGGAAGTGAGGGGTTCTAATGAAGGTTG CAAGCCTGTCCACCCAGGGCCCTGCTAAAGAAGGAA TGGTCCCCAGCCTGTTTTGTCCCCTCTGTGGCTTCT TAGTTCTGGACACTGAGCCAGTCTGGGCAGCAGGCA ATTCACACTGTGAATTTCTGTGGAAAGCATTTTGGG GGTTCTGAAAGCCCTGTACATTCTGTGTTAAGGACA GAGGGCCTCCTGCATG	346	K	*Fgf3/Fgf4*
IM000473	CATGGGGGCTATGTCCTAGGGTAGACACCCCCTTTA TCCCTCACCTCCTTCCCTGTCTTAGCAGTGGTGTCC CCCACTGTGACTCTACTGCATCTGGGAGCTGTCTCC CGGGGGACTTCCTCCTGCTGGAGTGAGTAGGTGGCT AGGGCGAAGCCTGTGTAAGAGGCAGGAGGTGTTTTG CACAACTCCAAAGGGTGCAGATCCTGCTGGCTCCAG CTTCCCAGGGCCAGACCCCCAAATACCCTTCACCCA GC	347	K	*Fgf3/Fgf4*
IM000474	GTGTATGTTCTCTGGTGAAAGTGTTAACCAGCTCAC TCCGTGAAGAGCACGCTGCTTTCAGATCAGTGTTCA GAGTCTTGAATAATTGGTTTTTAGAATCATAAAATT GCAGTCCTTTACAAAGGACTGGAAGTGACTCATG	348	D	--
IM000475	CATGTGAATTCTCTATTTGCAATGTGCTTGGTTCAT ACTTCCATACTCTACCCAGAGCCTGTTAGAAAAATC ACTCTTCCCCACCCTATTCTTCACCAGTCAATATGT ATCTAGTATTCTAAACTTCCTCCCTCCTAAGGCAGT GGGGAAG	349	D	--
IM000476	CATGTGTACTCTCACCATCAGAATTATGAGCAACCC ACAATTTCTTCACATTTATAACTGACCCAGTCTGAG GTATTGTGCCTTTAGCAACAGAAACTGAACTCAAAA CAATCGGCACAC	350	C	--
IM000477	CCATATCAGACCAACCTTCCCACACAACAGTAGGCC ACCAGGTGGGGGCAAAGTCCTGGGTAAGGTTCTTGG CACTGTAATTTTGAATCCCAATAATAATGACTGTGT TATTTGCTCATG	351	D	--
IM000478	TAAAACCTTTAGGGAGCTGATAAAAATCTATCAAAA CAACACTCTGTCTCTCGTATCCAGCCATCCATG	352	C	--
IM000479	TCTGCCCAGCCTTTGCTTCCTCCCTGGTAACAGGAT GCTAATTAGAATTCATG	353	B	AA117784
IM000480	CATGTAAAAAAAAACTTCATTAACAACTA CAACAAAGCAGAGACCTTGGCCCTTGGAT TGGGGCCCCTCTGAGAGCTATAGGCTGGG ATACTGG	354	D	--
IM000481	GTGCGTGATAACCAGGCTGGCAGTGCCCTCTGCATC CCACATTGGGAACAGCAGCCTGATACTCCAAGGCTG CCATG	355	D	--

IM000482	ATGTCAACATTGAGTCCAGTAAGGACATCGTATATG CTGGTCATTATTATAGCTCTAAGGGTTCATACATGA GACAGACCACCCCCTTACCCCCTCCCCCGTCTGGGC TAAAAGCAGACACACTGGGTTGGTGAGAGAGCAGCA G	356	K	*Wnt1*
IM000483	CATGAGACAGACCACCCCCTTACCCCCTCCCCCGTC TGGGCTAAAAGCAGACACACTGGGTTGGTGAGAGAG CAGCAG	357	K	*Wnt1*
IM000484	CATGAGAAAAATTTGTCTCTAATTCTCTTTGTTGAA TTTTTGTGTGGTTTTGATATCAGGTGATTGTGGCCT CATACAATGAATGTGG	358	R	--
IM000485	CCAGTGAAGTAAACCCAGCAGGACCCTTTACAAAGC CAGGACATG	359	D	--
IM000486	TCGGGGGAAAGTTATTTTTATACCTTCCCGCTCTGG ATTAAGGGAGGGTAGGAAAGGATTGGATGAAGCTAG AGACAGAGTGGCAGGAAGGTGGTAGACCTGAAATTG TCAGACAACCACTTATCGTTGGGAAGGGTATAAGGT GACCACAGCACTAGCAGACTGTTCTGGACGTAGTAA GGAGTTCCTGCAGGGGAGGAGTGGGTCAGCCTTTGA ATCCCATATGGTGGTTCACAAGTCAGCCTACATG	340	D	--
IM000487	CATGTGTTTTTAGCAACTGTGCTCATTTTCTGCTGC TGCTAGGAATAAAATCAAATCTAGTANAATTGCTTT AATACAAAGTTATTGTCATCCATCTCTGAAGATCTG AAGTATTGCTGGGGGGTCTCCAACTCACCCACC	341	D	--
IM000488	CAAGGGCCTCTCCTCCCACTGATGGTCGACCAGGCC ATCCTCTGCTACATATGCAGCTAGAGACACAGCTCT GGGGGGGGGGTACTGGTTAGTTCATATTGTTGTCCC TCCTATAGGGTTGCAGACCACTTTAGGTCCCTGGGT ACTTTCTCTAGCTCCTTCATTAGGGGCCCTGTGTTC CATCCAATAGATGACTGTGAGCTTCTTATAAGCATA AACTTTCACTTACCACATG	342	R	--
IM000489	CATGGTGTTAGCCTCCAGGCAGGAAGCATACCAGAG GAGAACTCCACAGGGAAGCCTTTGTTTTCTGCTGTT AAAAACAAAGTATGATGGGGCTTAGAAGAGGCTTTA AGAGGTCCTCTGGAGAAAAGAATCTATTTTCCATT	343	D	--
IM000490	CATGAGAGGTTTTTAAGTCCTGAAAGACCATCATAC CTAGAGTCTATACAACAAATAAACTTGGAATACAGT GAAGCTAGTAAAAATAACTTCCTGAGCTTATGG	344	D	--
IM000491	CACAGTCAGGAAGCAGAAAGATGAACGTTGACTCTC AGCTCTCCTTCTCCCTTTAGTTCTATGGAGGTCTCC AGCCCATG	345	K	*Fgf3/Fgf4*
IM000492	CATGATAAAAGTCTTGGAAAGATCAAGAATTCAAGG CCCATAAATAAACATAGTACAAGCAATATACAGCAA ACACAGTAGCCAACATCAAACTAAATAGAGAGAAAC TTGAAACAATCCCACTAAAATCAGGGACTAGACAAA GTTGCCCACTCTCTCTTTAACTGTTCAATAGAGTAC TCAAAATCCTAGC	346	R	--

IM000493	CATGGTAGCTTTCTAGTGAGGTCTCTTCC	347	D	--
IM000494	AGTACCCTTAGCCAATAAACCATCCCTCTAGTCCCT GTTTGTTTTGTTTTTTTTTTAAAGACAGGGTCTCAC CATG	348	K	*Fgf3/Fgf4*
IM000495	CATGAGCTAGGCCATCTGCAAGCTGGTCTCGTCTTG ACCAGGAGTACACAGAAGCCTGGCTCAGGACTTGGT AAC	349	D	--
IM000496	GTTGTTTATGCAGATCTCTCAGCGTTAGCATTCTAT GGGATTCTTTGGAAAGACCTTTTCAGTTATCTTCCA TTTCTGAGGCTGTTTCTAGGCAACGGAGTGGTACCT TCCTTTAATCTTCCCCTGACCTTTTCTGCCTATGAA GATGTTGACTAGTGAGCCCGTGGGGATGTGTATTAT CTGTTACATTTATTTATGGCTTGGTAGCGACTCCTT GGTTGTTGTTCAGCTTTTCATG	350	D	--
IM000497	CATGCCTCCCTCAGCCTCCTCCCACCCCT TCCTGTCCTGCCTCCTCATCACTGTGTAA ATAATTTGCACCGAAATGTGGCCGCAGAG CCACGCGTTCGGTTATGTAAATAAAACTA TTTATTGTGCTGGGTTC	351	K	*Wnt1*
IM000498	TCTAAGTCCAGTCTTTCACACACACTGACTTTGGTC ATCTGTAATCACAACATG	352	D	--
IM000499	CATGCACACAAACTGGCCCTGAACTTTTGACTTCCA GGCCTCTGCCTCTCTGCGCGCACACACACACTCGCA CTCCTGTATATGAAGCGTATATGTGTTTCTCTGGGA ACTGTTTTTATCAGGTGAAG	353	K	*Fgf3/Fgf4*
IM000500	GGGCTGAAGGAAAATGTTGTGTCATCTTT TGTGGCATG	354	D	--
IM000501	CATGTACCACTTTTGCTAATCCCCTAACC GCCCCTTGGTAAGCATCTAAAGTGATATA TCTCTTGGTCTACTGAAGTTCTGCCCTGT CTCCATCGGGGATTCTCGGGAGGCTAAAA TTATAGACTATTTGTGAAAG	355	D	--
IM000502	CATGTCCTTATGATATGGAAAAA	356	D	--
IM000503	CATGTGCCAAGAGCCATTACAGGCTCAGA CTAACATCTGCCTGTAAACAACGGTTGCT AAGTTTCCAGGGAAGCGTAAG	357	D	--
IM000504	CCAGATGACCTTGAACTCAGAGATCTCCTTGCCTTA GCCTCCTGGGATTCATAGCCGCTATGCCTCAAGATC TCCATG	358	R	--
IM000505	CATGTAGTTTGCAAACAAGACATCCCTGGTATATCC AGAACCTGAGCTATGC	359	D	--
IM000506	GGATATAGTGTCAAACAGTCTGATGTATTCATAGGT TTGTATCCATAGTTATCAAATCTCTCATG	360	D	--

IM000507	CATGTACCACACACAGACTTGGTAATAAGTTAGATG ATAATTACAAAAGCAACAAATAAAACCAACAAAACA AAACAAAGCTTGGTAATA	361	D	--
IM000508	GTTAGGAGCACGAACTGCTCTTTCAGAGGACCTGGG TTTAATTCCCAACACTCACATG	362	R	--
IM000509	CATGGTCAATGATAAACATTCCAAAACACCAAAACC ATCCTCTCTGTACAGGCTATGATGATTCAACTGCTG CCCTTCCTCATTTCTTGTTCCCAACTCCTACTGAAT ATTTCCTGCAT	363	D	--
IM000510	CATGATAGAAGACCACGTCTGGGATGGGGTAAGGGT TTCTCAGAGTACCTTGCCCTGGGGCCACATCCTAAA TCTACAACAAAGCTGACCCTA	364	D	--
IM000511	CAAGTTTTTGTAAGGGAGCTAAGAAAGGCATTGTTG GTTAGGTTGGAAAGAGGGGGCAGGACCTGGCTCTCG CTTCAGCCCACTCCCCTCTGCCCCCCAGCCTCAAAC ACTTTTACCCTAGCATAGCAGAAACATG	365	D	--
IM000512	CATGAACTCAGTGGGCAGATGAAGAGTTTTTGTGTG AACTGGGGCTTTGCCCTTATCATCCTGTGTGTTCTC CTGGTGACCCTCAAGCTTGGCTGCAATGATCCCCAC TTACAGAT	366	K	*Fgf3/Fgf4*
IM000513	GTTTATTACTCCAATGATTCGCACAGCCGGGTTGCA AGTCTAAGGCAGGCTGTCTGCCTTCCTGGAGGTACT TACCCCACCTCCCCCTCTGGGGGAGCTCCACTTGGC CATG	367	R	--
IM000514	CATGATTTTCAGTTTTCTTGCCATATTCCACGTTCT ACAGTAGACATTTCTAAATTTTCCAACTTTTTCAGT TTTCCTCGCCATATTTCACGTCCTAAAGTGTGAATT TCTCATTTTCCGTGATTTTCAGTTTTCTCGCCATAT TCCAGGTC	368	R	--
IM000515	GTAACCACTCATTTACCTGCCCCAATGATGTCTGGG CCAAGGCACTTTTAAATTCATATCTACTGTGACTAT AGGTGCCCATG	369	D	--
IM000516	CATGACACTGCTCACTGTTGCTCTCTAACCTTGGTC CAG	370	D	--
IM000517	GNGCTTGGCAGAGTAGAGAAACTCTTTGGGAAACTT GGTTCAGATCCAGACATG	371	C	--
IM000518	CACCTCTGCCTCAGTTTCCCTGATTATCA ACAAGTGCTCATG	372	D	--
IM000519	CATGTAACTCAAGAAAGTCTAGTAGGCGTAGTGGTA AATGCCTTTGATCCCAGCACTTGGGAGGTAGAGGCA GGTGGGATCTCTACAAATTCAAGACTGGTCTGGTCT ATATAGTGAGTTCCAGGCCAACCTTCACATTGAAAT TCATCTCAAAACAATAAAAATAGAGGAAGATATAGT CAGGCAC	373	R	--
IM000520	GAAGACATTCATTTTTTTCTTGGGAGGGGATAGAAT CCAAGGCTCCAAAGCAGAGTTCATG	374	D	--

IM000521	GACCACGCTGGCCTCGAACTCAGAAATCTGCCTGCC TCTGCCTCCCAAGTGCTGGGATTAAAGGCTGTGCCA CCACTGTGCTTACTGATCTCTTTGATGTCCCAGTTA TAGCTCTTGGGTTCCCCACCCATTTGTAGGGGGACC CAGGACACCTCAGAGCTCTCCCAAGTCTAAAAAGGG CAGGGTTCCTGGCTCCCTTAATGCCTTATCAAGCAC AACAGAACTCAGGGGCAGAAAATGTTCCCAGGAAGA ACTTAGCTGTGGGGAGAGTCATG	375	R	--
IM000522	CATTTTTCTTTATAGCTGAGTGTTATTCCACTGCAA AAATTTGAATATTCCACTATTCTGTTGATGAATGTC TAGGCTGGTCACGTTCTCTTGCCTTTGTGAATGGAG CAGCAATAAACATAAGTGGGCATG	376	D	--
IM000523	CTCCATTGGGCCGAGTGAAGCTGTGGTTCAGAGAAA CTCTATGGACAAGCTTGACTTCCAGAACATTGACCT GGTCTCTGAGATCAACAAGCGTAGGAAAGCCATG	377	D	--
IM000524	CATGGGAAAGTAATCCGTGGCTAACACAAAGGGGAA ATAAAGTAATATT	378	D	--
IM000525	CATGTAGGACCCTGAATGCCAGCAATGAACAATACC AGCTTGGTTTTCCGACTCTTGCTTTCTCCTCCCTCC ACTACTAACTAGCCTCACCGTTGCATCTTGTGACTC AGAGGTCTTGTTTCCAGGGCTTCCTTCCTTCCAGTG TTCTTCTAATGCATCTAAAGTGAAGGGGTGG	379	D	--
IM000526	CATGCAAAGCCTCTGCAGGGCCGACAGCAAGGAAGG CCCTTCTAGATCTCCAGCACTCTGTCAAAAGCCATC ACTCGGCAGGCAGGCAACCACAATGTAGGGAAGACC TGTAAAGCCTTCAGAGAGGAACAGCTGGCAGCCCCT GGGTCACTCAGAGTGGCCAACAGCTACTCTTGTGGA GACAGCAGGAGGAGGCCTAGACTATAGAAGGATGGA GGAC	380	D	--
IM000527	CATGCACACAAACTGGCCCTGAACTTTTGACTTCCA GGCCTCTGCCTCTCTGCGCTCACACACACACTCGCA CTCCTGTATATGAAGCGTATATGTGTTTCTCTGGG	381	K	*Fgf3/Fgf4*
IM000528	CATGAAACATTATTTNTTTTGGAAGTCTG CAGGTAAACTTAAATAGGTTAA	382	R	--
IM000529	AGCAAGAACAAAGGAAGTACTTCACCTGATAAAAAC AGTTCCCAGAGAAACACATATACGCTTCATATACAG GAGTGCGAGTGTGTGTGTGAGCGCAGAGAGGCAGAG GCCTGGAAGTCAAAAGTTCAGGGCCAGTTTGTGTGC ATG	383	K	*Fgf3/Fgf4*
IM000530	GATTTTTATTTTCCTTAGCATCCTGATTGGAGATGC CTGGGTGCACATG	384	K	*Fgf3/Fgf4*
IM000531	CATGTAGAGACTGCCATATCCAGGGATCCACCCCAT AATCAGCATCCAAACACTGACACCATTGCATACACT AGCAAGATTTTATTGAAAGGACGCAGATGTAG	385	R	--

IM000532	GACCTGTACCCTACCCTCTGATGGAGGCCATCTATT TGCCTGTCCCCAGGAGTCCCCAAACTGCTCAAAGAA CAGACTGTGGGCTCTGGAAAGCTAGCAGGTGACCCC GGGGGATGTTCTGAGCAGTGCCTTACTGAAGTTTAT CCAGGCCCTAGGGTCCCCTCAACTGCTCACACAGCC TAGGGTGGGTCTCTTGAGGAGTCACTTGTCACTTCT GTTGCTTCCCAAGAGACCCAGGGAAAAAAGGAAGGA AGGCCATG	386	D	--
IM000533	ATCTCACTCGTAAAATGAACAAAGGGACTGCAGAGA TGGCTCTGAGCTTTTAAGACCATAGCCTGCTTTTCC AGAGAGCCCAGGCTTCATTTCCCAGCCCACATATGG CAGTTCACAACCATCTACAACTCTAGTTCCTGGGGA TCTCACACTTTTGTCTTCTGTGGGCACTGCGCAAAT GTGCACAGAAATACACGCAAGGAAAACACCCATG	387	K	*Fgf3/Fgf4*
IM000534	AAGAAACACTCTTAGCTGGGCCTGGAAGTGCACATG	388	D	--
IM000535	CTAAAGCAGATTATTATACTTATTCTACTGACCATA ATGCAACCACTATTATATAAACAGAACATACTATAA AGTGAATAACATTAGGATACAAAATGTATAAAAGGG GAGAGAGGATAACCATTGTGAAGTATGTTTAAATAA AATGTTTGGGATTTGAGGAAATTAATAAATTAGTTA CCCTTTTTGCTTTGGGGAAAGAAAGGCAGCATG	389	D	--
IM000536	CAGCCCCAAACCCATCAGCCTGAGACTGATGCACAG GAGGCAGGCCAGTTAGTTATTCTCTGGGCCCCTCTA TTTTGCCTTCTGTAGGTTAATCCCACCGCTCCCAGT GCTGGAAAGTGCAAGCATTGTGGGAAGTTAAAAACG TGCCACCATG	390	D	--
IM000537	CATGGACAATGCACCCCTCAAGCAGTGTCTTCCATA CAGACAAGCATATTTATTTTCTATACAGACAGCAAC TTTGCTGAGGTGTAAGG	391	K	*Fgf3/Fgf4*
IM000538	GGATGAAGAAGCCCAAGGTATTAGGTCAGTCTTGCT CTGACTTCTCACAGTAAAAATACAACTCCCAGGGAC TAAAATGACACAGAACAGCTTAGCCTCTGGACATTG CTTTTGGATTGCAAAGTGATAAGTGAAAAAGTAATA AGTCTATCTACATTGGAAAACATTTGGTAACTTCAT TTAAACACACTTCCCCATG	392	D	--
IM000539	CATGTCCTACATTGGACATTTCTAAATTT TCCATCTTTTTCAGTTTTCCTCACCATAT TTCACGTCCTAAAGTGTGTATTTCTCACG TGTATTCGTTGGTTGTTGGTTTAGTTCCT GGGAGCTCTGGAAATCTGATTATT	393	R	--
IM000540	TGGAAAATGAGAAACATCCACTTGACGACTTGAAAA ATGACGAAATCACTAAAAAACGTGAAAAATGAGAAA TGCACACTGAGGGACCTGGAATATGGCGAGAAAACT GAAAATCACGGAAAATGAGAAATACACACTTTAGGA CGTGTAATATGTCGAGGAAAACTGAAAAGGGTGGAG AATTTAGAAATGTCCACTGTAGGACGTGGAATATGG CAAGAAAACTGAAAATCATG	394	R	--

IM000541	TGACATACAGAAAGAACACAAATACCTGTAGCTGCT GTGACAGGACCAACCATTCTAAATATCAAAGCAGCT GTTGACACCTAAGGACTGGTCTGACTGCTAGATCTA GGAGTTTCAACTTGCAAAAGCTGGCTTGATGCTCAT G	395	C	--
IM000542	TTATATATATATATCGTTTTCTCTTACTCCTGAATC AGTGACATG	396	D	--
IM000543	CATGTCAGCCCTCAGCTTTACACAGGTGTCAAAAAA AAAAAAAAACACTGACTGAGATCTTCCGTCTGCCAT TAGCTGTTATTGTGTACATTAAGTAGAATCCACTGC TTAACCCAGGCTACTGGGCTCACCCCAGTATTCAAG GAGGTGCCACAGGACTCAAAGGATACAGAAGTTACA TATTAAAACCCAATCTCGTAGAGGATTCAGAGGAAC TAAGTTTGGTAGGGGCACAGATTGTAGTACCATTAA GCCCCTCTGTTCCTCGTGGAGAACCACTACTGTCCA GCAAGGCGGGAAGGACCCAAATCAAGCAAATGAGAC TTGTTCTGG	397	D	--
IM000544	CATGATANATCCCTTTTTGTGAGCATTCC ATAGCCTCAGTAATAGTGTCTGACCTTGG GACCACGCTGTATCCCACTNTGGGACCTT CTTTTCNTCAGGCTACTCTCCATTTCCAT TNCTGTAATTCTTTCAACAGAAACATTTA TGGGTCANAGGTGTGACTGTGGGAGGACA ACCCCATCCCTCACTTGATGTCCTGTCTT CCTGCTGGAGGTGGGCTTTATAAGTTCCC TNCCCCTACTGNCCAGCATTTCATCAAAG ATCCCTCCCTAGGAATCCTGGGAACCTCT C	398	D	--
IM000545	GATAAGCTTATCTTGAACTTGAATGTATATGGAGAA GCAGAAACCTTGAAACAGCCCACAGAAACTGAAGAA GGATGAAGGTGGAACTCTCAGCTGGAATATTCATG	399	D	--
IM000546	CATGTTCCCAGCTGGGCAAGGCCTCGGGTTCCTCGG TGAAGAGTGTGGACCAGCCGATGAGCCCTCCGACGT GTGGATGAAACGGCTGGCTTTTGTTTAGTTTTGTTT TAACCTCCCCAACGAGACTTTGATCAGCTCCACCTC GAAAATGTTCGCGAAAGATGCGGAGAGCCTGAGGGA CTGCGGGGCAGCAACGGGCTCCGGCCTAGCCCGGCC CGCCGGCCCCCAGA	400	B	AI413288
IM000547	ACCAAGTGTTAATAATGTACTGATGGCTTCTGCCTG TGGCAGTACACTTGTCCTCTACACATG	401	C	--
IM000548	CCTTACTGCAGAGATGACTCGGCCAACGGCTTCGAG CCCCTGACCACTTCCTCAGGTTTGGTTTTGTTAGTT TTTTCTCACAGCAATGGGAAGCATAATCAATACAAC TTCCCAGAATGCGACCTGTGACAAGGCCAATGAGCA GACTCAAGGCTGGGCACATAAAAGCACCAAAAAAAA AAACTCCCTTGCAGTTATTGTTCATG	402	D	--

IM000549	GACTGAGCCTGCCTGGGGCCGTAGGGAAG GGGGGGTTGGACCCTCTGGTATTTGCAGT TACCACTGACAGGGTTTTTCCGAGATGCC AGTGTCAGGGTGTTCGGTGCTGACCCCCC AGGGACCGTGCAGCCCCGATGGCTGTCTC GGTCCTCTCANCTTTTCCGCCACCCCTGG GATATTTCAGGACTCANTCCCCGCAACAG CTCTGACTGAGGTCAGCTCTGTGACCAGG GNCCCTGTCCCCGGTGTGNNGTGTATTTG CATG	403	K	*Wnt1*
IM000550	CATGTAGAAGGCAGAGGACAACCTTCAGGGATTATT TCTGCCCTTTCAC	404	C	--
IM000551	GTTCCTCCATTCTGCTGCTTCTCCCTGATACATTGA GTTACAGCAGCCCACGCGTACACACTCTCGCACATG	405	K	*Wnt1*
IM000552	CATGCCACCAACAAATAAGTAAGTAAAAAAGAAGGA AGGAAGGAAGGAAGGAAAGAAAGAAAACATTTTAAA TCTGTAAT	406	D	--
IM000553	CGGAGCTTAGGTCTATCATTTAAAGATACAACCAAA TAGGCAGAATCATTTCCTGAGGAGCCCATTTTCTTT ATCTCAGGTCCTGCAGATTTCTCCCTGGTATTATCA GGGAGGAGCAGCAGCTGAGCTATCCTATCTCCTTTA CTAATAGAAAAAACGCCTTTAGGGCTTGAGCACAGG ACCTGTATTTCAGGGGAATGTTGACAATCCATAACT CCAGGGTGGACTACTAAGCCCTGCAAGGTGAGTGAA CCCCGGCCGAGAATAAGGCCCATG	407	R	--
IM000554	CATGGCCTGAGAGTTGGAAAGAGTATTGTAAGCAGG GGTTGTTCCAGAAAGTTTAGAATATACAGACACTAT ACTCTATCCAGACTTCTTGGCACAGGGAGTTCAAAT GTAGACTCTGAGCCCCGTCCTGGGGCAGCTTCTTCC ACCTGCTTTGGGTAGAAGCAGGCAGACTCTGGGTAG ACTCTGATTCCAAGGCTAAGTAACCCCTGAACCCAG AACAGTGTTTTC	408	D	--
IM000555	CCAGATATCATACTGAGTTCGTAGGTGGTTTTAATT AATCACGGGCCCCTGGCATG	409	D	--
IM000556	TTGGTGATCCAAACCCAAAGAGACAAATGCTGAATG TTCACTCTCATTTTCTGTTCTTAGCTCCAAATCTTC AGATATGAGTAAGCAACACATAAATTATGAAGGGAC CATACTGGGATGTAGGGGGCTTGCATG	410	D	--
IM000557	CATGAGCACTGCTCTAGGGACACCTCCCA TCCCTTCCTAGCACCCCAAATGCCCCTTC CCATCTCTCCTTCCAGAAGTTGGA	411	K	Wnt-3
IM000558	ATATAGCTGTCTCCTGAGGGCCTATGCCAGTGCCTG GCAAATACAGAAGTGGATGCTCACAATCATCCATTG GACAGAGCACAGAGTCCCCAATGAAGGAGCTAGAGA AAGTACCCAAGGAGCTGAAGGGGTCTGAAGCCCCAT AGGAGGAACATCAATATGAACTAACCAGTGCCCCCA GAGTTCCTTAGAACTAAACCACCAATCAAAGAAAAC ACATG	412	R	--

IM000559	CATGATAAGGTTAGAGTTTTGTGAGCCTCCTTAACC TTGCTCAGCAAGCGTTGGGCTCTTGGCAGCCGAGCT GCCATCTTTCTCATCCCCGATAGAGCCAGCCGCCCT TGTCGTGTCTTGAATAAGTTAGAGGAGGCATTATAG AGCGGACCTAAACATTTGCCTTGGAGCCTGAGGGAT GGGGATTGGCTGAATGTGAAT	413	D	--
IM000560	CAGAACTGTGCTCTTTAGGAAGCCAGACGCTATGCC TTAGGCCCTGTTCCCTCCAGACCTTGCTCTGTGCTA CAGTGTAAAAGCGAAGATCATG	414	D	--
IM000561	GAGAATTAGAAAAGAGATAACAAAGGCGAGAAAGAG AGGCGTGTGAGAGCATG	415	D	--
IM000562	GTTTCCAGATTGTCCTAGTAGCTGGGCTGCAGGAAC AGCCAGCATG	416	C	--
IM000563	GGGGGTGGGGGTGGTAAGAGAAGATTAATTAGCCTA GCATATATAAGGTTTTGGATTCAATCTTCAACTCCA CCCCTTAAAGAATAAATAAACAAGTAGATAGATTAT AGACAGACAGCTAGATGGATAGACAGATAGCTACAT AGATACATAGATAGATGATAGATAATAGACAGACAG ACAGATAAATGATAGATAGATGATAGGAAGTCCCAG TTAACAAATGGAAATAAAAAGACAAAAGTCCCCTTT GTCCATG	417	D	--
IM000564	GTATATGGAATATGGCAAGAAAACTGAAAATCATG	418	R	--
IM000565	CATGGTAAAGGTCAGGAGTACACCTGTGCTTCTGTG TTCTTCTGTGTTGGCTGACAGCTGGGCAGAAGTGAG TTCAGGAGGNCAACCCATACGATGAGACAAGCCGGG GCAAAGTGGGATATGTGGACCGCAGCACATCAGAAG GGTGTGCCCGACATAAAC	419	B	AA111354
IM000566	CATGAAGTATATTATTAGAGGGGAACTAGTCTTACT GCTGAGCAGCGTGTTGTCTTCTACAGAGGATGTTTG TGTTCTGGAATTTAAAATTACTTAAAGTAATAGTGT CAATGAAACGTTGTCCGGTGACTTGCTTCTTTTAAA TGATCACTGTTAGACAGGGA	420	R	--
IM000567	AATAATCAGATTTCCAGAGCTCCCAGGAA CTAAACCAACAACCAACGAATACACATG	421	R	--
IM000568	CATGATTTGATAGGGTTATTTGGTTCTCTGGAATCT AACTTCTTGAGTTCTTTGTGTATATTGGATATTAGC CCTCT	422	R	--
IM000569	GCAAATAGTCCTTTGTACCGAACTTCCACACACTAA TGTAGTGAATTATTTAAAATTTATTCCTTAATCTTT TTTTAAAGTCCAGACTCTATCCCCCTCCTTGTCCAC CCTCTGATTGTTCCACATCCCATACCTCCTTGCCTC ATG	423	R	--

IM000570	TTCCATCTCTTGTATTCTGTTGCTGATGCTCACATC TATGTTTCCAGATTTCTTTCCTAGTGTTTCTATCTC CACTGTTGCCTCACTTTGGGTTTTCTTTATTGTGTC CACTTTCCTTTTTAGGTCTTGGATGGTTTTATTGAA TTCCATCACCTGTTTGGTTGTGTTTTCCTGCAATTC TTTAAGGGATTTTTGTGTTTCCTCTTTAATGTCTTC TACCTGTTTGGTTATGTTTTCCTGTAATTCTTTAAG GGATTTTTGTGTTTCCTCTTTAATGTCTTCTACTTG TTTAGCAGTGTTCTCCTGCATTTCTTTAAGTGAGTT ATTTAAGTCCTTCTTGATGTCCTCTACCATCATCAT G	424	C	--
IM000571	CATGAGTTTTCTACTTTTTTATAAAATTATATAAAG TCATTTAGTAGAACCTAGCTTTATTTAATTTTACCA ATTAATATAAGGCCACTGATATTATTGACTTTTGTC ACTACAAAATACAGCAATGAAATAATCTTTCTTCTA GGCTCCTTCCTCATCAAACTAGTTCTTCAGCTCACA TTAATACTTTTTTCAAGTTGTAAGGGACCTCAGGGA CAGGGGGC	425	D	--
IM000572	CATGAGCTTATAGTTTCAGTAAGAGAGCATAGATAG AATATAGGTGCCTGTGCGCTGGCTCTTTTGGTTGTA TTTAAATCCTTTATCTCTGAGAAGTCGGAACTGTTG GCAACAGACAATATGGTAGCC	426	D	--
IM000573	CTGACACAGGTATGCCCAGTCCATAGTGTGCAGAGC ACAGATGGCCAAGGATAACTAGGAATGAGACCTACT TAACCCAAACTCCAAACATTATGAAACTTTAAAAAA ATGACTTCAGTTGAACTTTGCAGGTAACCACATCAT G	427	D	--
IM000574	ATTGTGTCCTTTTAACATTCTTGCTTTAGTAGAACA TCCTCTGACCCGTATCTGATTCAGTGAAAAATTCCT TCACGAGTCTGCCTTAGCAAAACATCCTTTCACCTG TGTCTGCTTCAGGAAAACACCCCTTCACATG	428	R	--
IM000575	CATGTTGGTAACAGATACAACAAGCAGACTTAAACT AATAAGAAAACAGCTATGATTAATATGTTTATAACT TAGCTGAAGAGAATGTATGGAGCTTTGAAGTTAATC TTTTCATATACACAGGAATGCCTTCAAAAAGCATTG CAGCAGATTTCAAAGGATTAAACTCAT	429	D	--
IM000576	CATGTGGCGAACCAGCATCACTTTTGCTCTTTCCTT ACTAACCCAGGACATCCATCATTATTTTAATAGCAT CCACCCTAGTAGATATAAGGTGATACCTTATTGTGA TTTCATTTGCCTTTCTCTGAAGATCACTAACAATCA AAATCTGGTTCATTTTATTTATGAATTCTCATTTGT CTTTTGCTAAATATATGTTCACAATTCTTTTCAATT TAAAAGCAAATTGTTTTGTTAATAATGAGCTAACTT TTCATACATTGAAG	430	D	--
IM000577	TTGCTGTGGGCCTAATTCAAGGCTGATAG ATCACCACAGAAGGACACTGTTTTCCTCC GGGCAGCAGGAAGTACAGGGTAGGGACTC TAGAATCACTGCCCTAGGGCATG	431	B	AI663969

IM000578	GTACTTGAAGTTTTAGCTAGAGCAAAAAGACAATGG AAGGAGATCAAGGGAATACAAAGTGGGAAAGAAGTC AGAGTATCATTATGTCCAGGTGATATGATAGTATAC ATAAATGACCCTATAGATTACACCTAAGACCTCTAC AGTGGATAAATACTAAAATATTTACTACACAGAAAT CACCCCATG	432	R	--
IM000579	CATGCAAGGTATGAACTCACTAATAAGGG GATA	433	D	--
IM000580	CATGGTTCACACTCCATAATATCTTGTTCTCACTAA TTCCTCTAATCCCATAATATACACCAATAATTTAAC AAGGGAATTTCTACATTGATTTGTAATAAGGGAGAT ACTGTGTGAACTTACCCAACAAAAGTCTCCAATAGA AGTGTGGATACCACAGGAAGTCTTGTGACAACCATT AAAATTTGGGTCTGATAAGAAGATAACCCTTTAAAT ATATAGATTTATGTAAAG	434	D	--
IM000581	CATGGGCTGGGGAAAGGCAGAGAGAAGAACATCTGG ATTGTTCCTAACTTTGCCTTTAAAATGAGACTTCAA TAATACTTAGACGTACCAGCTTCTCACAGTCAGTTA AAATGTGACACACACACCTCTCAGCAGACTGAATGG GTGAG	435	D	--
IM000582	AGAGATGGTTGGGATTTAAGTTACCAGGG TAGGGTCACCACAATCAACCCTTGATGCC TTTATAGGAAGAAACATG	436	D	--
IM000583	CATGGAAGTCTAAAAGACATTAGGTTCTGGATGGAA GAAGAGAAAATTATCTTTAAGTTTTAGAAAAGGGAT GATAAAACAAGTCTTAAATCTTCTCAATTTTGCCAT AATTCATTTGAATTAATATTGGTAAATGCTTTGTGT GGTCCCATAAAGTTCAATGTGTTATATCACTAAGTA GTTATTTGTAAAATTATAAATAGCCTCTAT	437	C	--
IM000584	CTTGTGAATTGTTTAACTGTTTTGAAAAAGTAGATG TTTTCTCTATTTATTTTTGGGACAATTATCAGAATT TGAAACAAACTGTGTATCTCTTATTTACTTTCTGCT TAACCCCCATG	438	D	--
IM000585	CATGGTTGCTATATTCATTAACACAAATCATTTAAA ATCCTTAATGTAAAATGGGCACATTTTCAAAATTAA AATATATGAAAACCAATAAAGATAGAAAATTTAGGA AAAAAAATAATCCAAGCAAGATGTTAACATCCAACC ACAGCAGCATATTAGCAGCAGGACAAAAATAAGGAC AACAACCAAGAAAGGGATTGTGGTTAATGTATGCCT CATTGGAAGGGATAATAGGATGTAAAAGTGTGACAA TAAAGAGAAAAAAATCTCTTTTAAAATGTAAGTTAA AATAATAAAAATAATTTAAAAATTGGTGTTCTCAGG GCTGGATAATATTACTAACAAAACCAGGGAATTATT AATAAAAAATCTCTTATCAGTTAT	439	D	--
IM000586	AACAAGTTTTAAATGGGGCATAGTGGATCACATTTG TGATCCCAGCACTTGGAAGGTAGAAATAGGTAAATT AAGAGTTCAAGGTCATTTCTCAGTTATGTAGTTGTA CATTTCTAGCGATGTAGTTGAGTTCAAGGCCATG	440	D	--

IM000587	GTCCTCCAATGTGCATTTCTCATTTTTCACGTTTTT CAGGGTTTCTCGCCATATTCCATG	441	R	--
IM000588	AATTGCATTGAATCTGTGGATTTCTATTAACAAGAT GGCCATTTTTTTCCTATGTTAATCGTACTGATCCAT CAGGATGGCAGTCTTTCCATCTTCTGATATCGGCCT CAATTTCTTTCTTCAGGGGCTTGAAGTTATCGCCAT G	442	R	--
IM000589	GGCTAGGTACTCCTAAACCTTCCTCTGCTATCCTAG GCCCAATAGAAAAAAAGTGGCCCATG	443	D	--
IM000590	AATAATACTTTCACTGTACTTTAAAATATTATCTCC TATCTCACTCTAATACTTCTGTGAAAGAAGCAATAT CGTCTCTTTGTAGATAAAAATGGCTGAGAAGGGCAC CTTCAAGACACTAAGTGACTAACTCAGACTCAGAAG TTCAGAGACCATG	444	D	--
IM000591	CATGCTCTACTATGTTCACAGCAGTCTTATTTATAA CTTCCAGATACTGGAAGCAACTCAGATGTTCCTCAA TGTAAGAATGGATACAGAAAAAATATGGTACATTTA CACAATGGGGTACAACTCAGCTATTAAGAACAATGA C	445	R	--
IM000592	AAAACCCAAGAACAATTAAGCTGTAGTTC CCAAGTGTAATTATATTATGGTTGTTTCT GCTTGCTTTATATCCCTATATACAATTTA TGATTCAAGTATTAGTGGGAATAGACTAA TGGCATG	446	C	--
IM000593	CATGCCAAGCCTTCTGGTATCACCCTAAAGGC	447	C	--
IM000594	CATGCTCTTCTCTGCTGTTCTTACTGAATTTTTAAT AAGAACAATTCCACACAGCTCGAAAGCACTGCTCAA TTAAGAGATATTCCTACCAGGCATCTTTGGAATCCT GCAAGCACCTCTTCTCTGTTTCCTGATGACCCTCAA TTTGGTTGTGTCCAGAGGTTGGTGGGGAGGAGGGGA GGGGAAACGAAGCTTATTTTTTTTTAATTGCAAGTT CAATTTTACAATGTTCTCGAT	448	D	--
IM000595	CATGCTAGGCAAATGCTCCACTGAATGAATTACATT TCCAATCCTTTAGATGCATTTTAAAGAGAAAAGATT GAGTACTGAAGTTTTGAATAGAATACAGGAATAAGG GACTAAACATATATATAGCCTTATATAGAGAAATAT TAAGTAAGTAGTAACTTTGCTTGTGTGTGTGTGTGT GTTGCACAC	449	D	--
IM000596	CATGCCATTAGTCTATTCCCACTAATACTTGAATCA TAAATTGTATATAGGGATATAAAGCAAGCAGAAACA ACCATAATATAATTACACTTGGGAACTACAGCTTAA TTGTTCTTGGGTTTT	450	C	--
IM000597	CATGCACAGCTGGTGAGTGAGTTGTCTTCTGGTACA AAAATCTCCTCACAGGCACATTTACAAGTGCCTATA TCTTTGCTAGCTTCAAGAACACAAAGAAGGGACACA CAAAAGCTCTTCTGAGTCTCCTTCTCCTGCTGTTAT TTTG	451	D	--

IM000598	ATCGTCAAAGTTAGCAAAATTATAAATGTGAAAGTC ATG	452	D	--
IM000599	CATGAATTATGTTTGTTTTATTTCTTTTG TACATCATTCAATGCAGTAATCTAAAGTT TGGGGTCTTGGTCTTATATCTTGGAACTT CAGTGACTTATTGGTTCTAACG	453	D	--
IM000600	AGAGACAGTCACAAAAGGGGCCCATTCTTGTTAAGA ATGGGCCAGTGGAGAAGTTCGGGTTAGTGGAGTAGC CTGCCTCAGTTTCCTCCTGTCTTCTGTAGTTAAATG TGTTAATGGTTAACATG	454	K	*Fgf3/Fgf4*
IM000601	CATGTAGCATTTATCTTAGCCAGCAC	455	D	--
IM000602	CATGTACAGACTATGAACAGGAAATGTTTTTGCAAA TAACTCTGTGCATTAGAATTTTCTTCAGAAATATAA CCATTTTGACAGTTGTAGGTTACACTTTTAAAATTA CAAAATCAATAAAATTGATCTACAAACCGAGGCCTA CAAAACCCTTGCTGGATATTGAAGACGGCATAATAT TAAAG	456	D	--
IM000603	AATTCCCACCACCCACAGGGTGGCTCCATAACCATC TGTAACTCCAGTCTCAGGGACTCCAAGGCCCTCTTT TGGCTTGCAAGGGCTTGCACACACACAGCGCACACA TG	457	K	*Fgf3/Fgf4*
IM000604	CATGGTGAATGATTGTTTTGATGTGTTCTTGGATTT GGTTTCGAGAATTTTATTGACTATTTTGGCATTAAT ACTCATAAGGGAAATTGGTCTGAAGTTCTTTCCTTG TTGAGTCTTTATGAGGGTATCAATATAATTGTGGAT TCATAGAGCAAGTTAGATTGTGTTCCTTCTGTTTAT ATTTTGTGGAATATTTTGAAGAGTATTGGTATTAGA TGTTCCTTGAAGGTATGATAGAATTCTGAACTAAAC CCATATGGTTCTGGATTTTTTTTGGTTGGAAGACCA ATGACTGCTTCTATTTCTTTAGGTGTTATGGGACTG TATAGATGGTTTATCTGAACCAGATTTAACTTTGGT ATTTGTTATCTGTTTAGAAAATTGCCCATTTCATCC ATATTTCCCAGTTGTGTTGAGTATAGGCTTTTGTAG TAGGATATAATGATTTTTGAATTTCCTCAGTATGTT TTCTTATATCTCCCTTTCCATTTCTGATTTTGTTAA TGTGGATACTATCTCTGTGTCCTCTGTTTAGTCTGG CTAAGGGTTTTTCTATCTTGTTGATTTTCTG	458	R	--
IM000605	CATGGGTTAACAGTGGGCCCTAAACTTGAACTAGAA AACTTAAAGATGCTCATAGGGAAGAAGAAAAGAGCA GAAAGCTTAGCTTCTAGACAGGGGTAAGGCTTAGAG CTCAATAAAAAAGGAACCCC	459	K	*Wnt1*
IM000606	CATGGCCTGTCTCAGTTTACTTCACAGCTGAACAAG AGGCAGAGAGTGACAGGTAG	460	K	*Wnt1*

IM000607	CATGCTCGCCAGTCCCAGAACCTGGAAGG CTGAGGCAGGAGGATTAAAAAGCCTTGGG GACACCAGGCTTGGTGGCACCGGTCGTAA ATCCAGCACTGGGGAGTTAAGAAGCAAGT GAGTCACATCTGTGAGTCTGAGGCTATCT TGGTCTACGTAACCAGCTCTAGTATAGCC AGCCTGGGATACATAGTAACCAGTTCTAG TATAGCCAGCCTGGGATACACAGTAACCA GTTCTAGTATAGCCAGCCTGGGATACACC	461	D	--
IM000608	CATATGCGTATTCACATTTGTGTGGGAACGTCCTTG GAGAAAGCAGGAGCAGGAGTTACAGACAGTTATAAG CTGCCTGACCTGGGTGCTGGGAAACACCTCAGGTCC TCTGGAAGAGCAGTAAGTCCCCTTAACCAATGAACC ATCTATCCGTCCAGCCTACATTTAATTTGTTTTCTT ATTTACTTTGTCTGCATG	462	R	--
IM000609	CACACACACACACACACGGCTGGGGATCCAACCCAT CTCGTCCTTACACGTGCTCTACCATCACGCCACACA TTTCCAGCACNTTTATCTGAAGTGTTTCCTTTTATT TGTGCATG	463	K	*Wnt1*
IM000610	CATGCCTGGTGCCTGCAGAGGTCAGAAAGTGTTGGA TGCCCTGGAATTAGAGTAACACATAGTTATAAGATG CTGCGTGGGTGCTGGGATTTGAACCCTTGTCCTCTG CAAGAGCAGCCAGTGCTCTTAACCACCGAGCCATCC CTCCAGCCCCTGATTACTCACTCTTCACGGCCTCAA TCTTGTAAGGAATATTGAGGCTGCCAAGTGACGCAA GAGCACCTAGGAAGGCAGCCACATCGGTGGCACTCT GGAAGCACTGCGAGGATGACTGCACACATTGCCGGT TGTC	464	K	*Notch1*
IM000611	CATGCTGGCCATTTATTTTGATTTAAGTTATACTCT AGACCTTTGTAAATATTAGCCATTGCATATTACAGA AATTTCTTAGCAGAGATAGTCTCTCACTCTTAGTGA TGAGCAAGCTGGAGCTCAGCATTATTCTCCCAGCTA AGATACAGAATTACAGACGTTTATGACGGACACATC TTGGATGTAGTTACTTAGTCCAC	465	D	--
IM000612	CCCCCCCCGCCCCTGCCAGACCGCAGCCCCAAGCAC AGCATG	466	D	--
IM000613	CATGCCTCCCTCAGCCTCCTCCACCCCTTCCTGTCC TGCCTCCTCATCACTGTGTAAATAATTTGCACCGAA ATGTGGCCGCAGAGCCACGCGTTCGGTTATGTAAAT AAAACTATTTATTGTGCTGGGTTCCAGCCTGGGTTG CAGAGACCACCCT	467	K	*Fgf3/Fgf4*
IM000614	CATGAATTCAATGGTGTGCTTGCTATAAATGCAAAT AAACCATATATATCATATTACACTCAATTTTAAATA TTTTTCCTAATATTAATAAAGGTGATGGGGAACTT	468	D	--

IM000615	CATGTCTACTTTATTGCATATTAGGATGT CAGGTCCTGCTCGTTTCCTGGGACCATTT GCCTGGAAGACATTTTTCCATTCTTTTAC TCTGAGATAGTTCCTGTCTTTGTTGTTGA GGTGTGTTTCTTGTATTCAGCAAAATGCT GGATCTTGTTTGCGAATCCAGTCTGTTAG CTTATGTCTTTTTACAGGTGAATTGAGTC CATTAATATTGAGAGATATTAAAGAGAAA TGACTTTTGGTTCCTGATATATTTGTTTT TCTAGTTAGTTTTGTGTGCTTGGGACTCT CTCCCTTTGACTGTGTTGTGAGATGCTTA ATATCTTGTCCTATCTTTGGTGCAGGTGT CTTCCTTGTGTTAGAGTTTTCATTCCAGG TTTCTCTGTAGTGTTATGTTAGAAGACAT ATACTGCTTGAATTTAGTTTTGCCTGGAA TATTTTGTTTTCTCCATCTATGTTGATTG AGAGTTTTTCTGGGTAAAATAGCCTANCC TGGCATTTGTGTTCTCTTAAAAGTCTGTA TGACCTCTGACTANGCTTTTCTGGCC	469	D	--
IM000616	CATGGTGAATGATTGTTTTGATGTGTTCT TGGATTTGGTTTCGAGAATTTTATTGACT ATTTTGGCATTAATACTCATAAGGGAAAT TGGTCTGAAGTTCTTTCCTTGTTGAGTCT TTATGAGGGTATCAATATAATTGTGGATT CATAGAGCAAGTTGGATTGTGTTCCTTCT GTTTATATTTTGTGGAATATTTTGAAGAG TATTGGTATTAGATTTTCTTTGAAGGTAT GATAGAATTCTGAACTAAACCCATATGGT TCTGGATTTTTTTTGGTTGGAAGACCAAT GACTGCTTCTATTTCTTTAGGTGTTATGG GACTGTATAGATGGTTTATCTGAACCAGA TTTAACTTTGGTATTTGTTATCTGTTTAG AAAATTGCCCATTTCATCCATATTTCCCA GTTGTGTTGAGTATAGGCTTTTGTAGTAG GATATAATGATTTTTTGAATTTCCTCAGT ATGTTTTCTTATATCTCCCTTTCCATTTC TGATTTTGTTAATGTGGATACTATCTCCG TGTCCCC	470	R	--
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Table 3

MOUSE NOMENCLATURE
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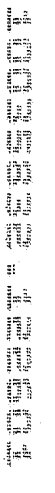
HUMAN NOMENCLATURE
HGNC SNL
Celera hCG15970

MOUSE SEQUENCE - GENOMIC

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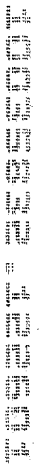
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MOUSE SEQUENCE - mRNA
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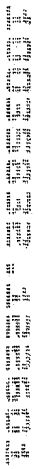
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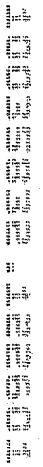


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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 4

MOUSE NOMENCLATURE

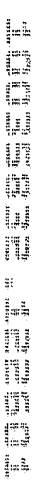
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HUMAN NOMENCLATURE

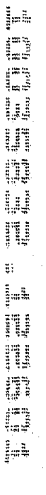
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

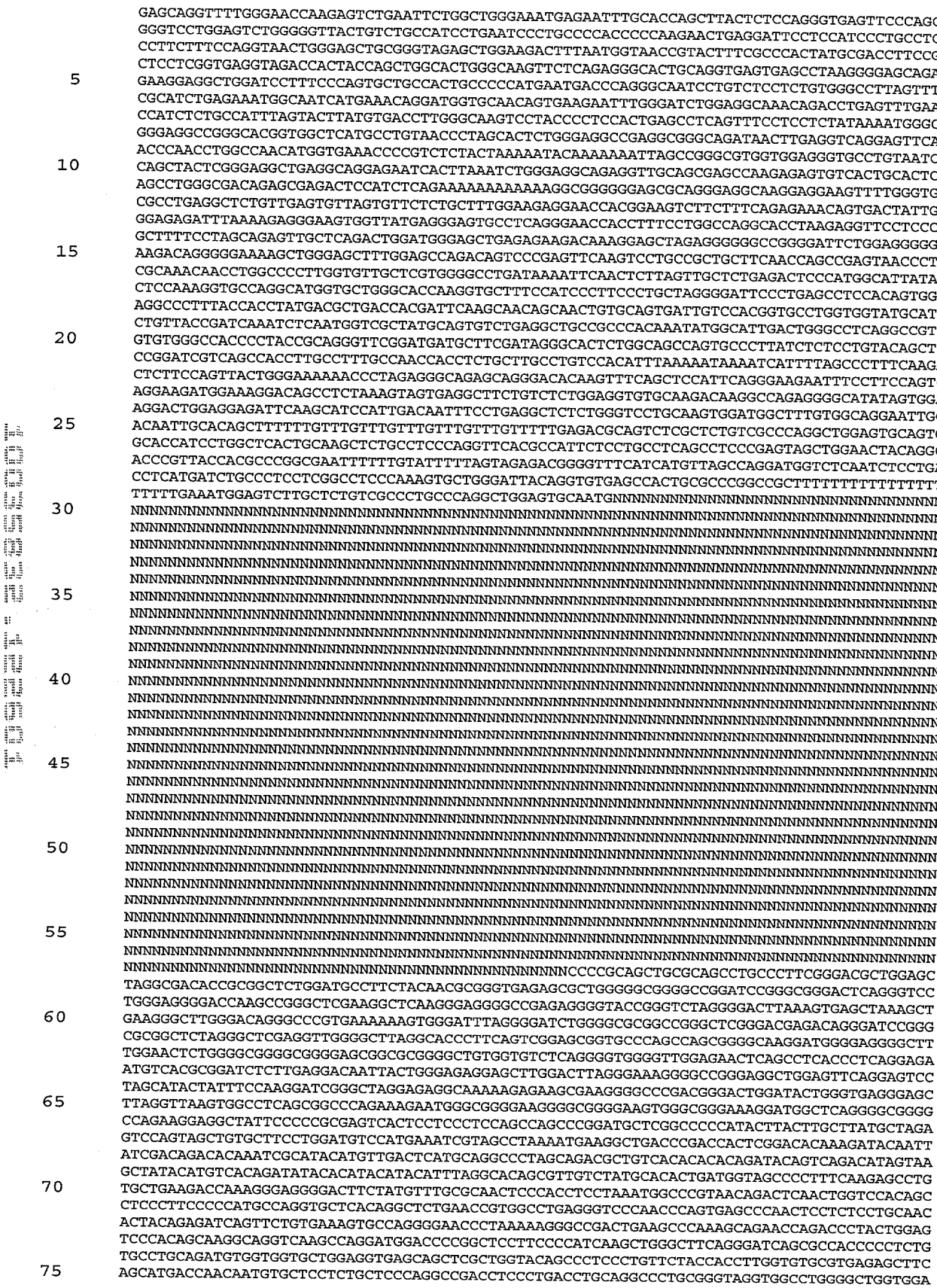
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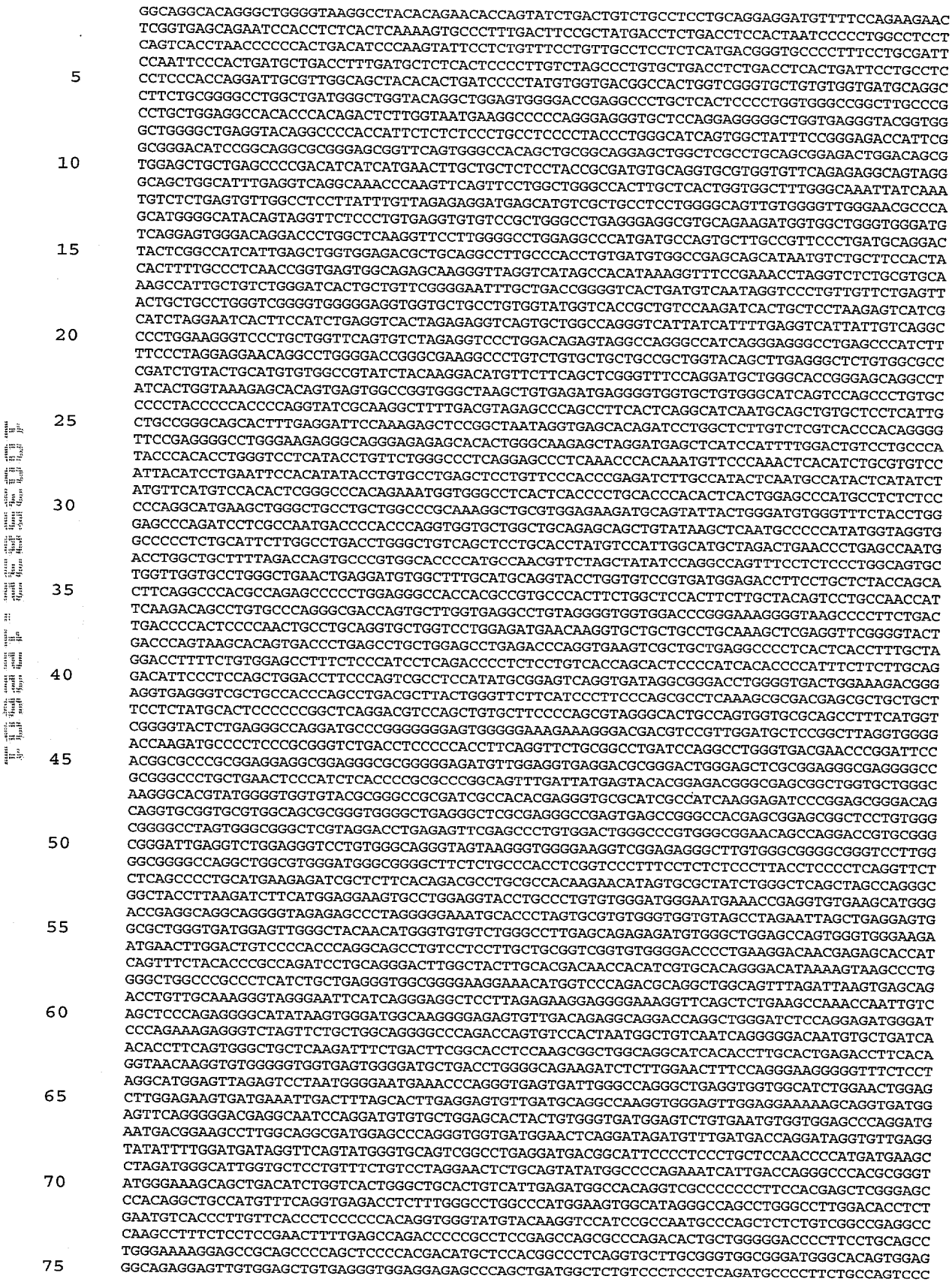
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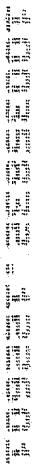
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HUMAN SEQUENCE - CODING

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Table 5

MOUSE NOMENCLATURE
ICSGNM Fosb
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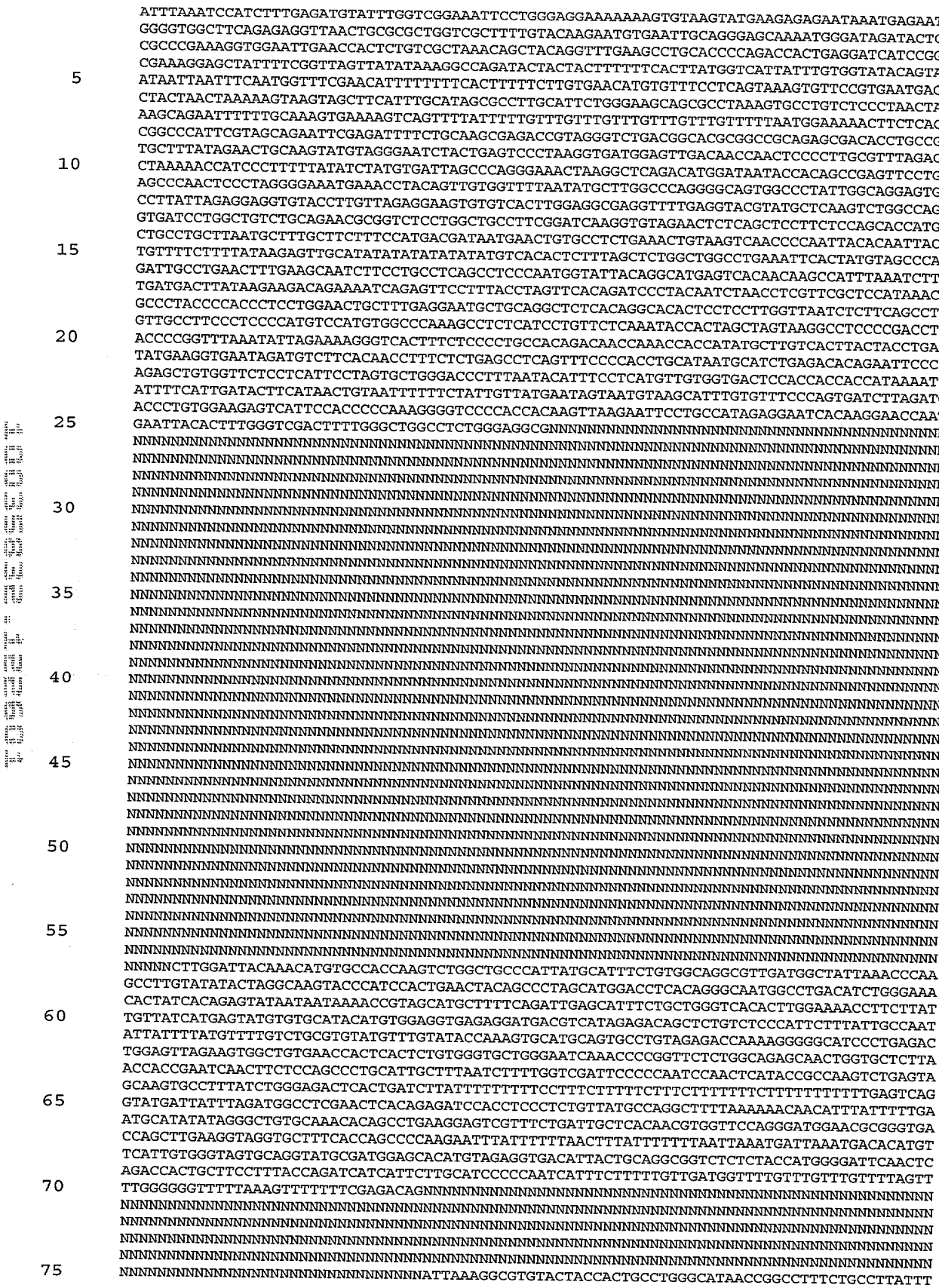
HUMAN NOMENCLATURE
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA
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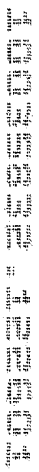
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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Replacement Sheet
Amendment Dated April 27, 2005

Table 6

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Celera mCG15362

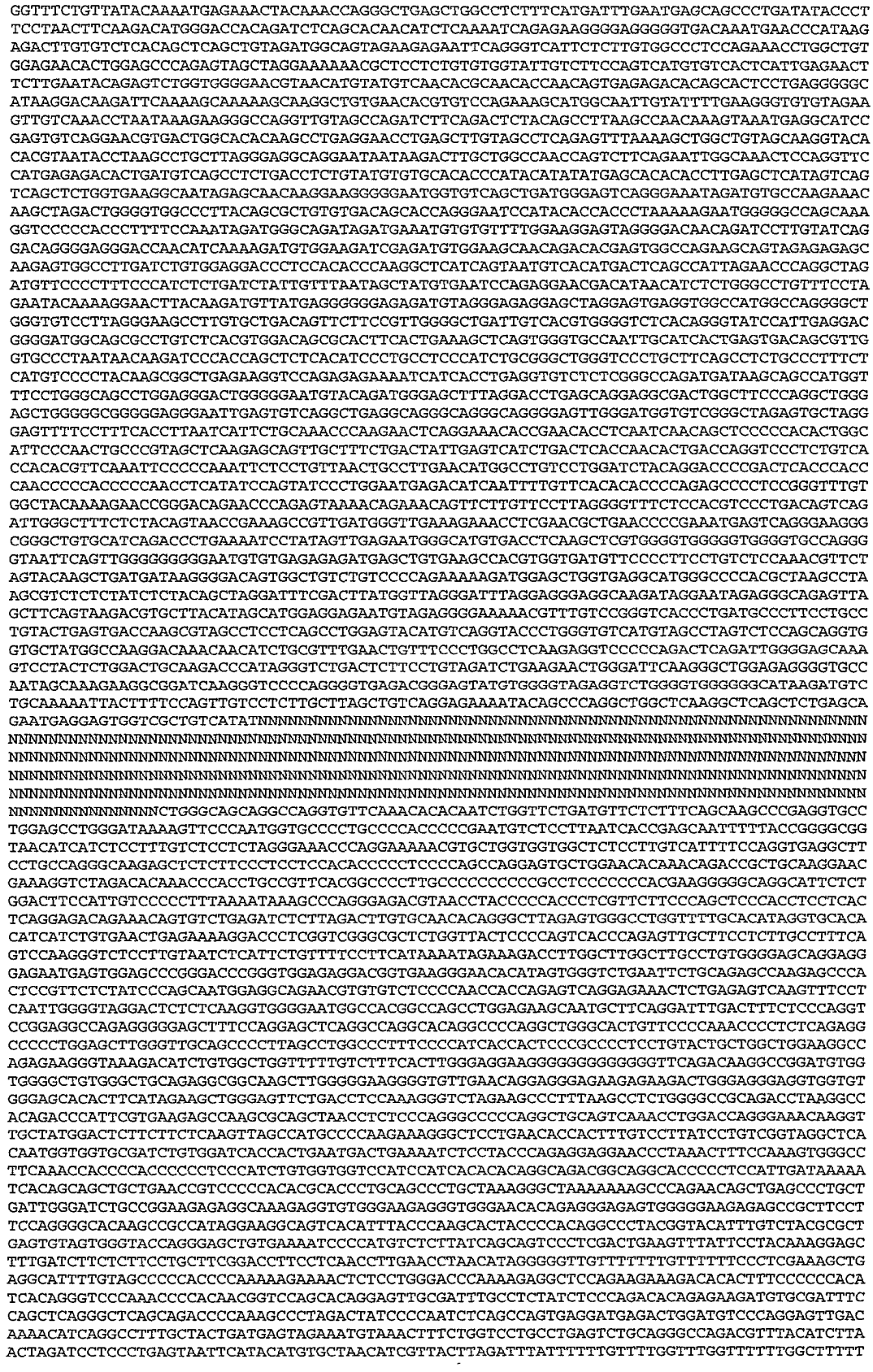
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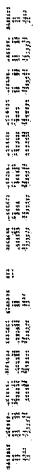
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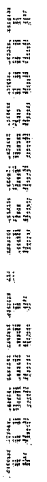
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Replacement Sheet





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MOUSE SEQUENCE - mRNA

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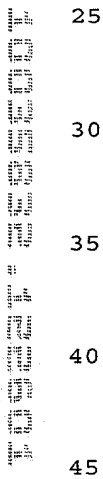
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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

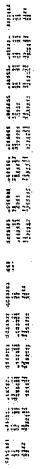
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TTGCTTGCACTAGTATCTCTTACCTGCCACCTGCCCTCCTCCACACACCCCGATTTCAGGGAAGCTCAGCTGCTGAGAGTGCTATT
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

ATGGACCTGGGGAAACCAATGAAAAGCGTGCTGGTGGTGGCTCTCCTTGTCATTTTCCAGGTATGCCTGTGTCAAGATGAGGTCAC
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Table 7

MOUSE NOMENCLATURE
ICSGNM Ccnd1
Celera mCG21251

HUMAN NOMENCLATURE
HGNC CCND1
Celera hCG27985

MOUSE SEQUENCE - GENOMIC

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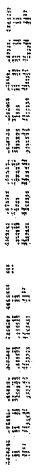
MOUSE SEQUENCE - mRNA

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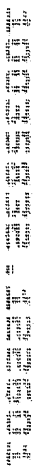
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MOUSE SEQUENCE - CODING
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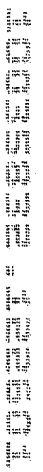
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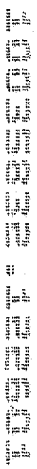
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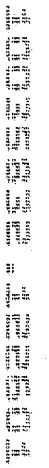
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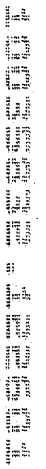
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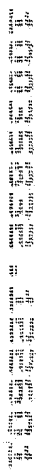
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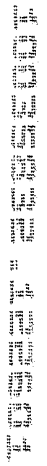
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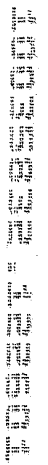
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MOUSE SEQUENCE - mRNA
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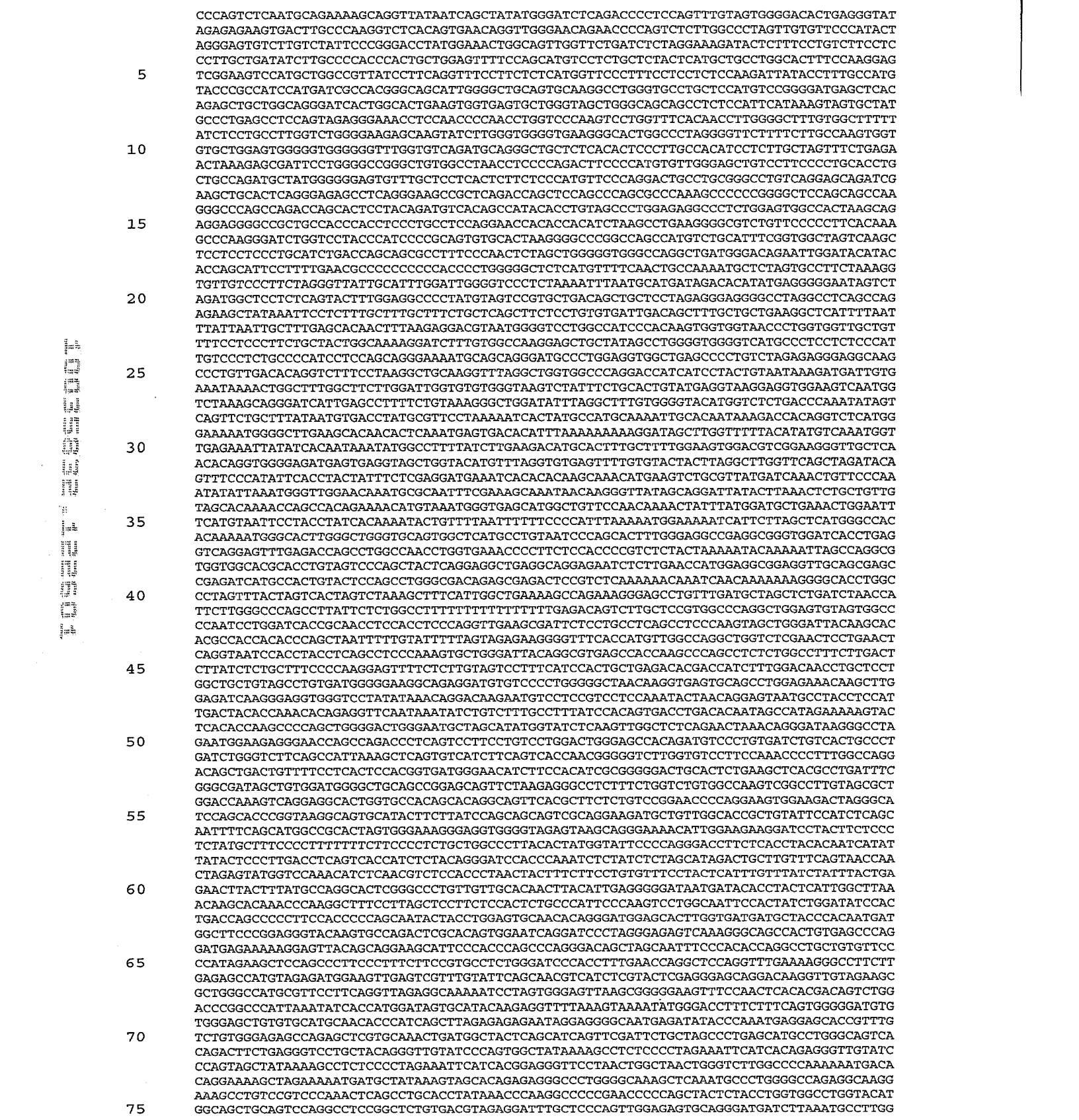
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - *CODING*

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Table 9

MOUSE NOMENCLATURE
ICSGNM Wnt3
Celera mCG19162

HUMAN NOMENCLATURE
HGNC WNT3
Celera hCG27972

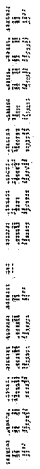
MOUSE SEQUENCE - GENOMIC
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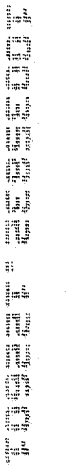
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Art Unit: 1635

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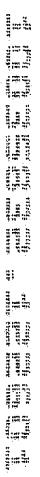
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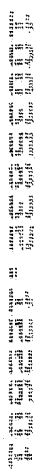
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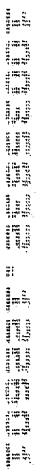
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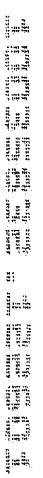
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MOUSE SEQUENCE - mRNA
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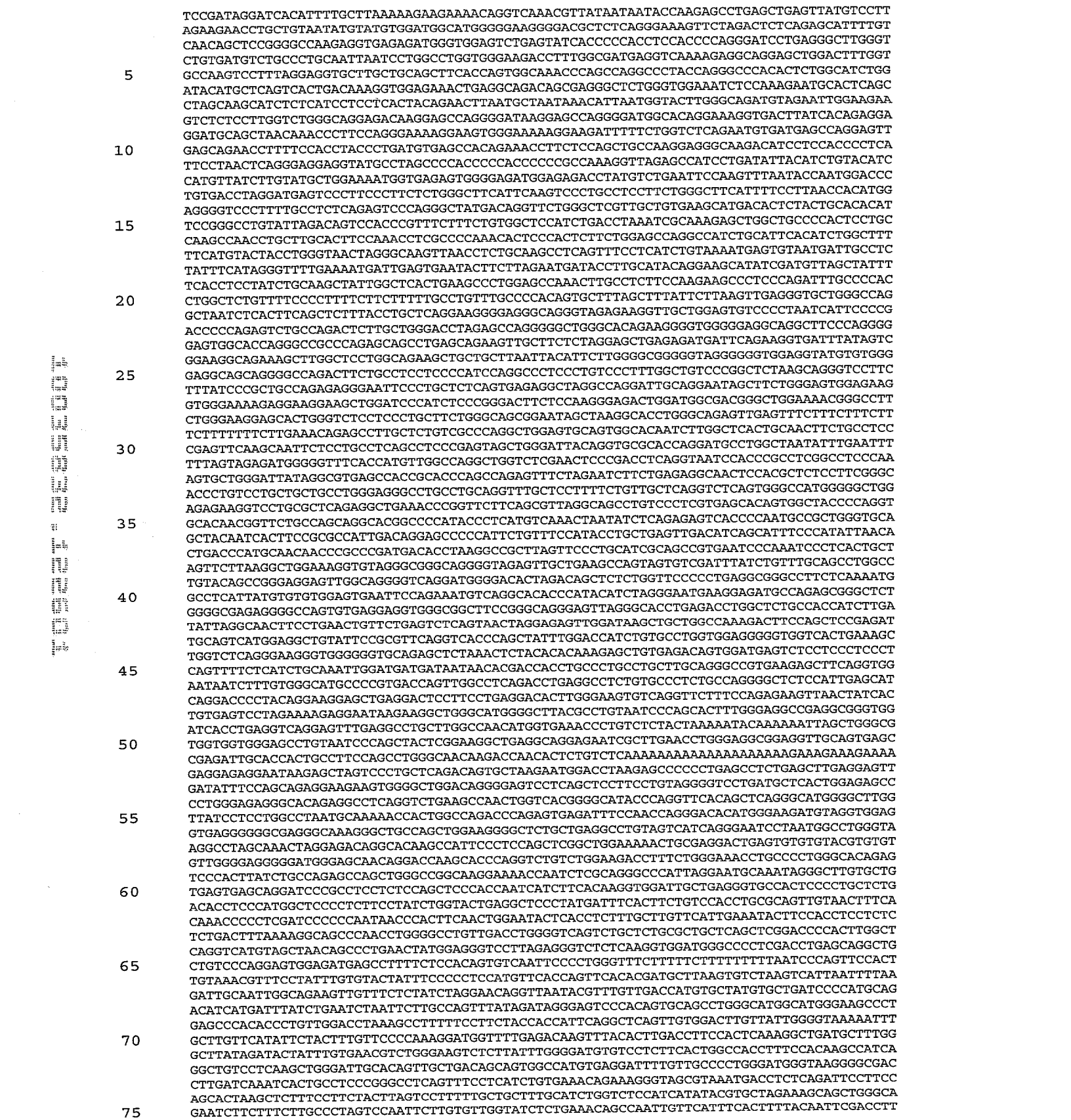
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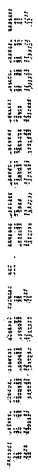
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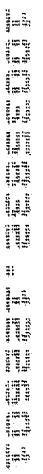
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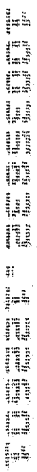


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70 HUMAN SEQUENCE - CODING

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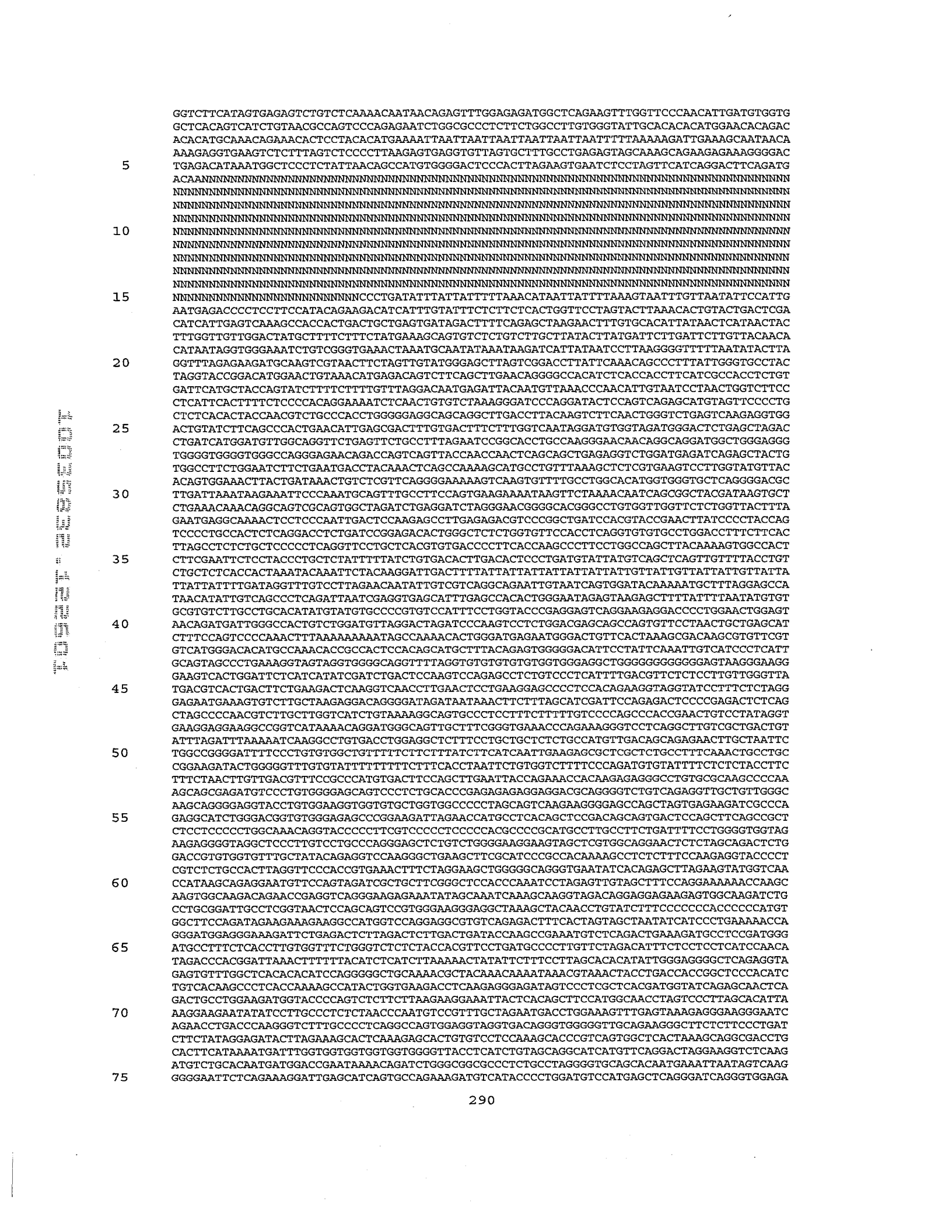
Table 10

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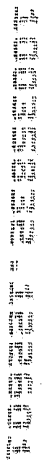
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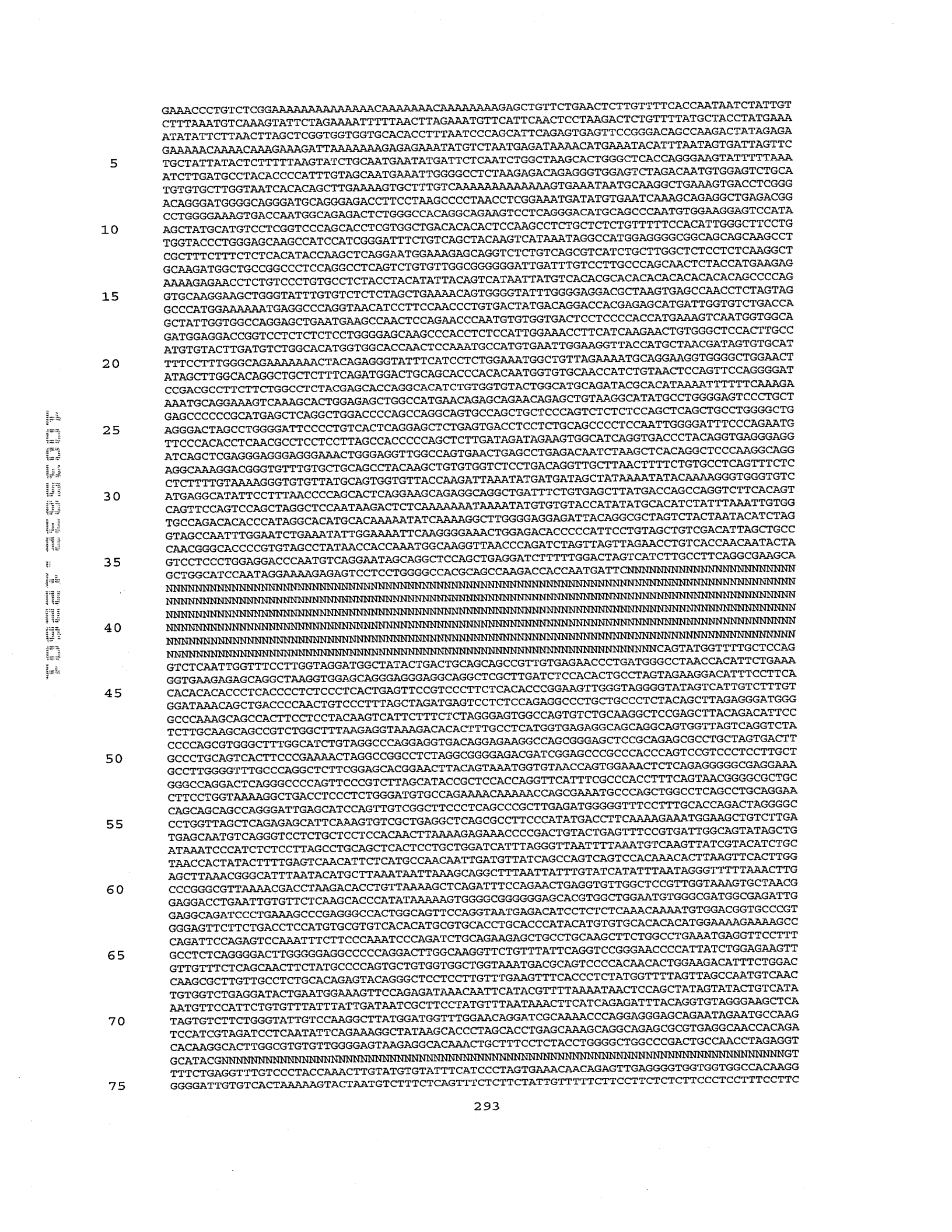
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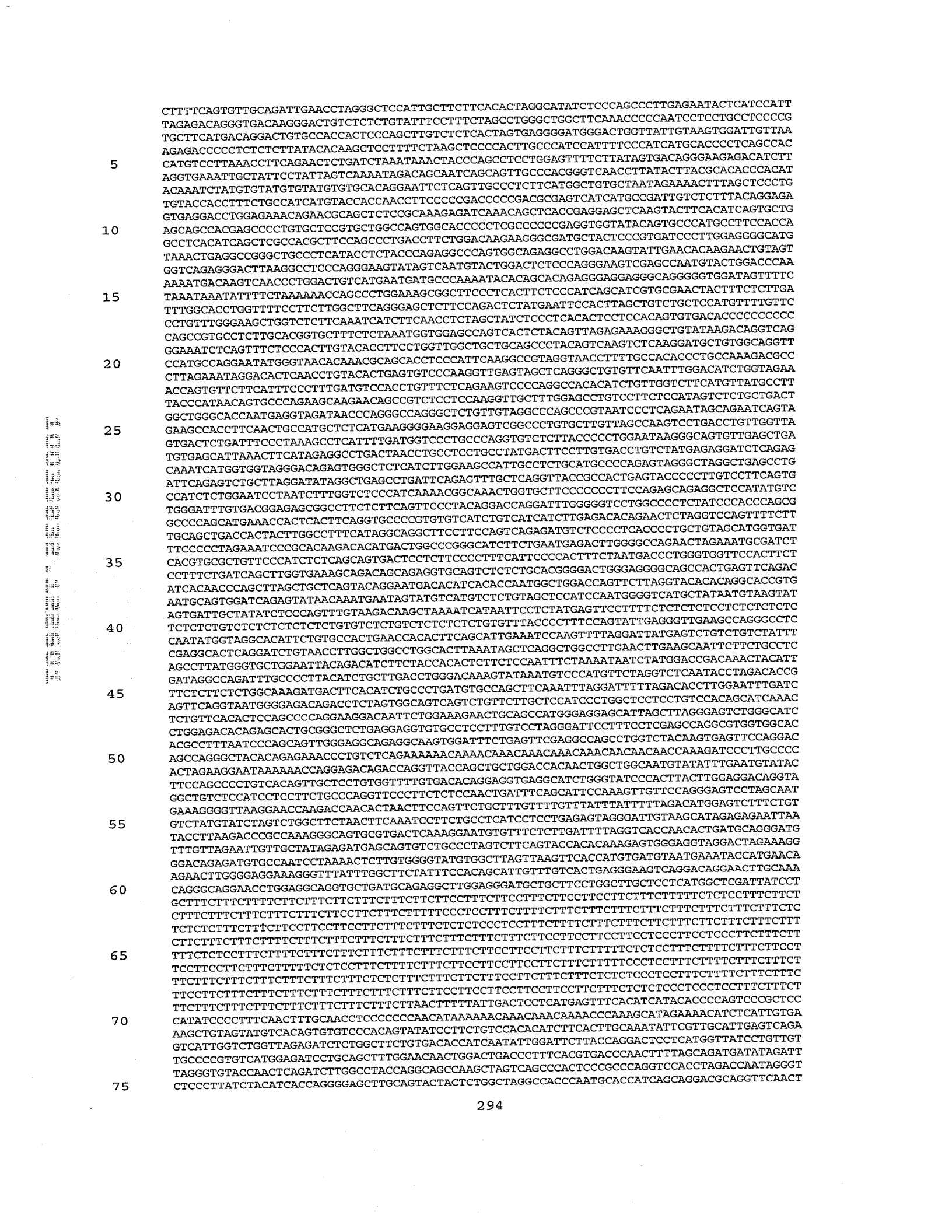
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MOUSE SEQUENCE - mRNA

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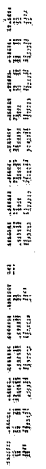
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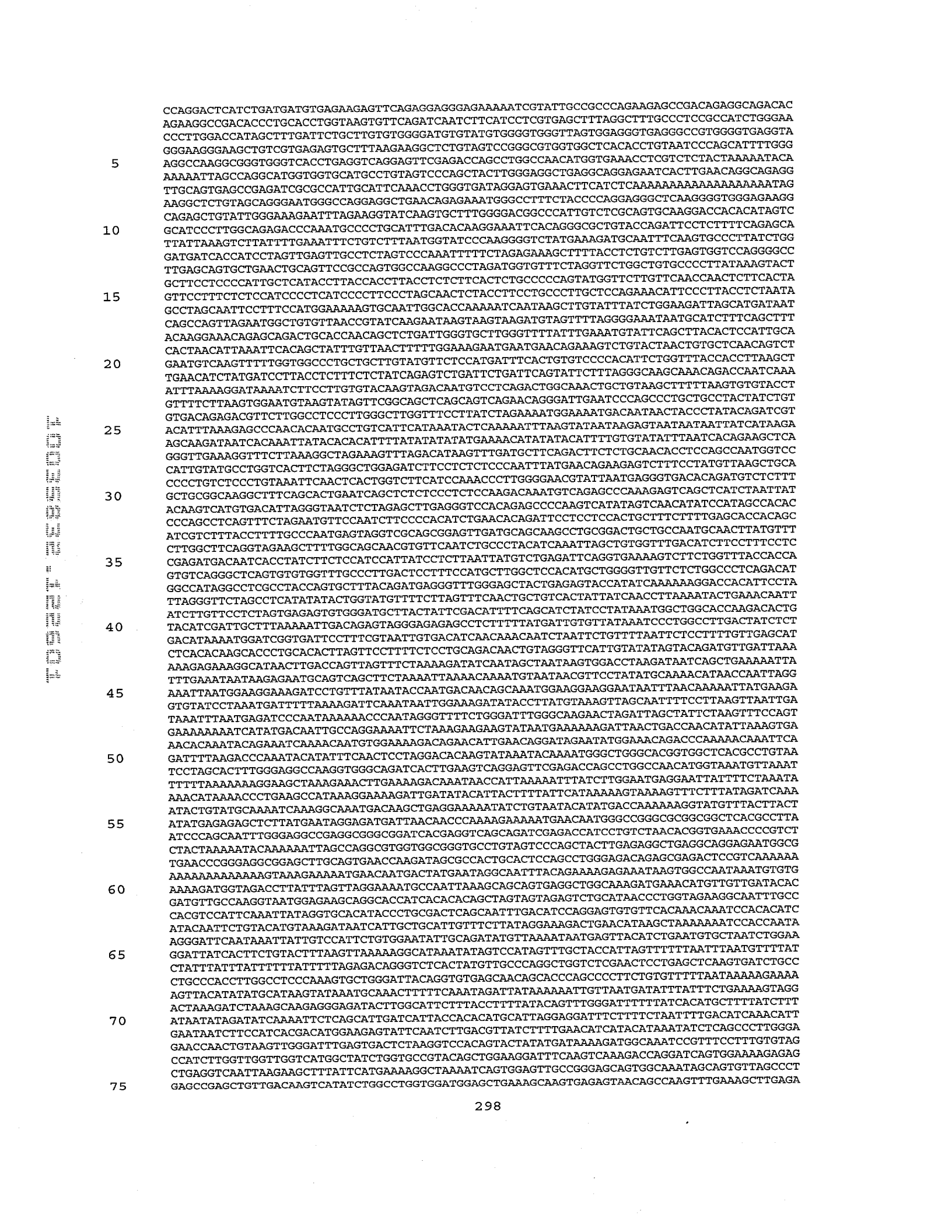
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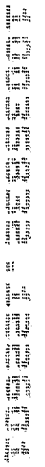
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HUMAN SEQUENCE - CODING
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Table 11

MOUSE NOMENCLATURE

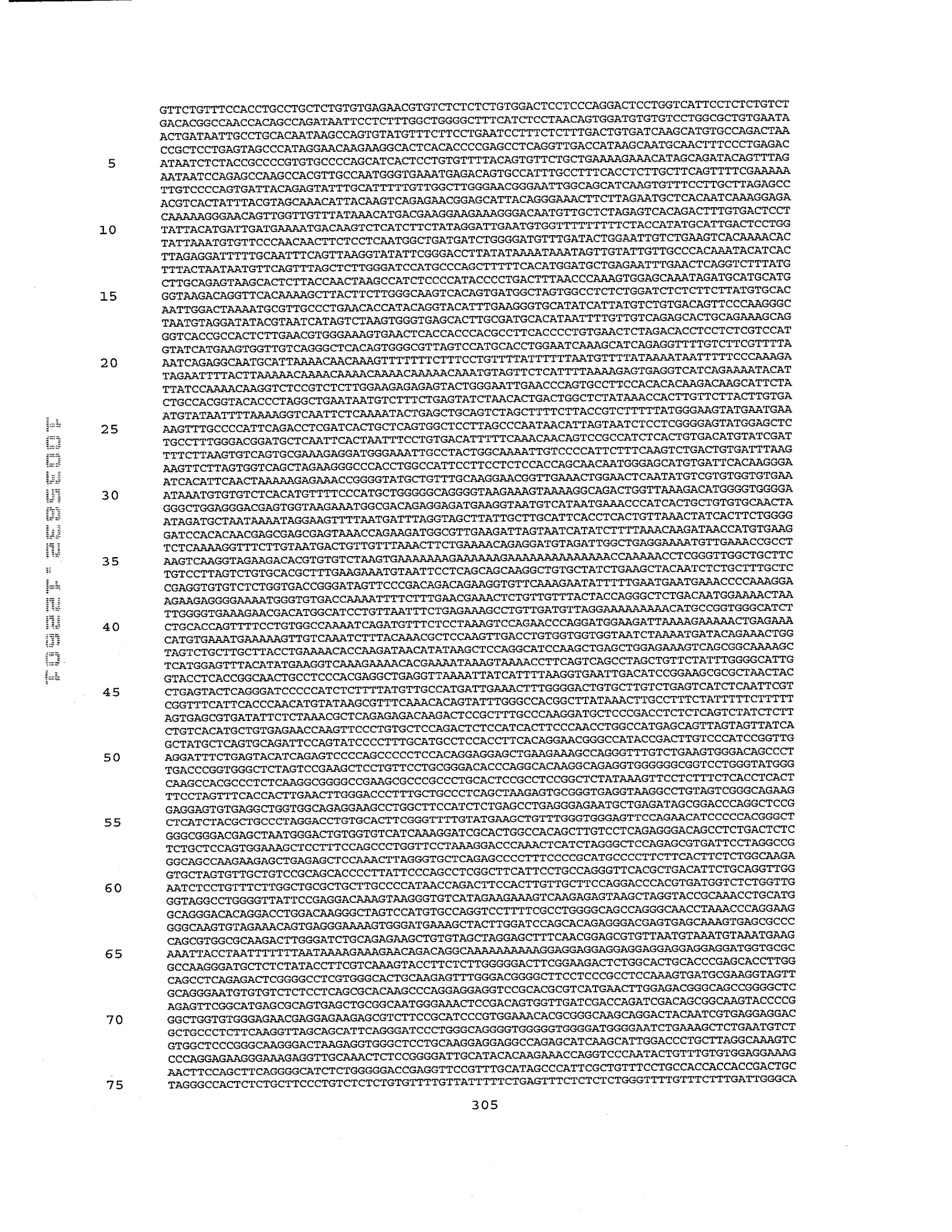
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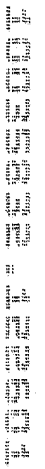
HUMAN NOMENCLATURE

HGNC	IRF4
Celera	hCG20902

MOUSE SEQUENCE - GENOMIC

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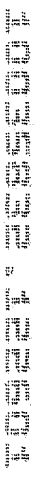
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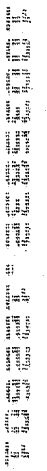
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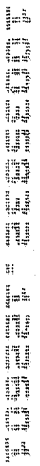
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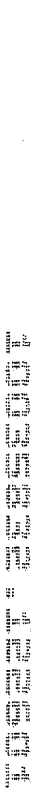
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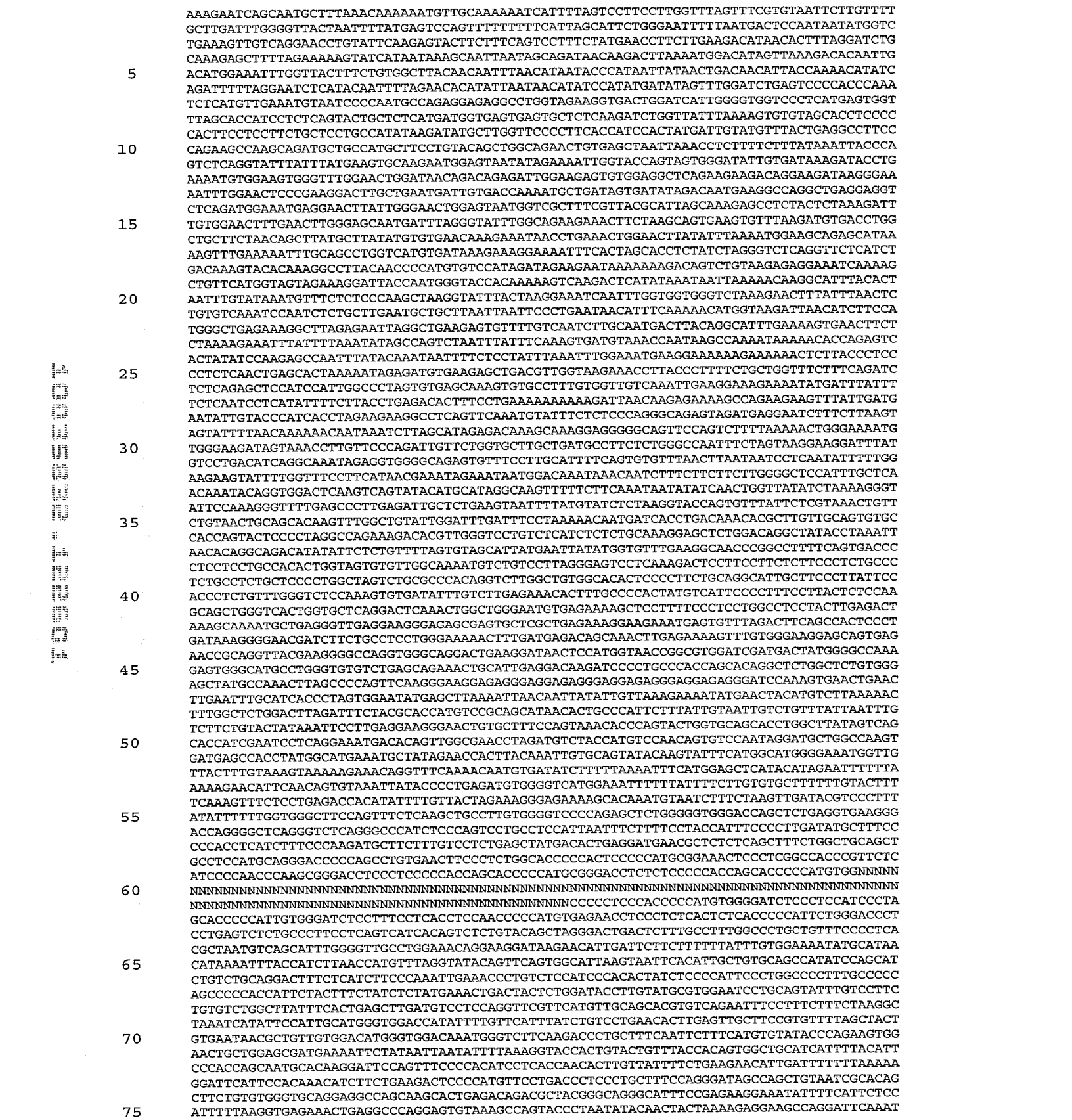
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 12

MOUSE NOMENCLATURE

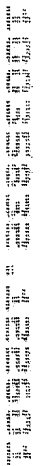
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HUMAN NOMENCLATURE

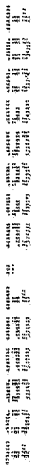
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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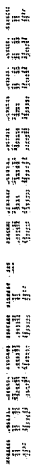
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Table 13

MOUSE NOMENCLATURE
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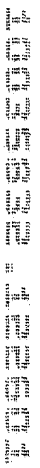
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MOUSE SEQUENCE - GENOMIC
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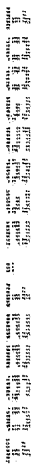
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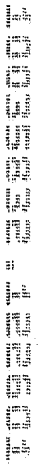
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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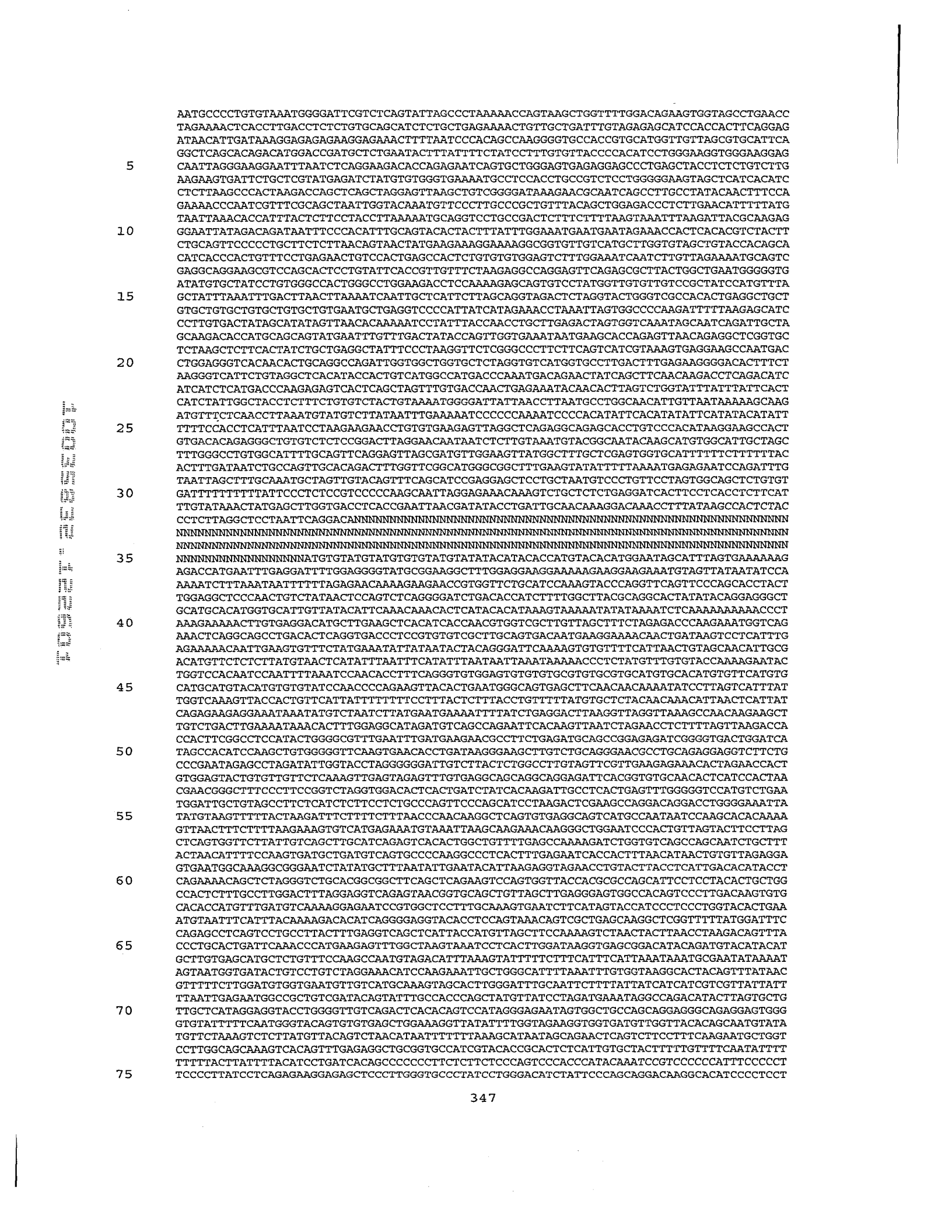
Table 14

MOUSE NOMENCLATURE
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Celera mCG12764

HUMAN NOMENCLATURE
HGNC BACH2
Celera hCG33075

MOUSE SEQUENCE - GENOMIC

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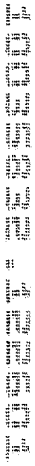
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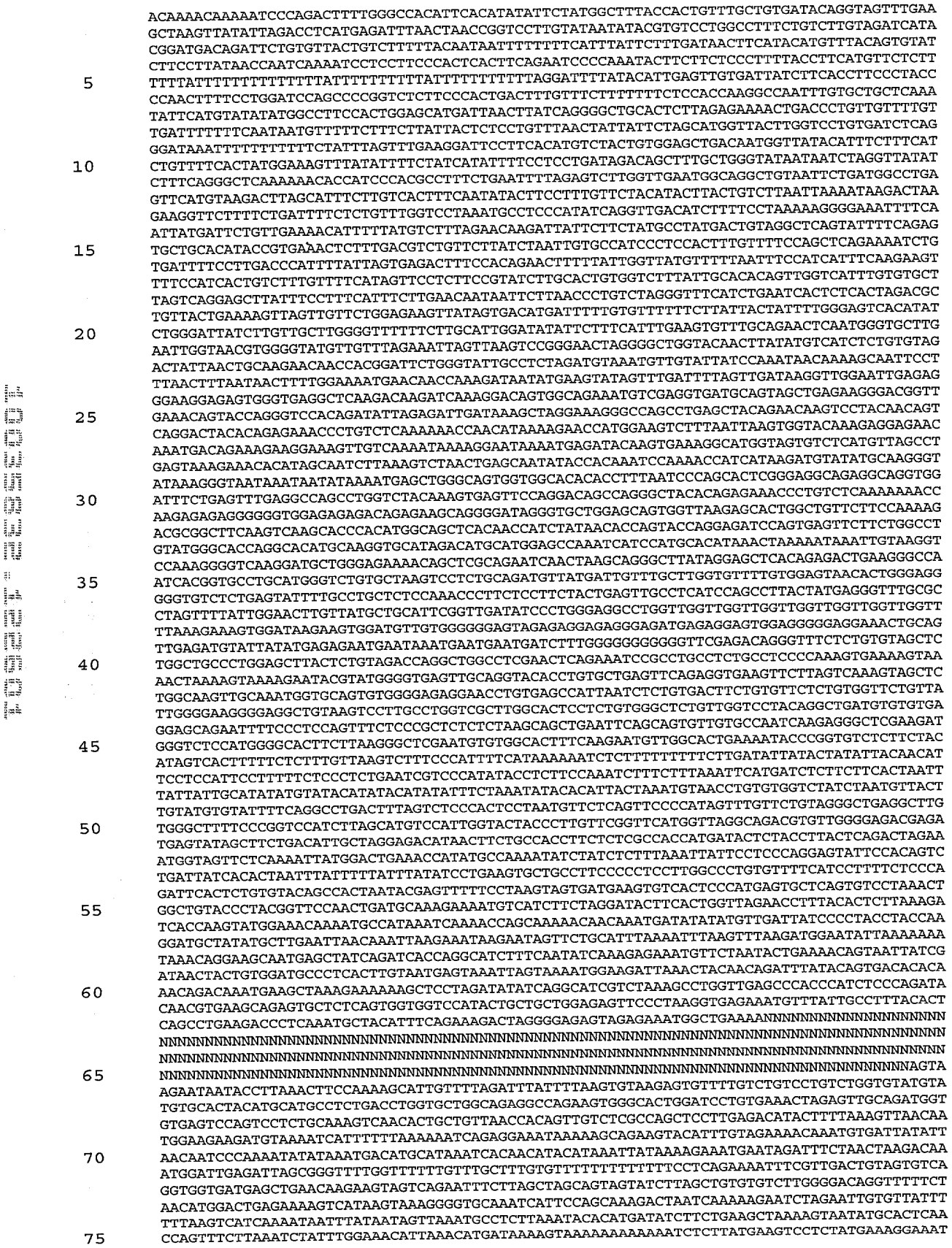
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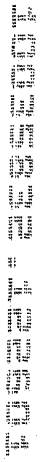
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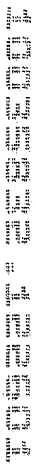
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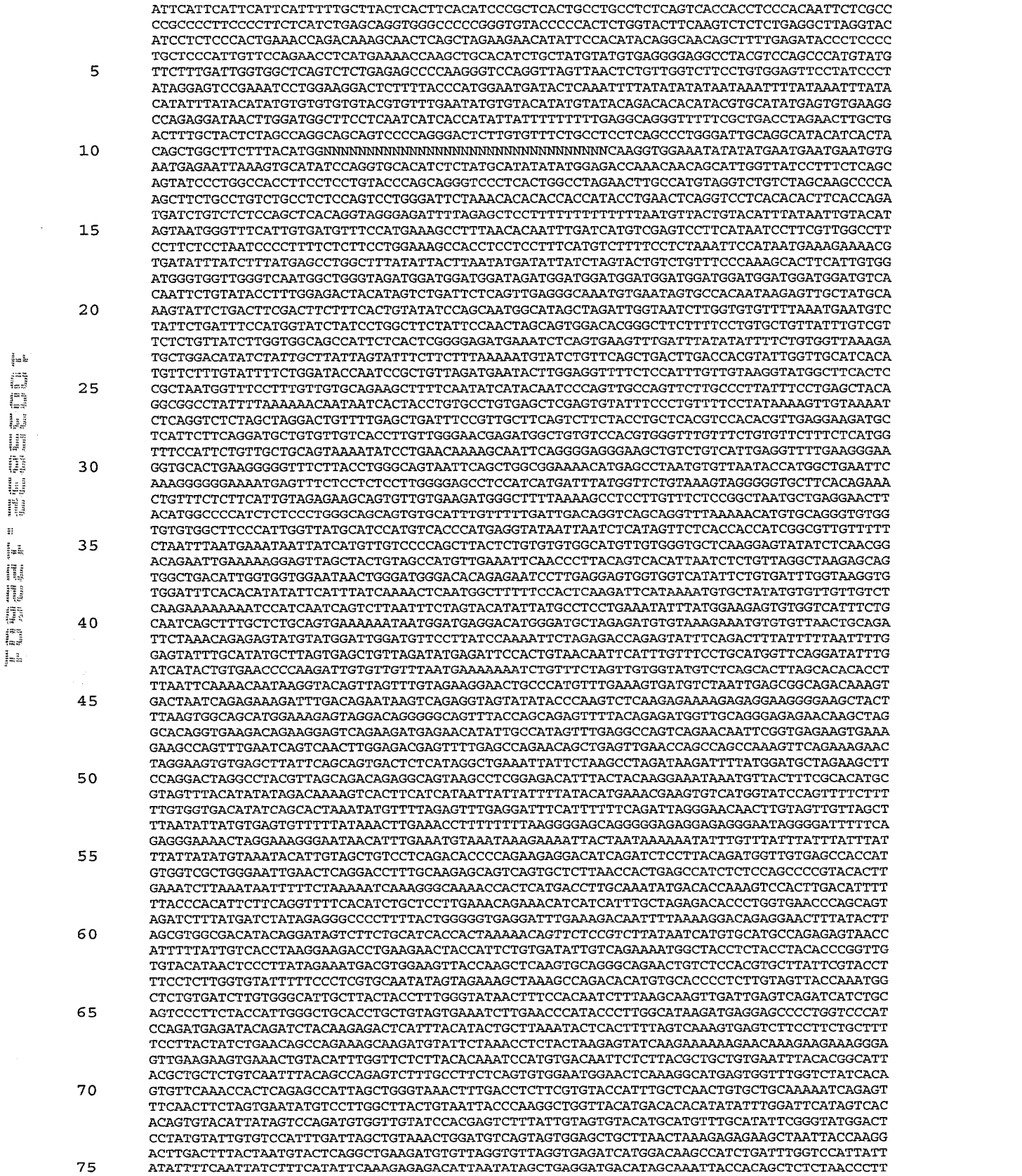
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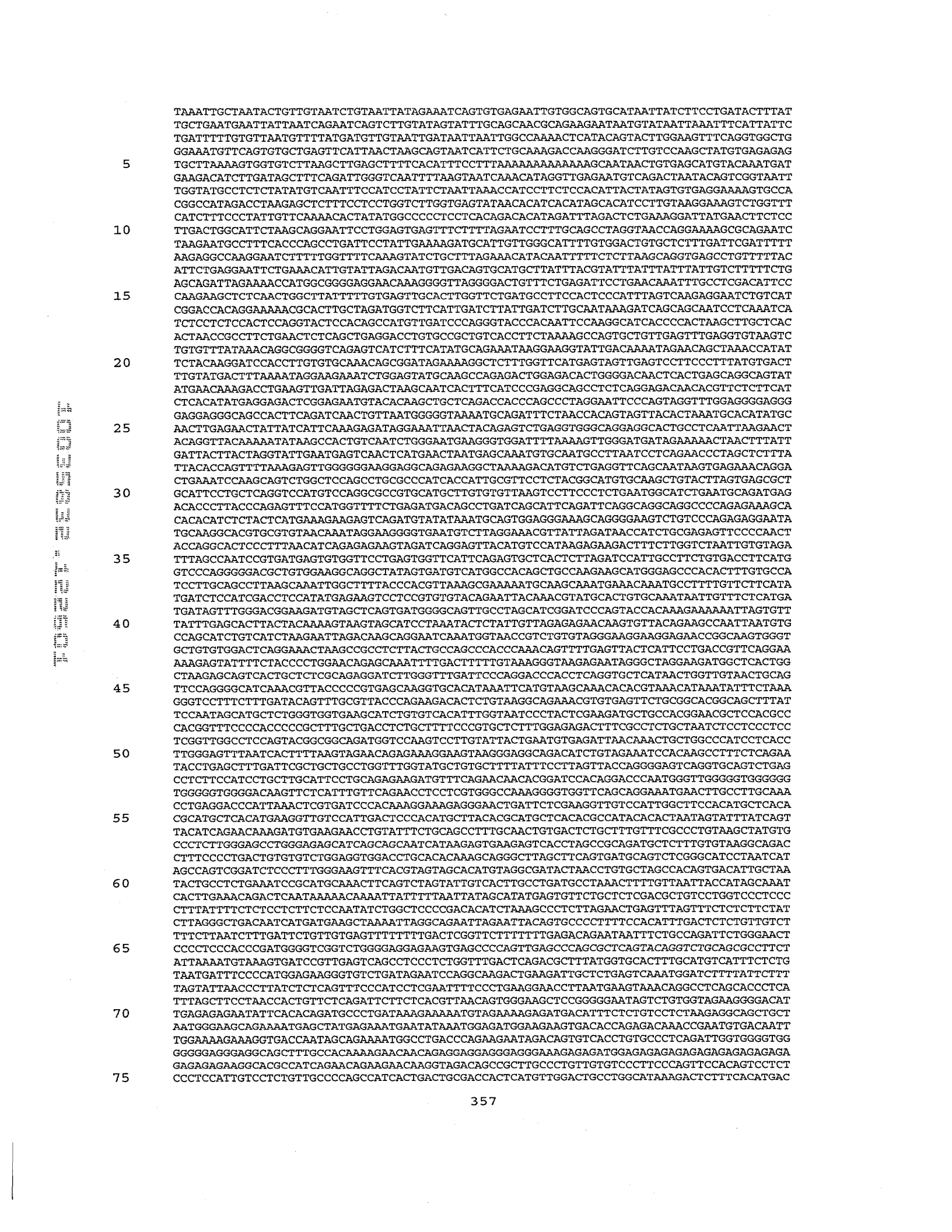


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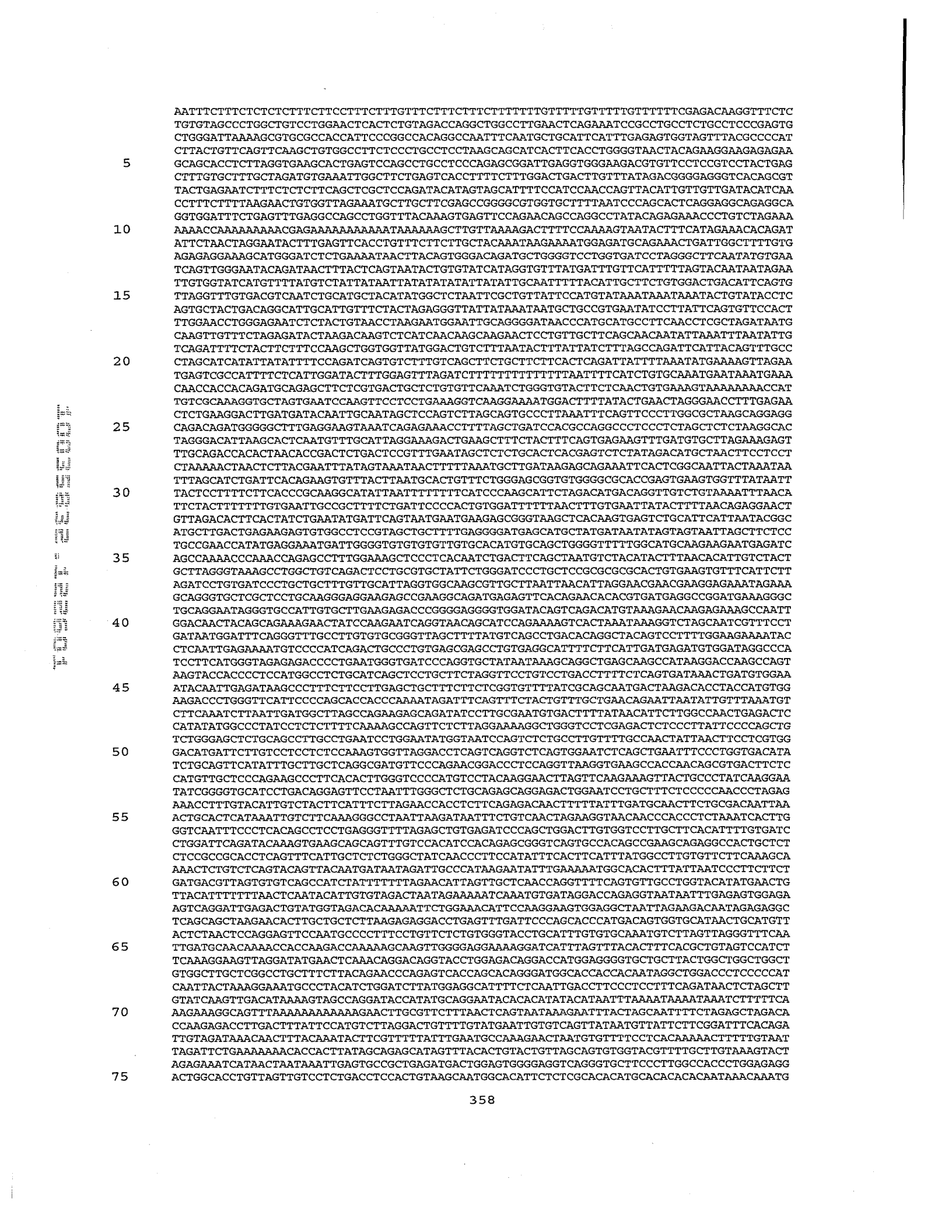


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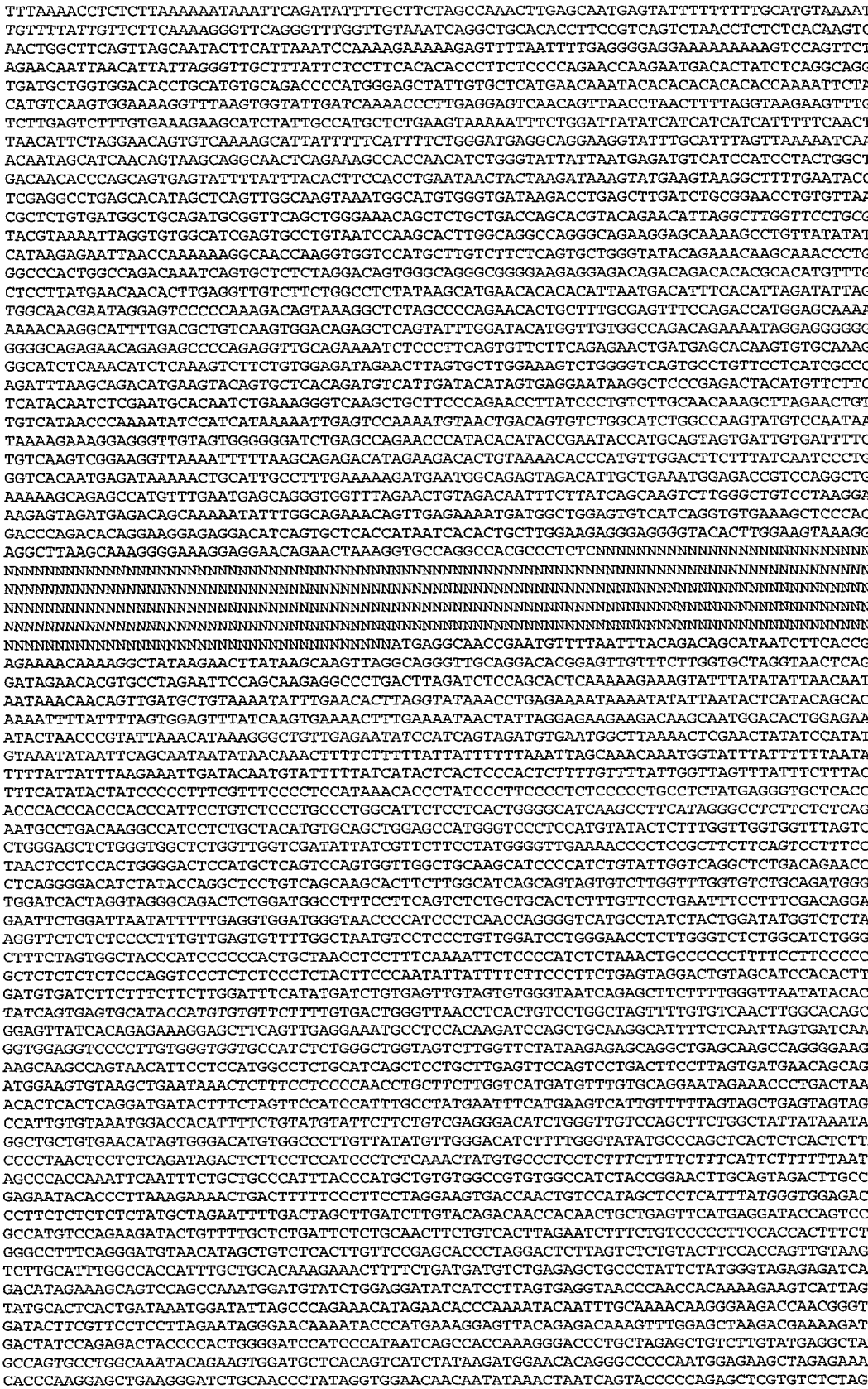




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MOUSE SEQUENCE - mRNA

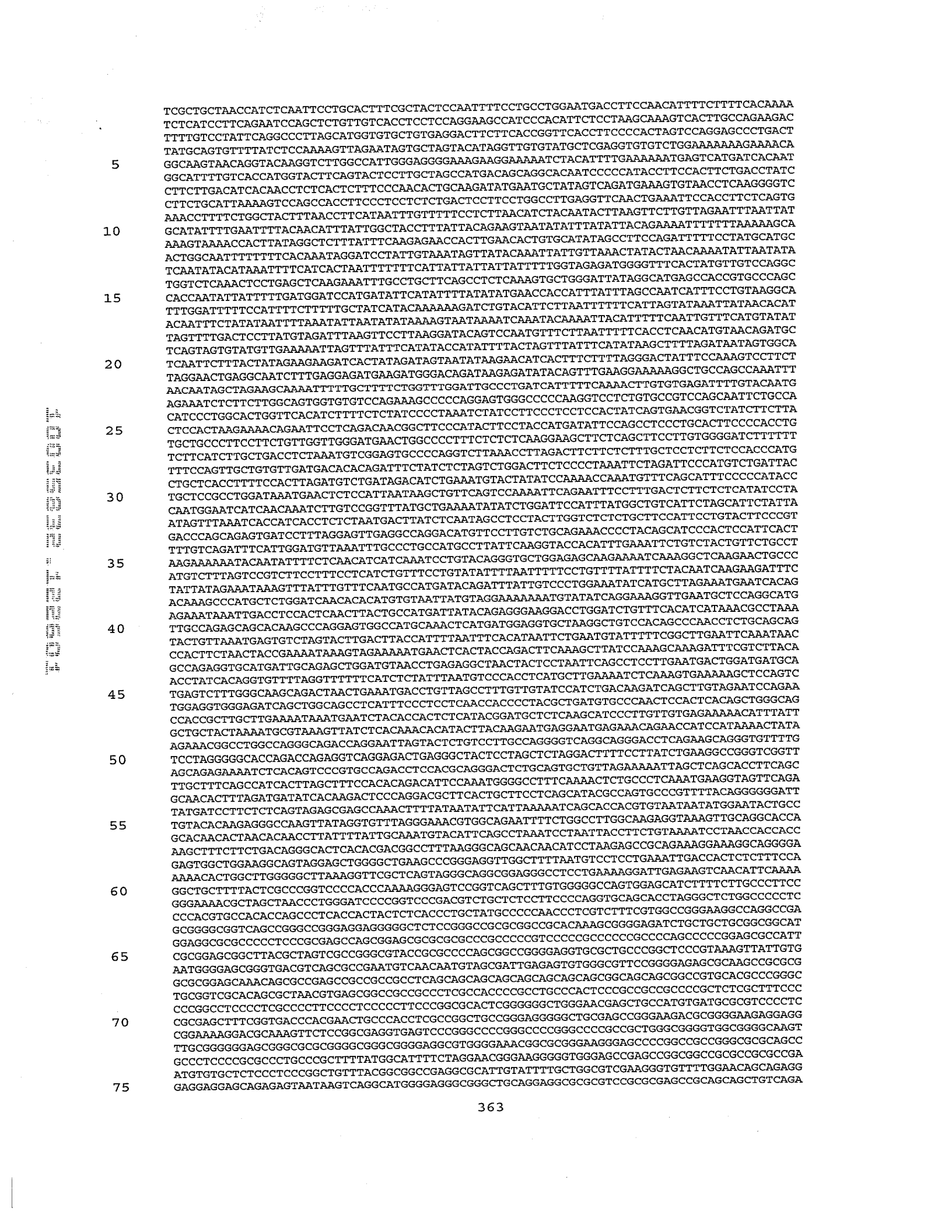
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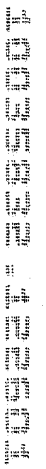
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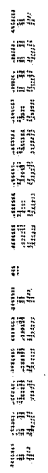
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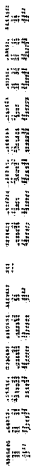
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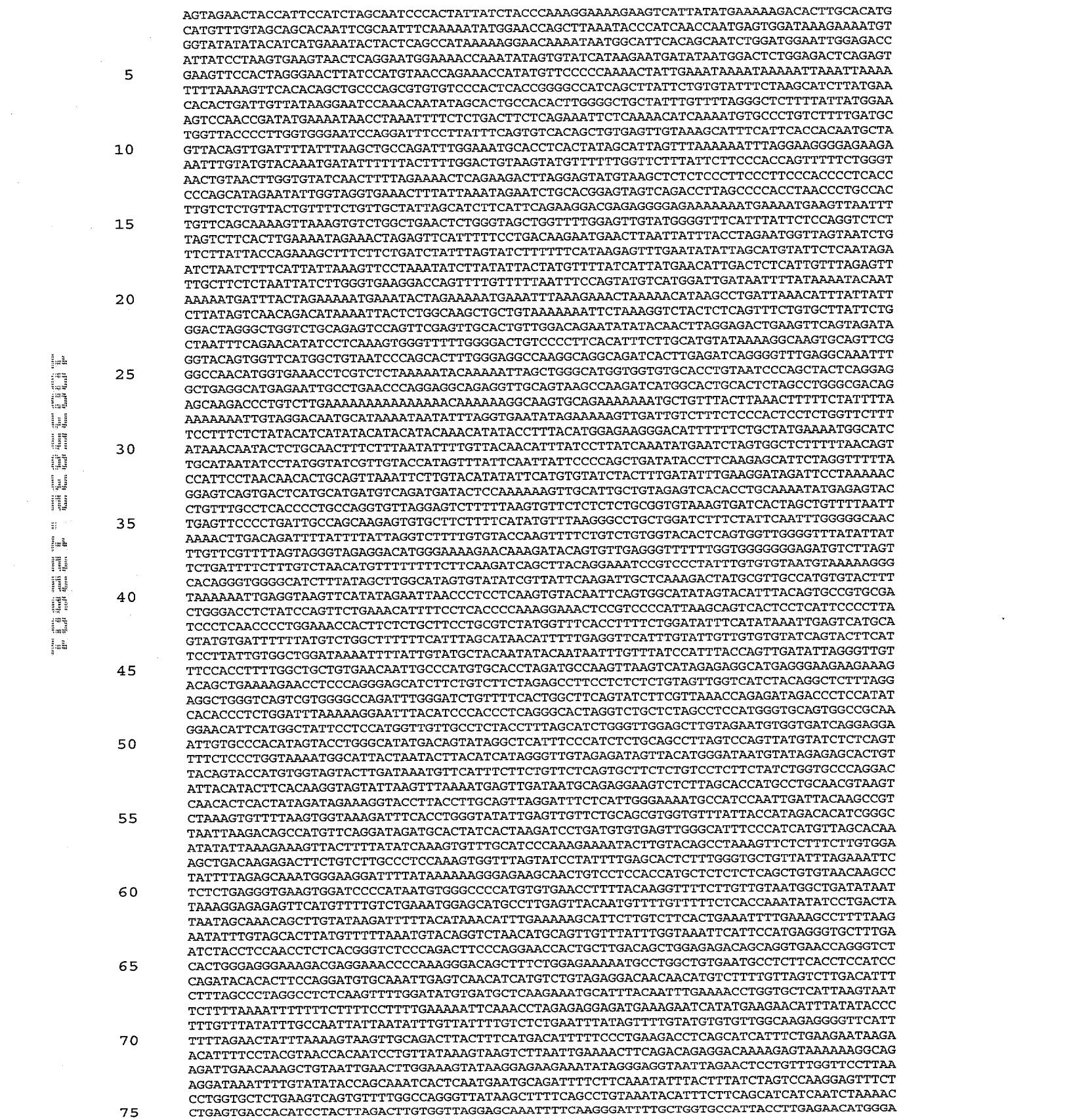
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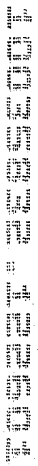


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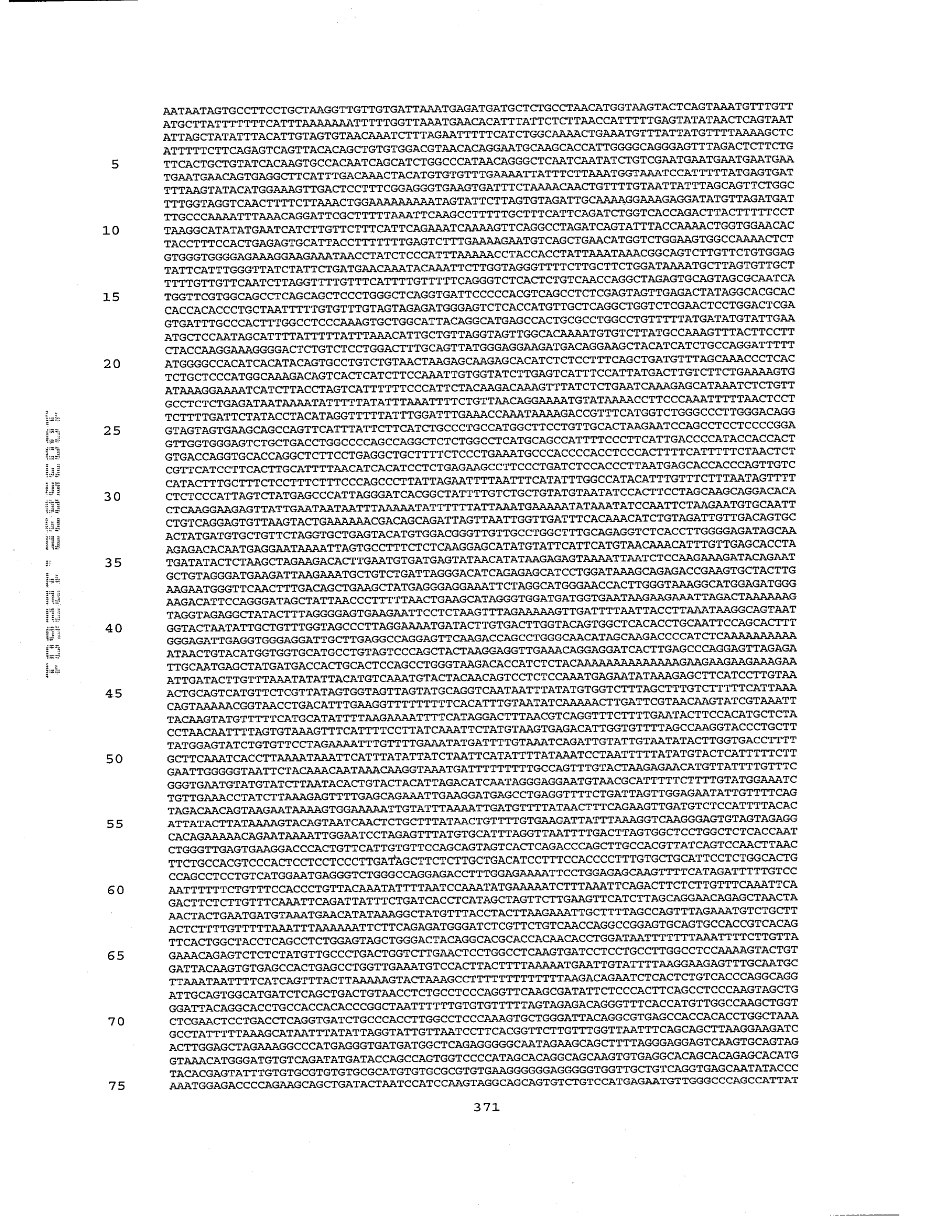


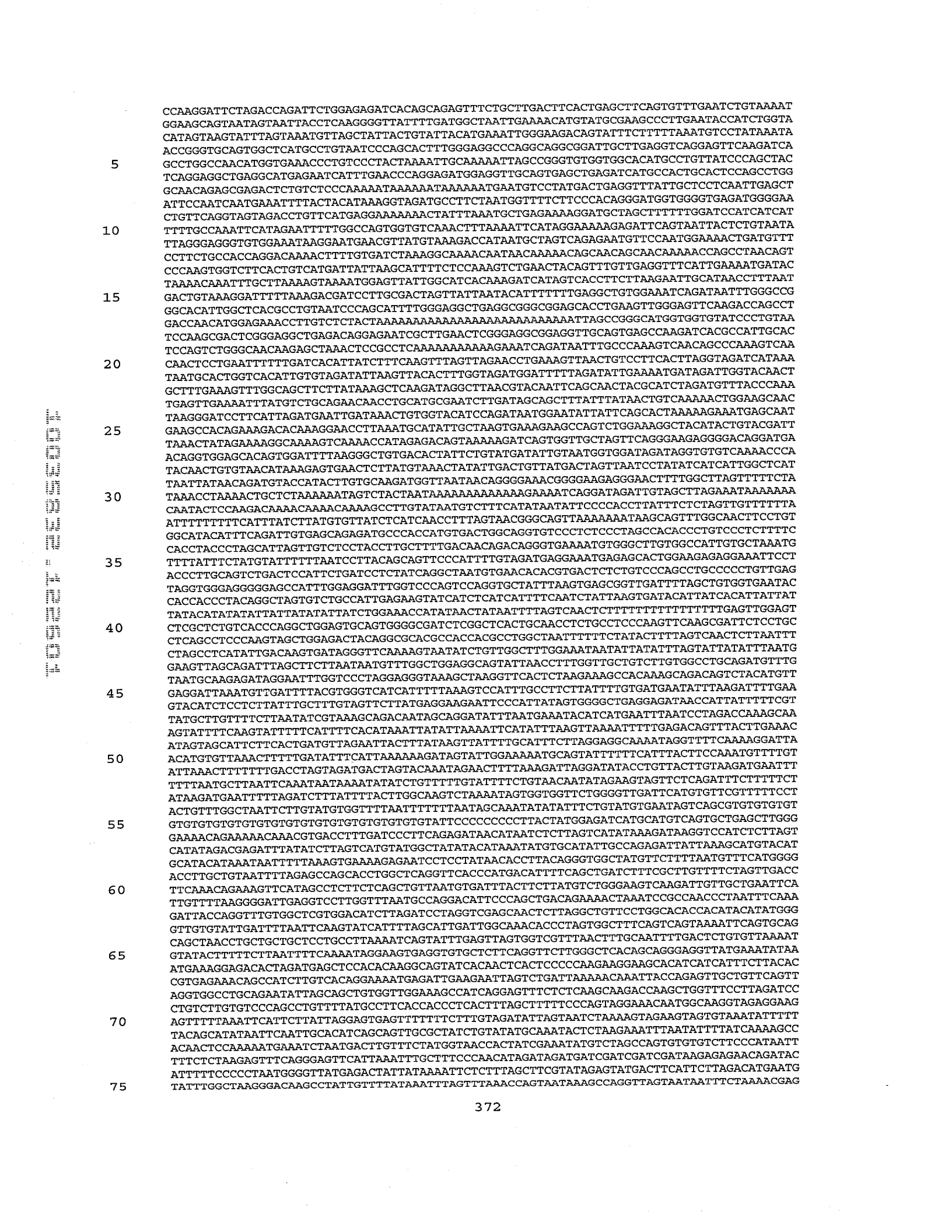
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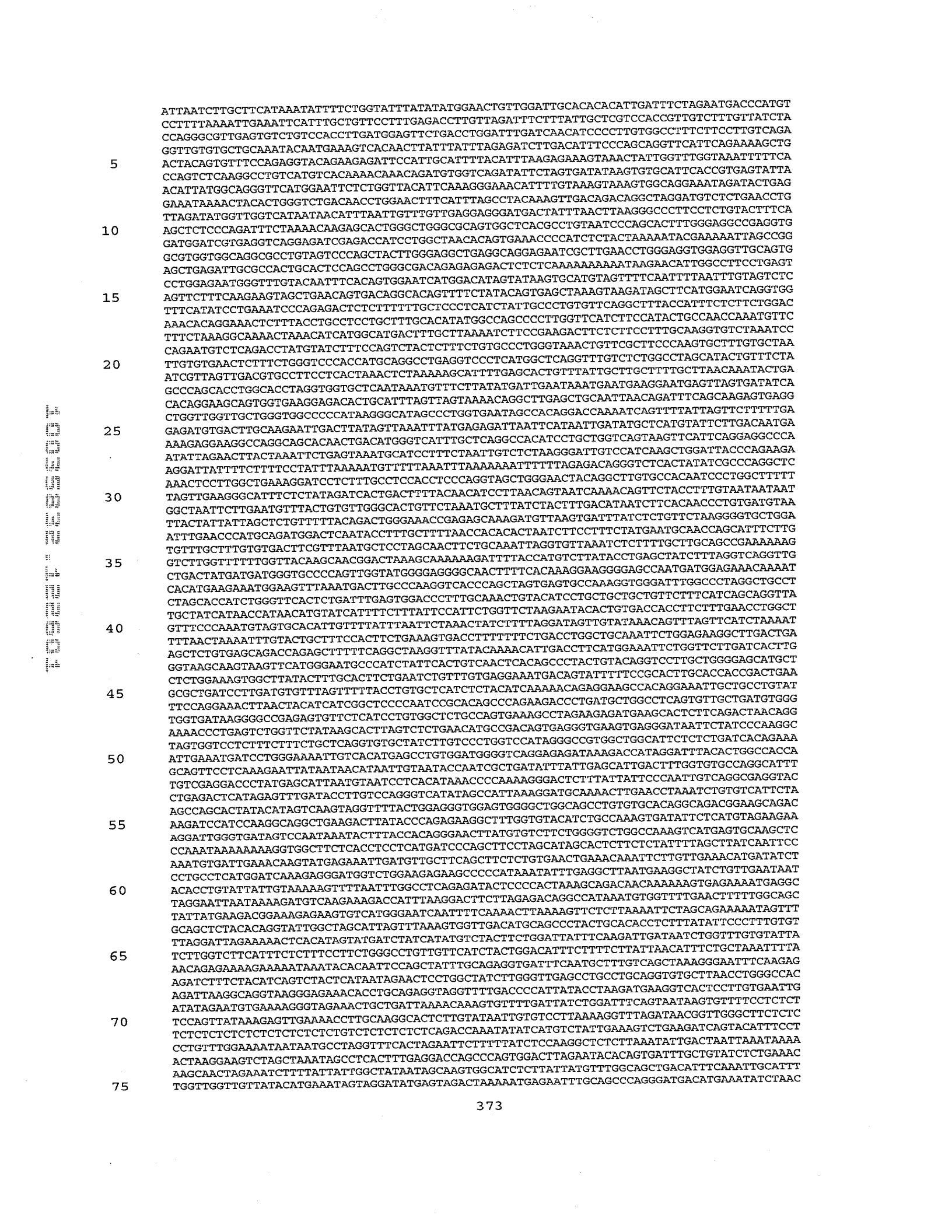


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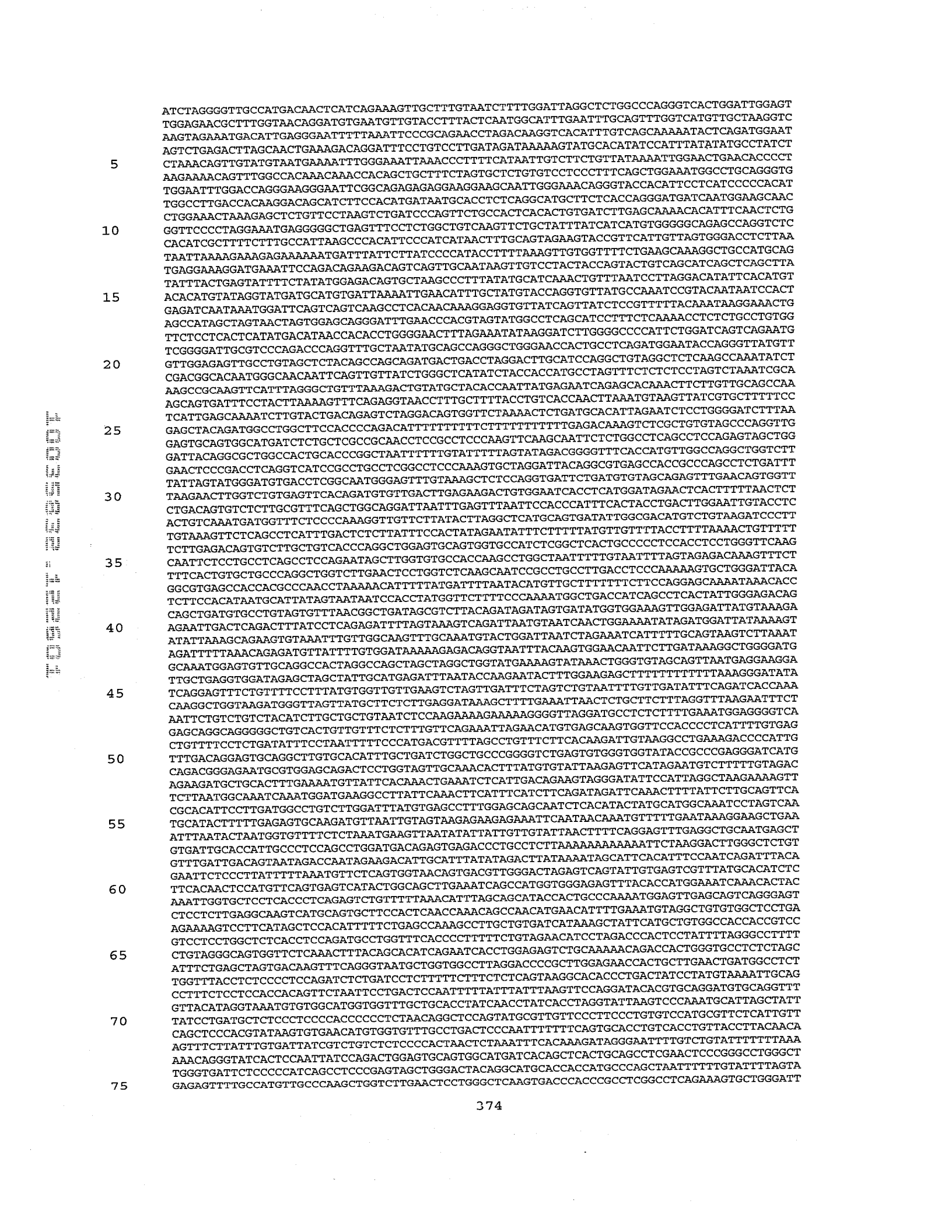


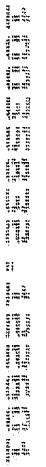


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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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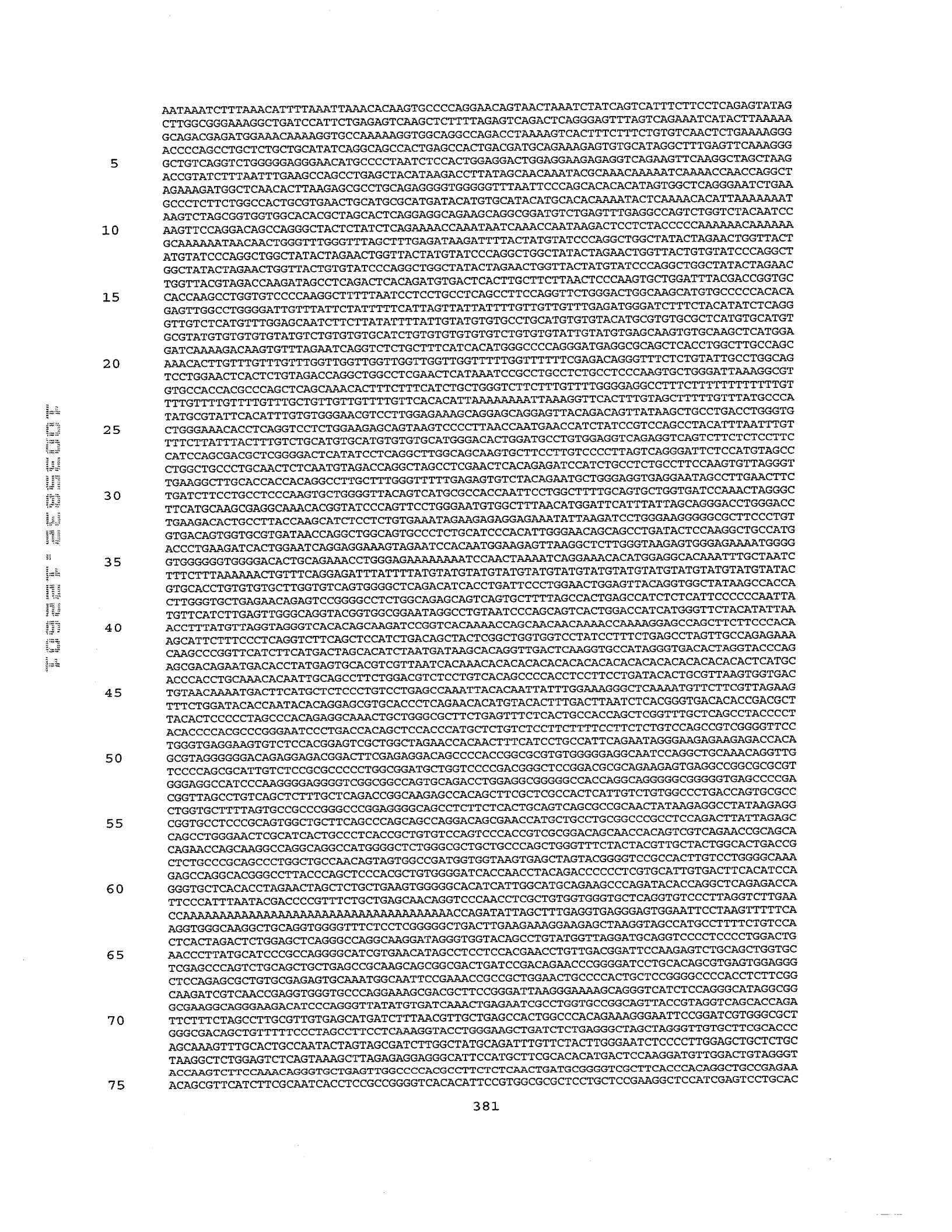
Table 15

MOUSE NOMENCLATURE
ICSGNM Wnt1
Celera mCG18420

HUMAN NOMENCLATURE
HGNC WNT1
Celera hCG41496

MOUSE SEQUENCE - GENOMIC

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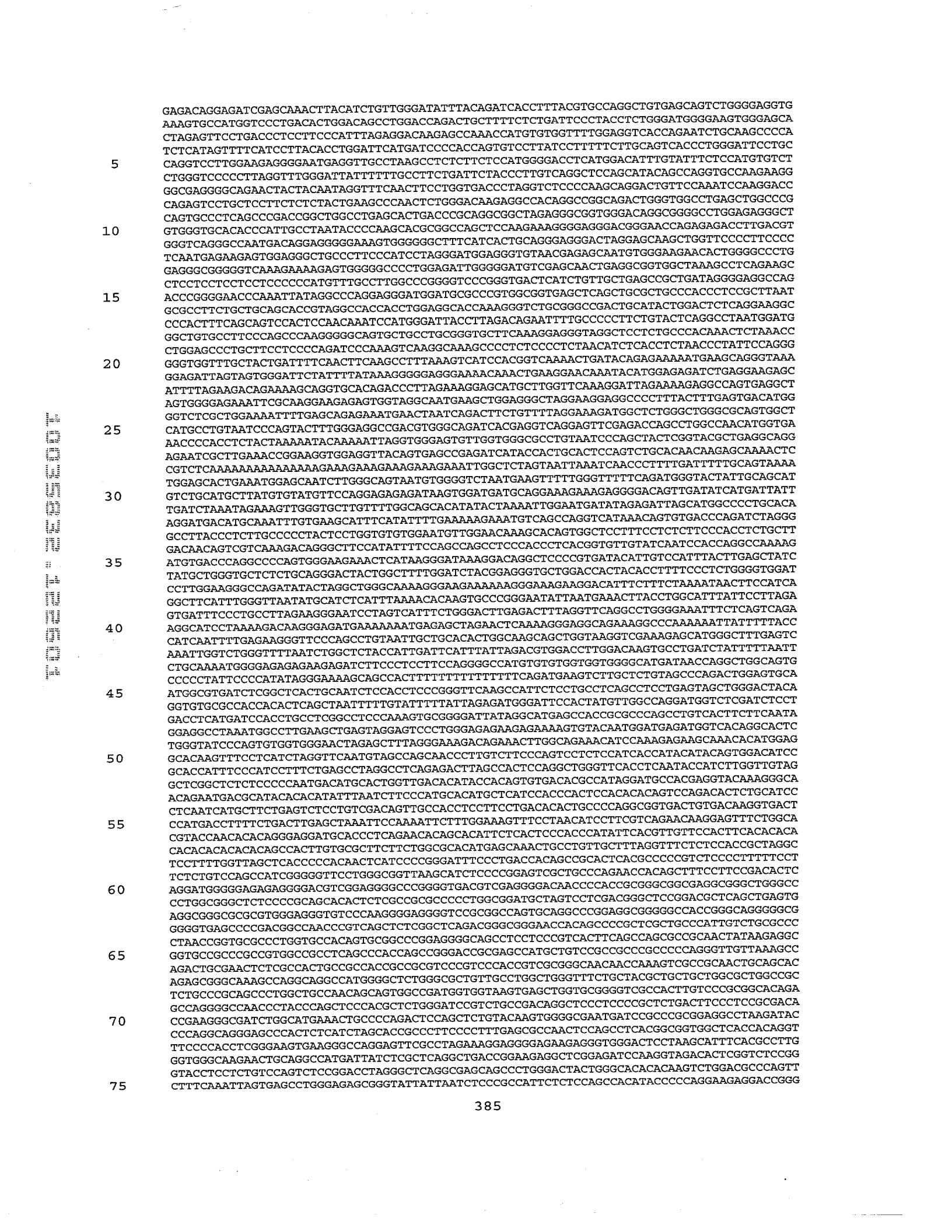
MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 16

MOUSE NOMENCLATURE

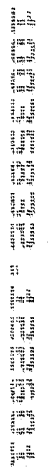
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HUMAN NOMENCLATURE

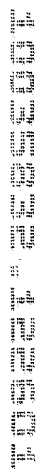
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MOUSE SEQUENCE - GENOMIC

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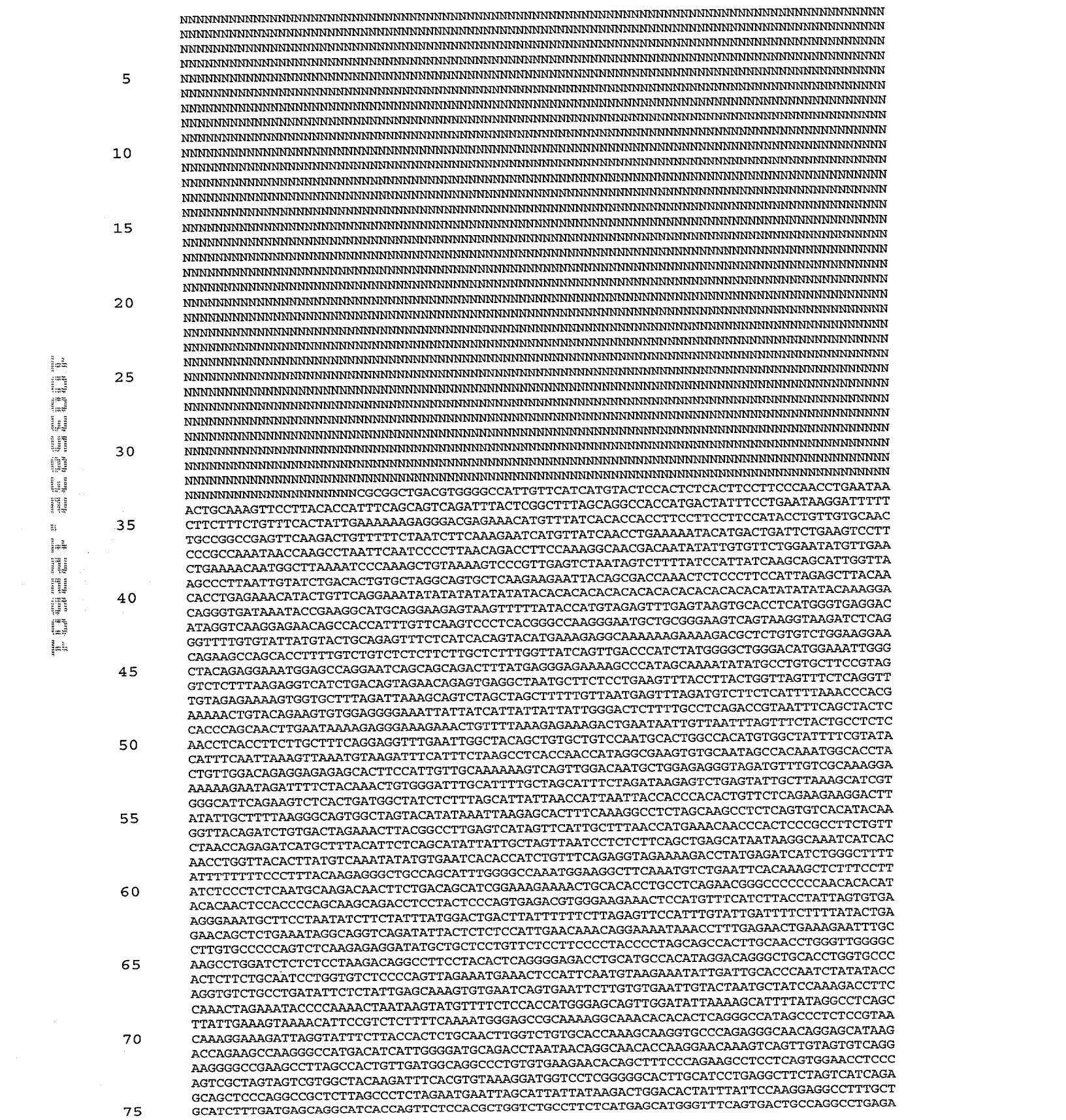
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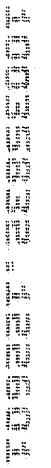
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HUMAN SEQUENCE - GENOMIC
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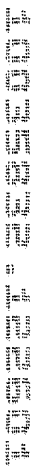
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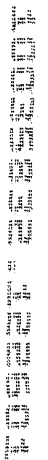


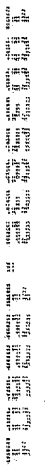


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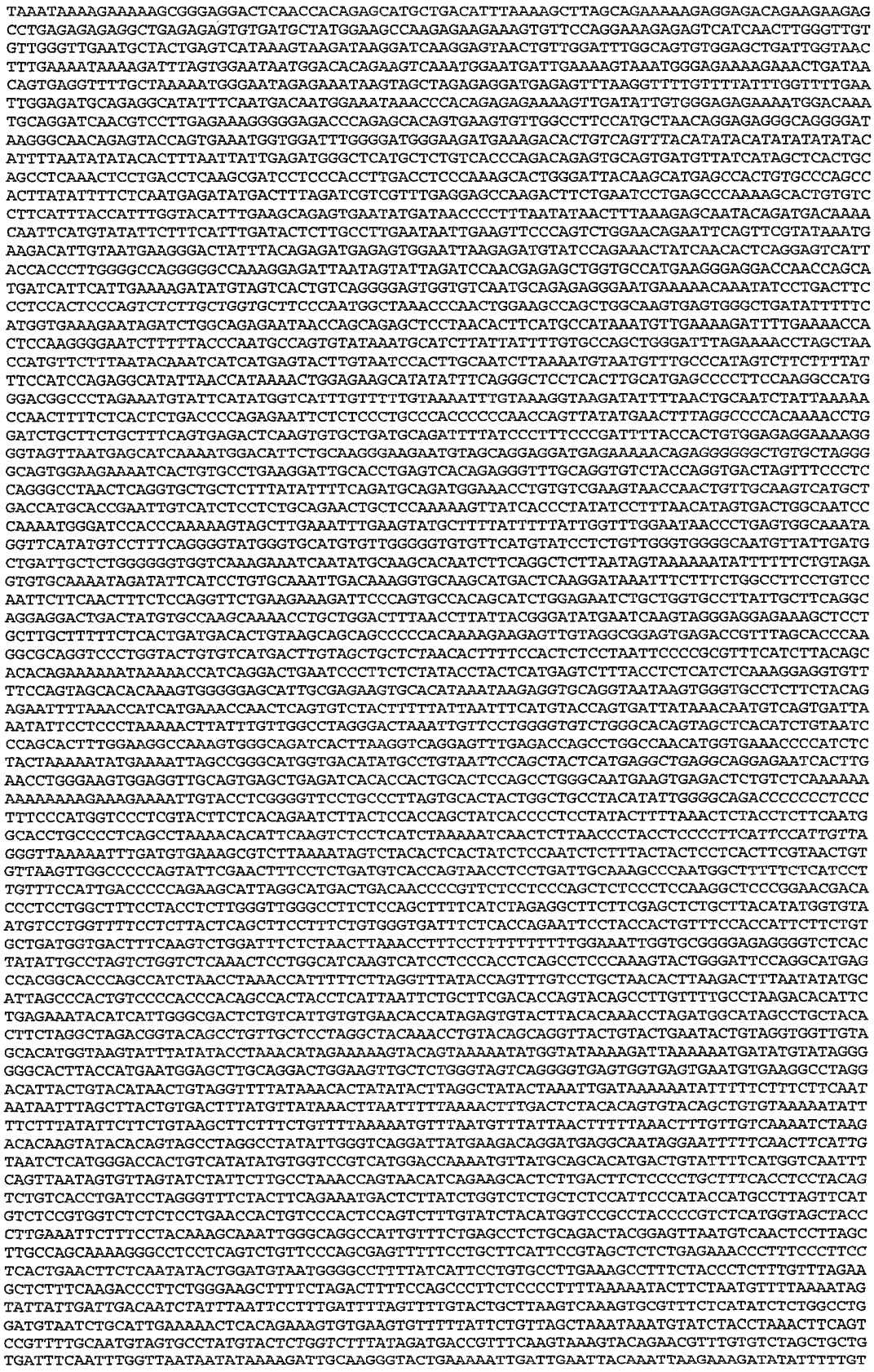


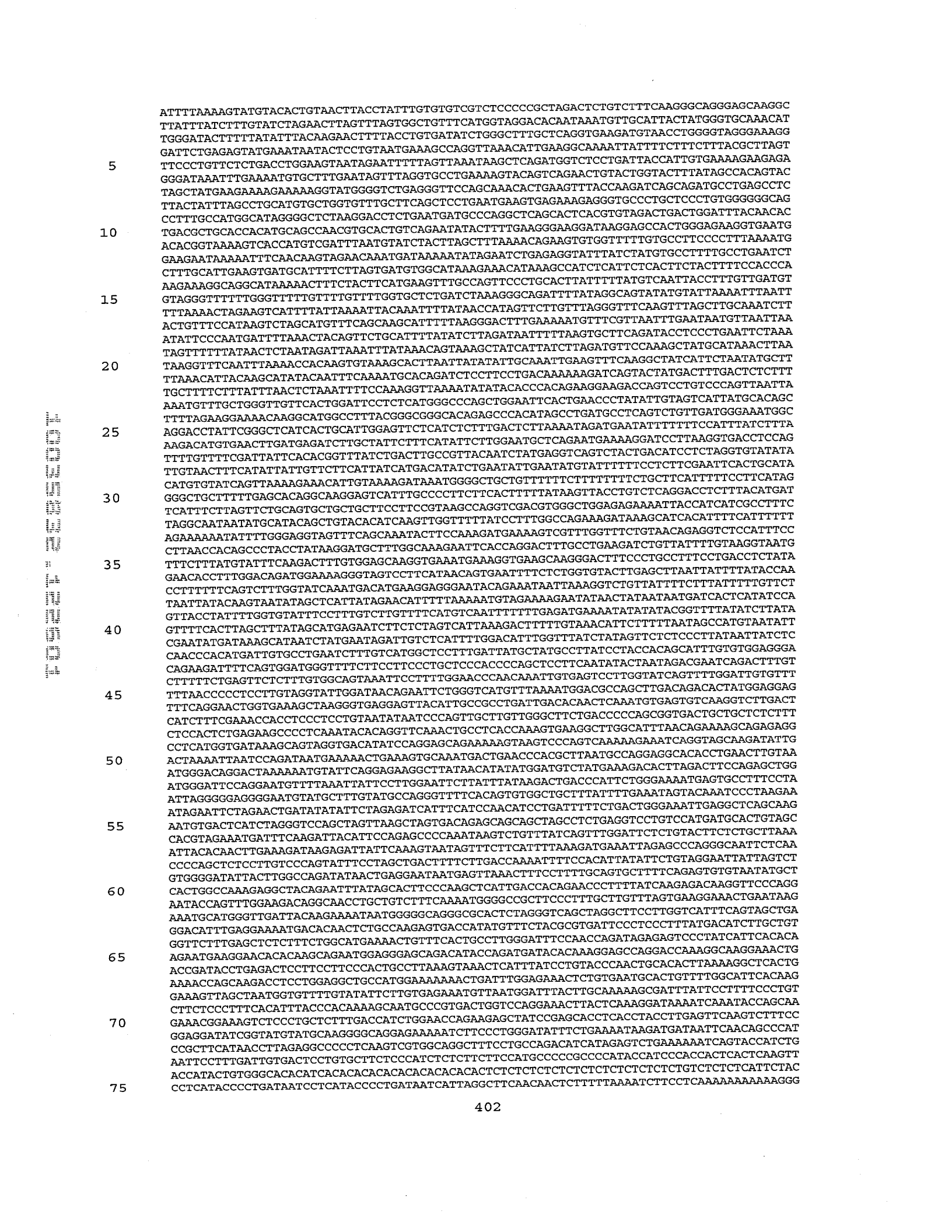
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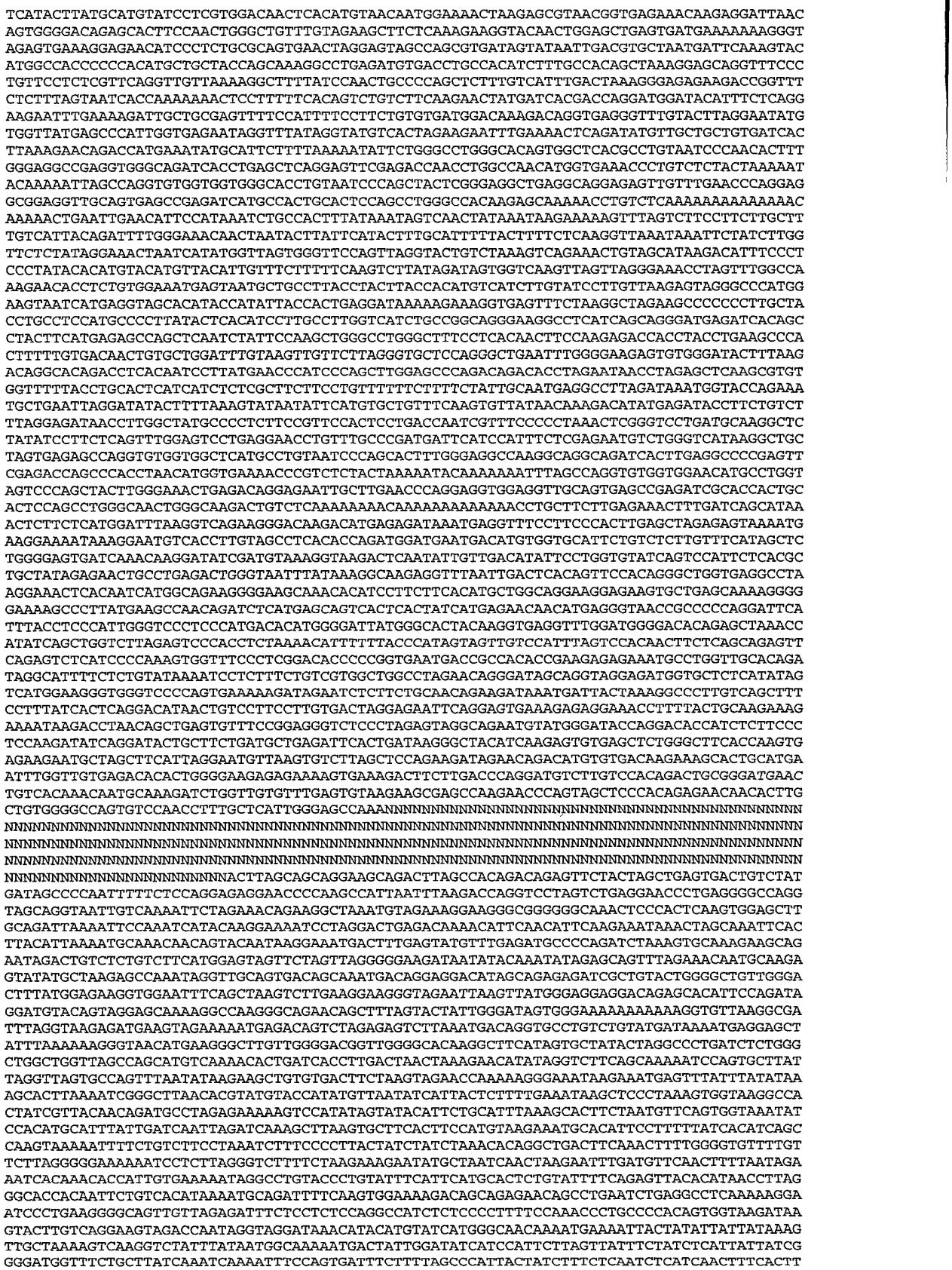


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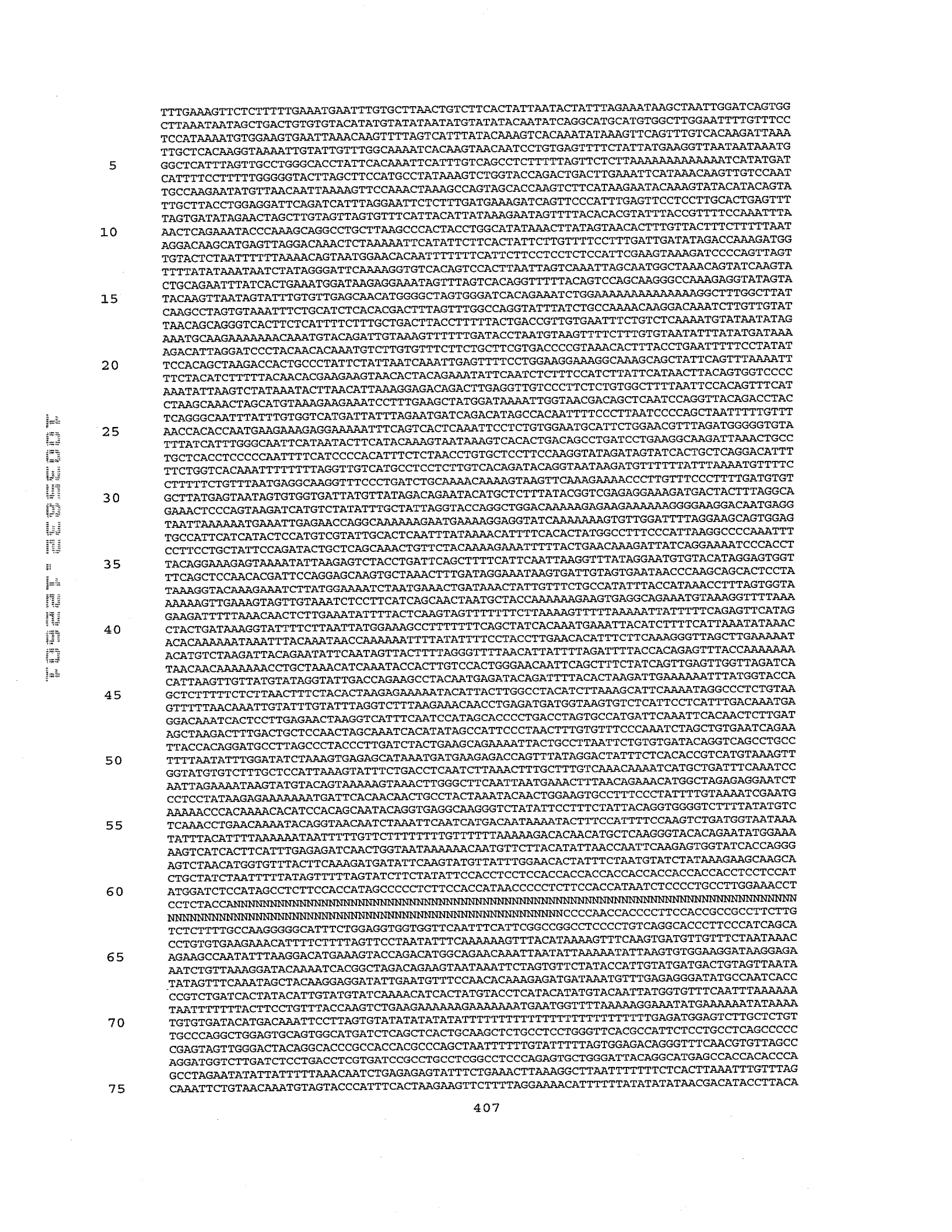
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Please add the sequence listing

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HUMAN SEQUENCE - mRNA
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AGTCCATGTACCCTCCTTCCTCACTACAGTCATAACACATGAGCATATCTACCTAGAAGCCAATTTCTACTGATGTAGCCACAACT
TTTTAGAGGCCTATTAAACATGACGTTATCCAATTGCAGGTCAACTTATAGTTGTAGCCTTACAACTTACAGGCATCAGAAAATAA
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CATCTTTCTCTTCTGAAGTAAACTATTTTGAAAGTTCTCTTTTTGAAATGAATTTGTGCTTAACTGTCTTCACTATTAATACTATT
TAGAAATAAGCTAATTGGATCAGTGGCTTAAATAATAGCTGACTGTGTGTACATATGTATATAATATGTATATACAATATCAGGCA
TGCATGTGGCTTGGAATTTTGTTTCCTCCATAAAATGTGGAAGTGAATTAAACAAGTTTTAGTCATTTATACAAAGTCACAAATAT
AAAGTTCAGTTTGTCACAAGATTAAATTGCTCACAAGGTAAAATTGTATTGTTTGGCAAAATCACAAGTAACAATCCTGTGAGTTT
TCTATTATGAAGGTTAATAATAAATGGGCTCATTTAGTTGCCTGGGCACCTATTCACAAATTCATTTGTCAGCCTCTTTTTAGTTC
TCTTAAAAAAAAAAAAAATCATATGATCATTTTCCTTTTTGGGGGTACTTAGCTTCCATGCCTATAAAGTCTGGTACCAGACTGACT
TGAAATTCATAAACAAGTTGTCCAATTGCCAAGAATATGTTAACAATTAAAAGTTCCAAACTAAAGCCAATAGCACCAAGTCTTCA
TAAGAATACAAAGTATACATACAGTATTGCTTACCTGGAGGATTCAGATCATTTAGGAATTCTCTTTGATGAAAGATCAGTTCCCA
TTTGAGTTCCTCCTTGCACTGAGTTTTAGTGATATAGAACTAGCTTGTAGTTAGTGTTTCATTACATTATAAAGAATAGTTTTACA
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HUMAN SEQUENCE - CODING
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CAAATCAATGCCCGTGACTGGTCCAGGAAACTTACTCAAAGGATAAAATCAAATACCAGCAAGAAACGGAAAGTCTCCCTGCTCTT
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CAACTGATGGTTCTCAGCCGCCCCACGCCGCAGCTCCGAGCAGAAGTCTTCATCAAGTTCATCCAGGTGGCTCAGAAGCTCCACCA
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CTTGGTCAGAAAGCGGGCTTTTGTCAAGTGGGAGAATAAAGACTCCCTCATAAAATCAAAGGAGGAGCTCCGTCACCTCAGACTGC
CTACCTACCAAGAACTGGAACAGGAAATAAATACTCTGAAAGCAGATAATGATGCCCTAAAGATCCAACTGAAATATGCACAGAAG
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Table 17

MOUSE NOMENCLATURE
ICSGNM Nmyc1
Celera mCG19753

HUMAN NOMENCLATURE
HGNC MYCN
Celera hCG1783900

MOUSE SEQUENCE - GENOMIC
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ATAACTAACCAGGCCATCTTAGCCGACTTTCCCAGTCCCCTGCTGCTTGAGGGAGTTCTAGTAGGCTGGTCAAAGTGTCCTTTACG
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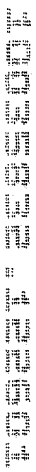
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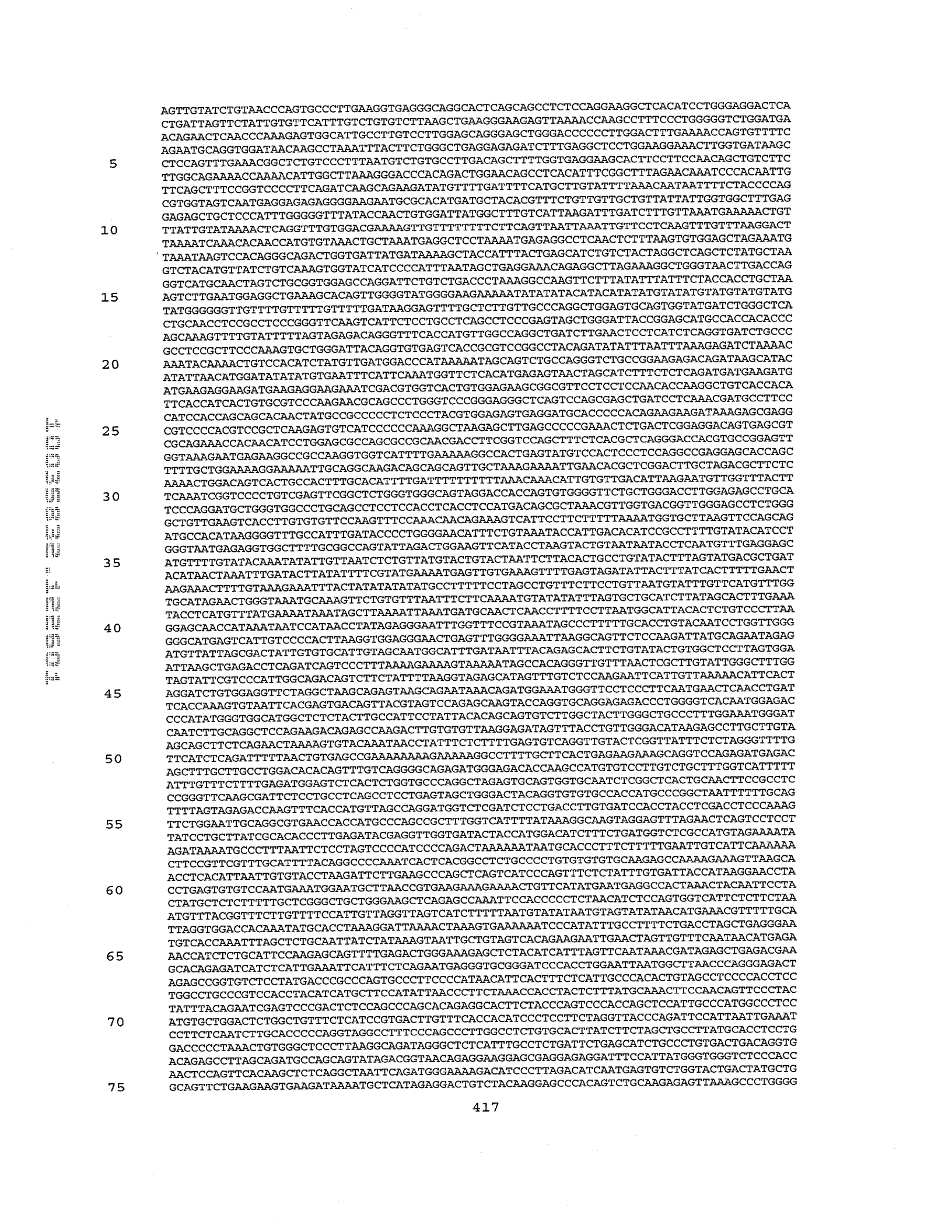
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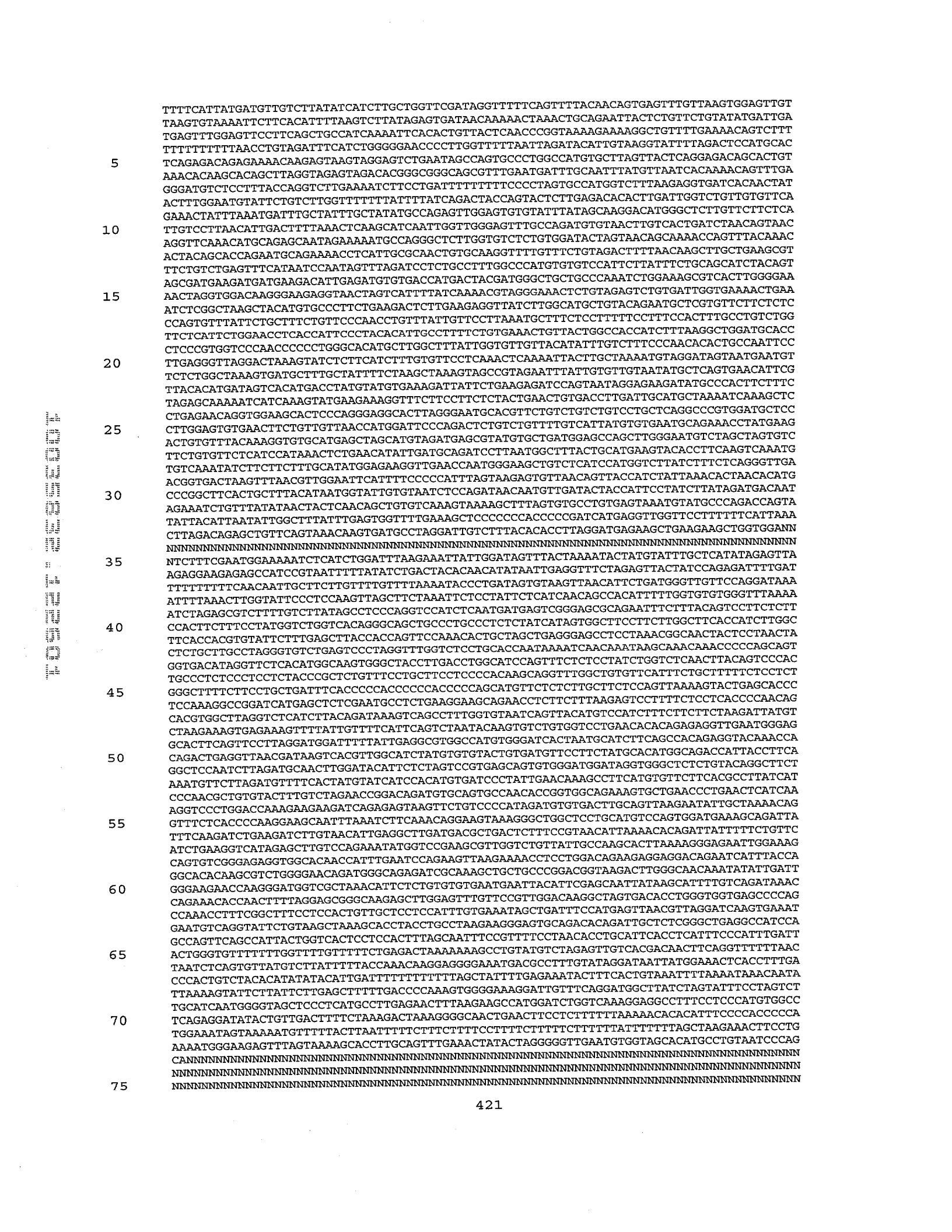
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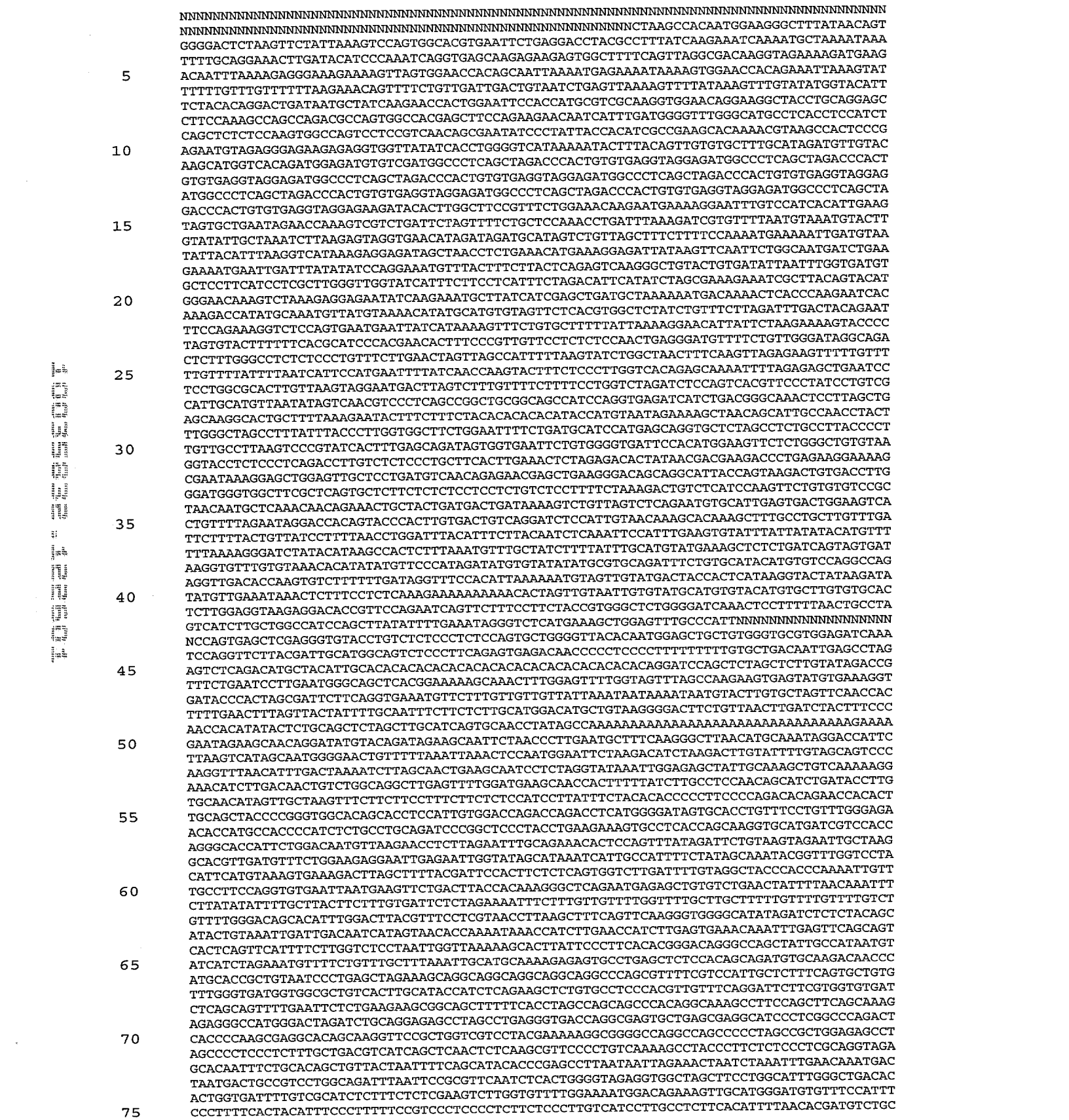
Table 18

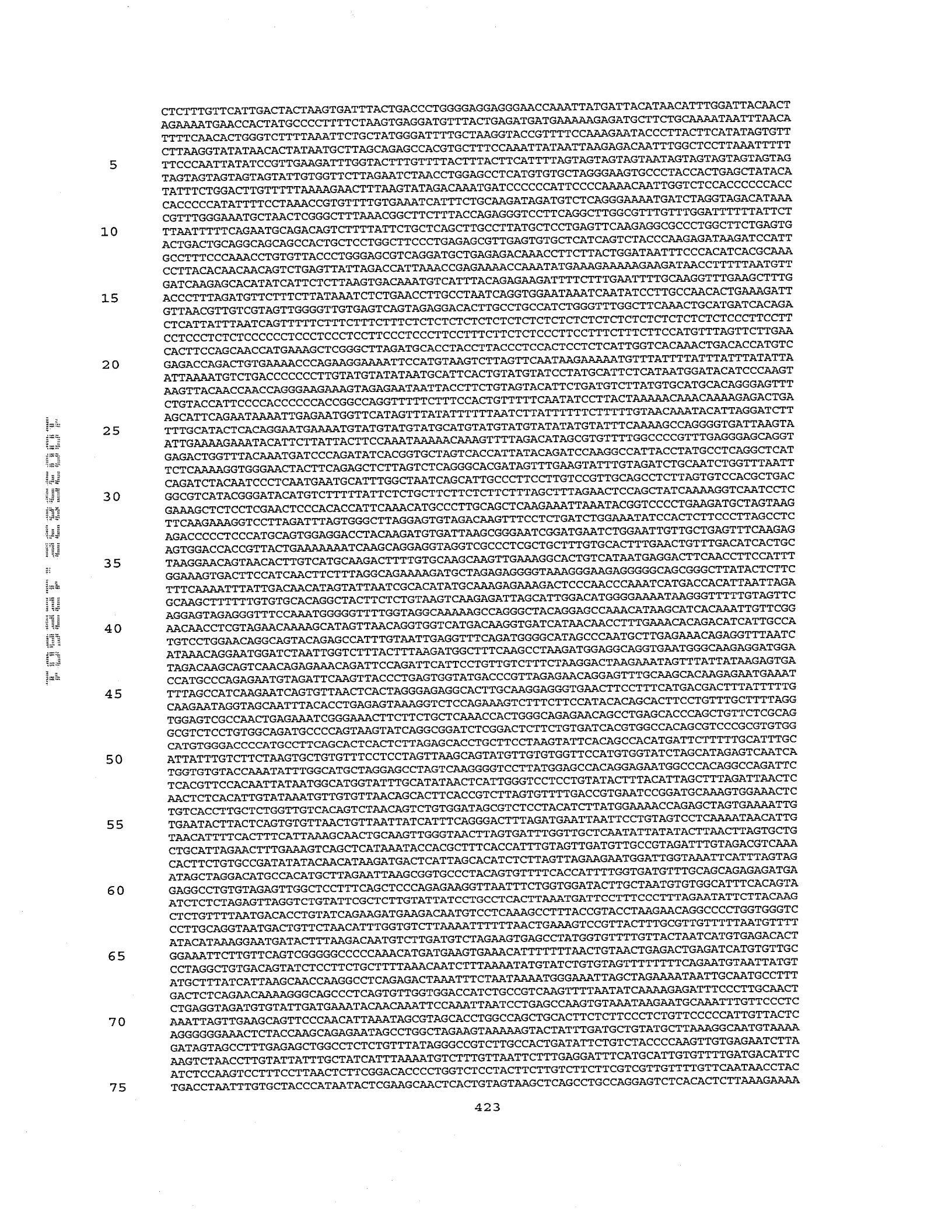
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MOUSE SEQUENCE - GENOMIC
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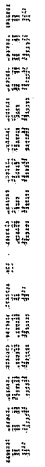






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MOUSE SEQUENCE - mRNA
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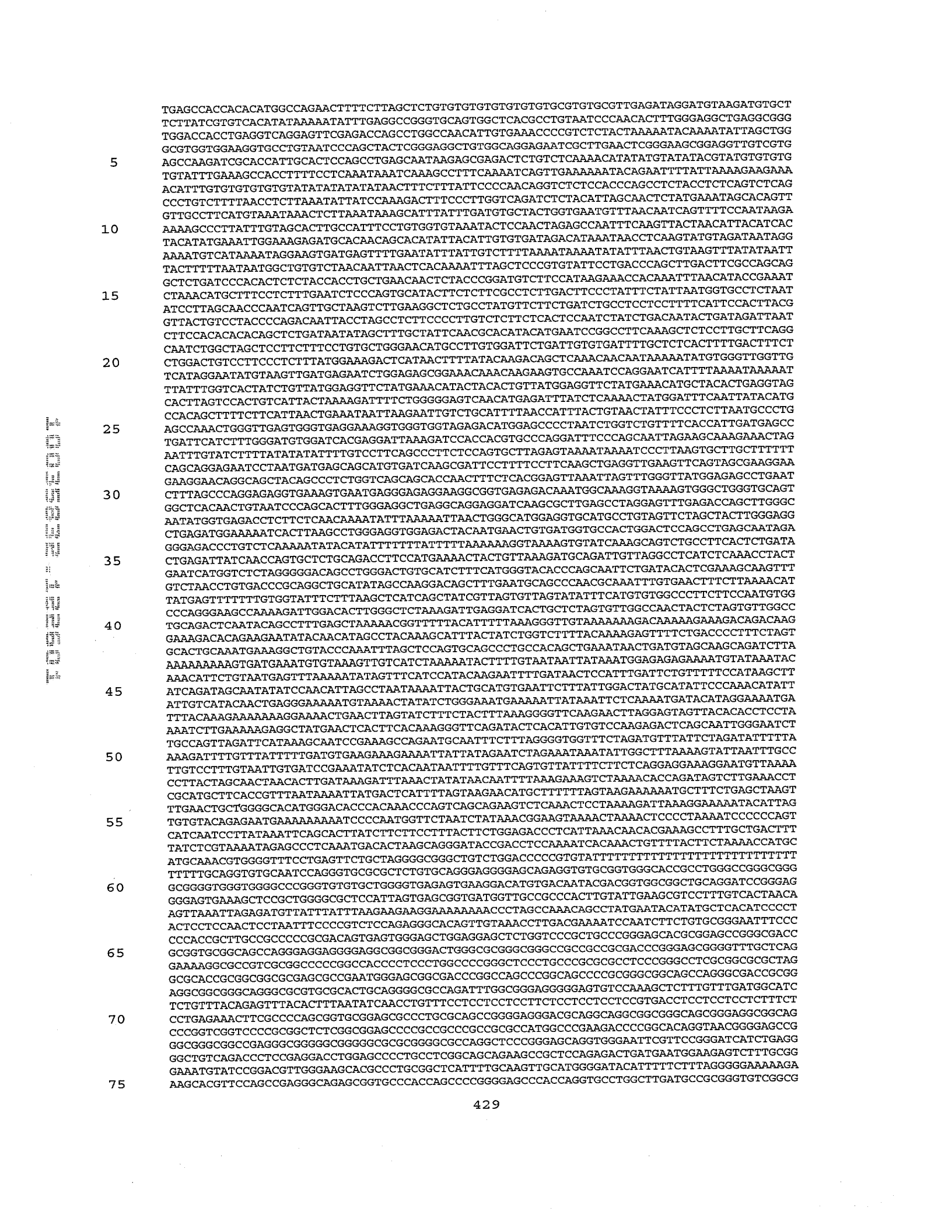
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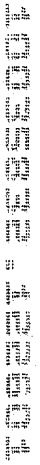
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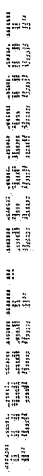
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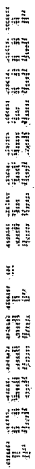




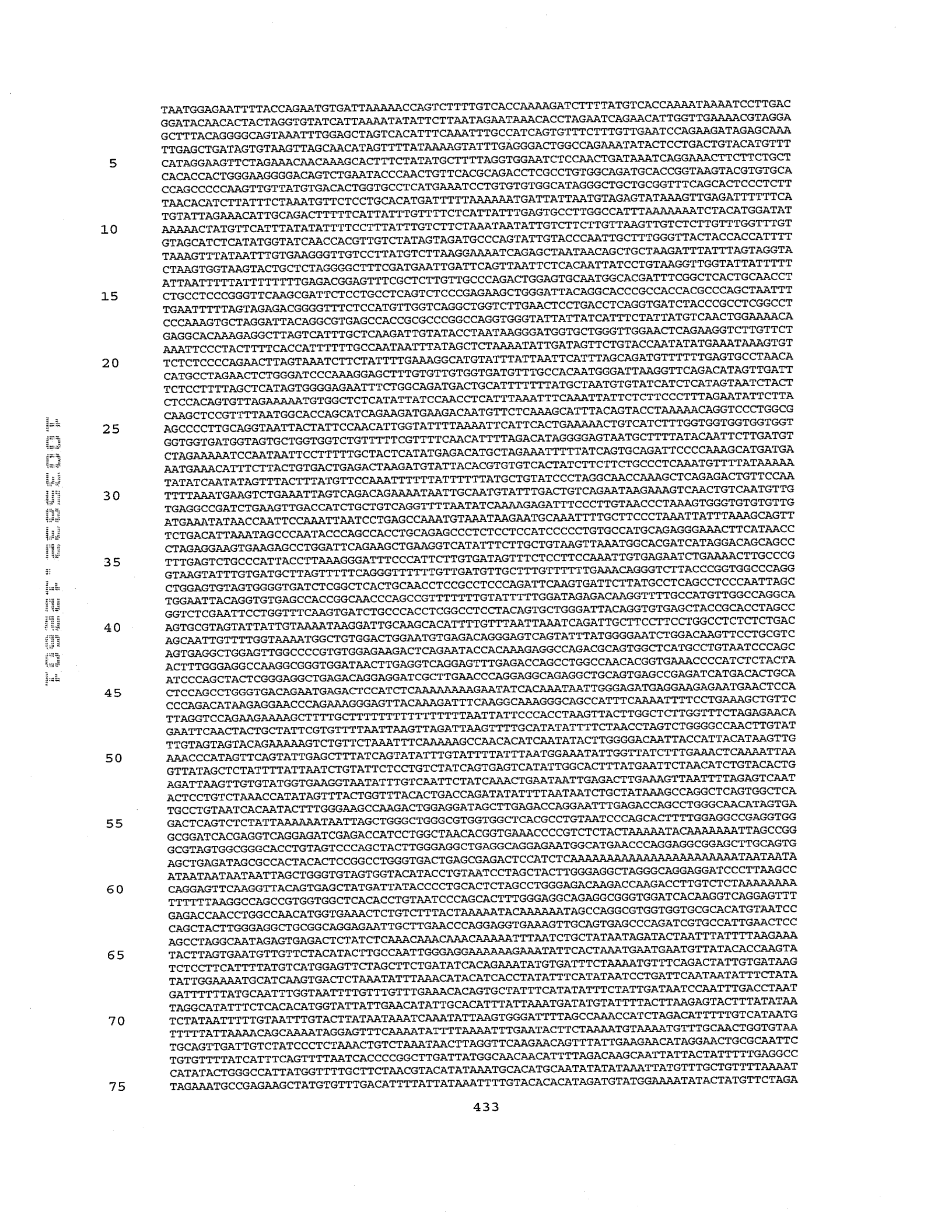
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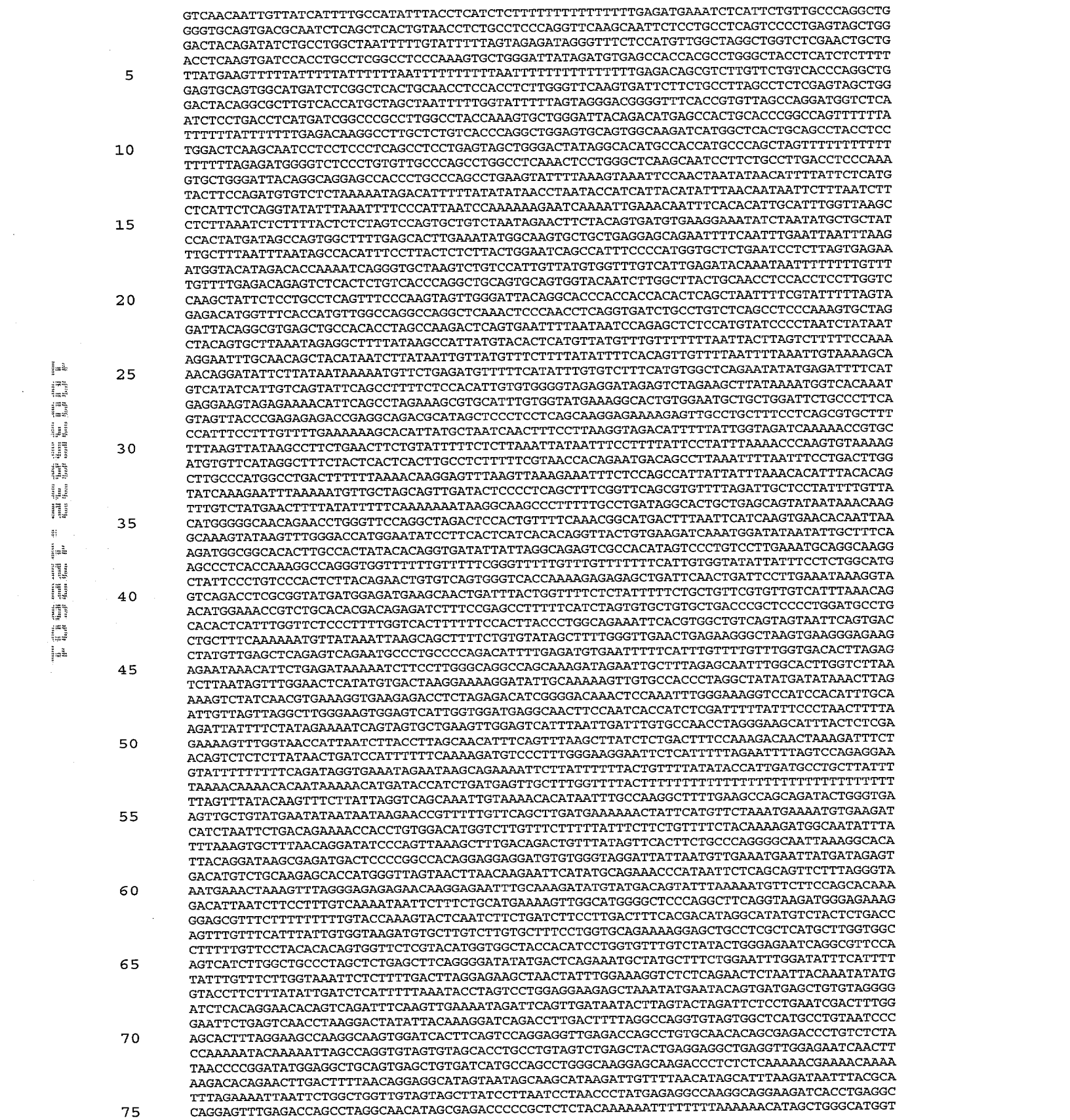
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 19

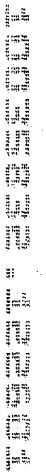
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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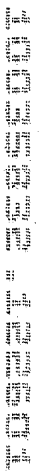
MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC
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HUMAN SEQUENCE - mRNA
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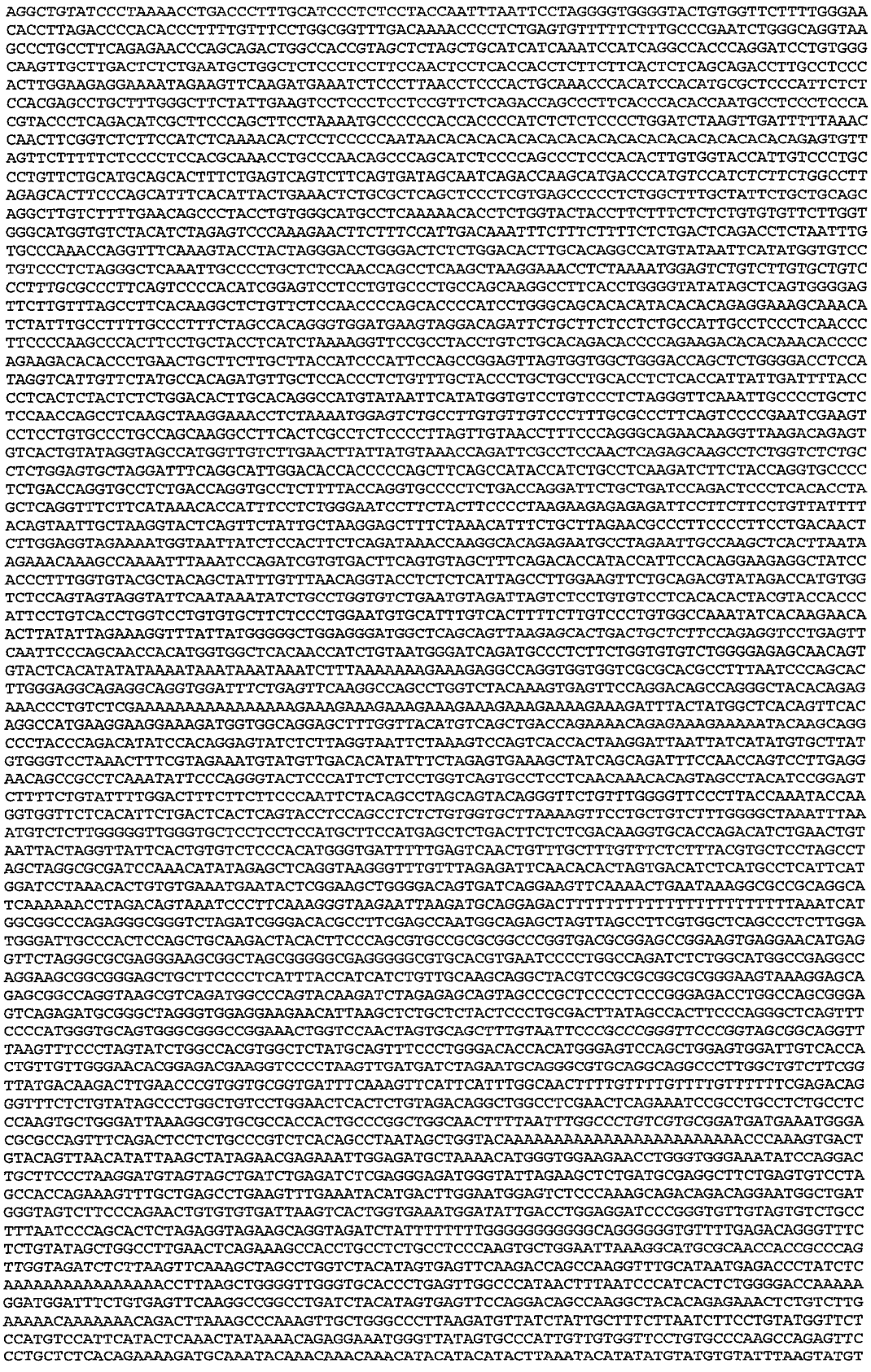
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Table 20

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HUMAN NOMENCLATURE
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Celera hCG38609

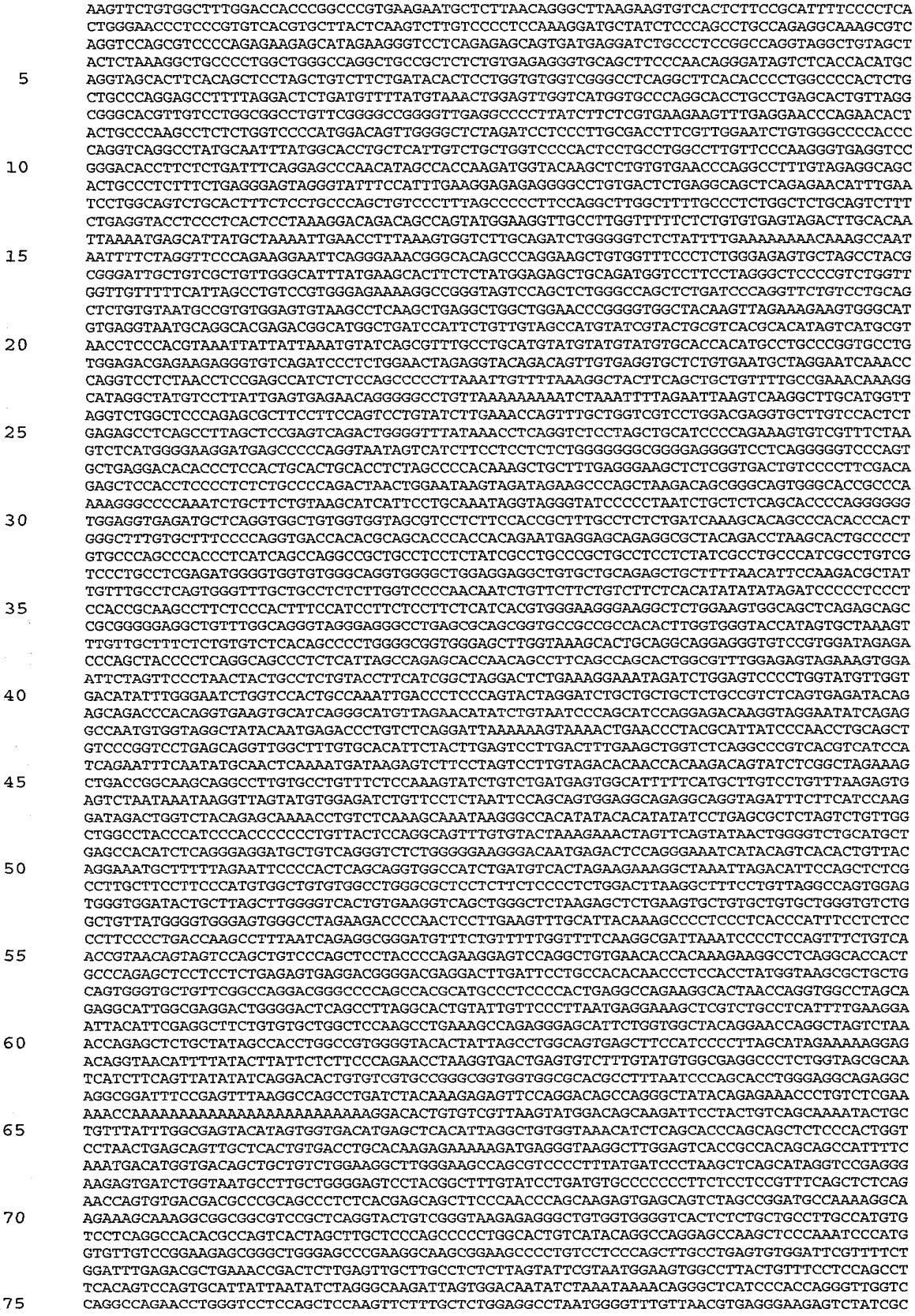
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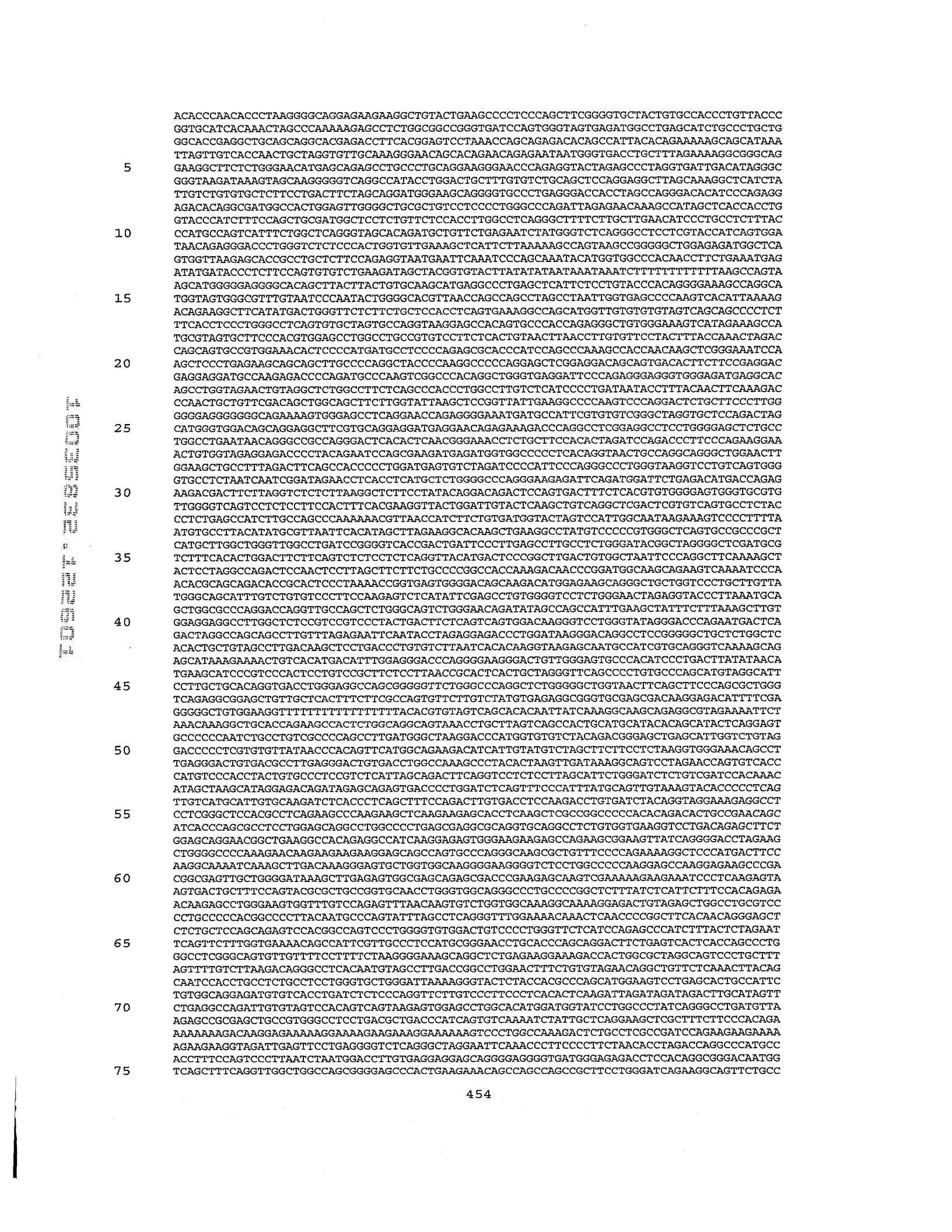
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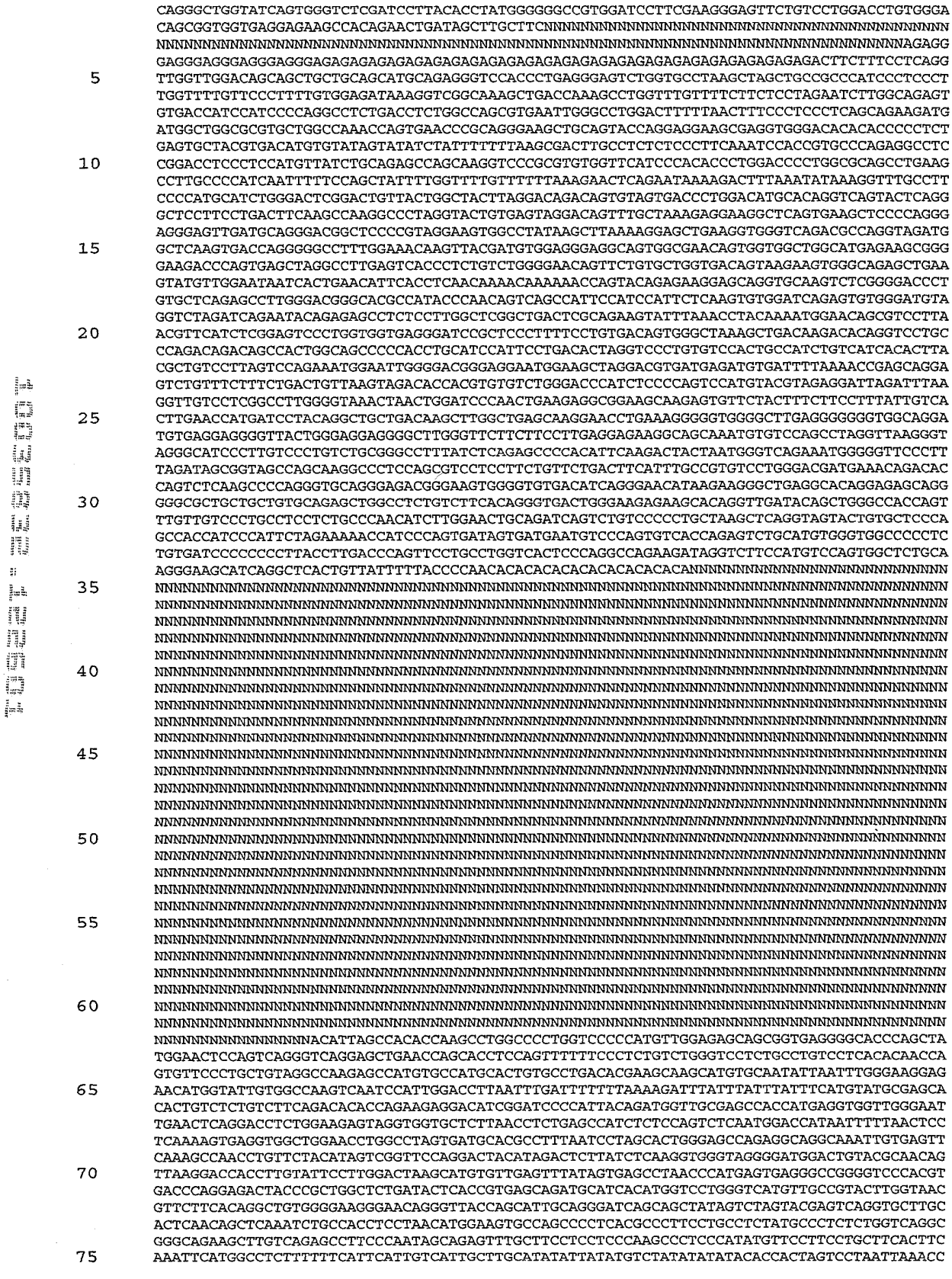
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Replacement Sheet





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MOUSE SEQUENCE - mRNA

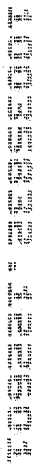
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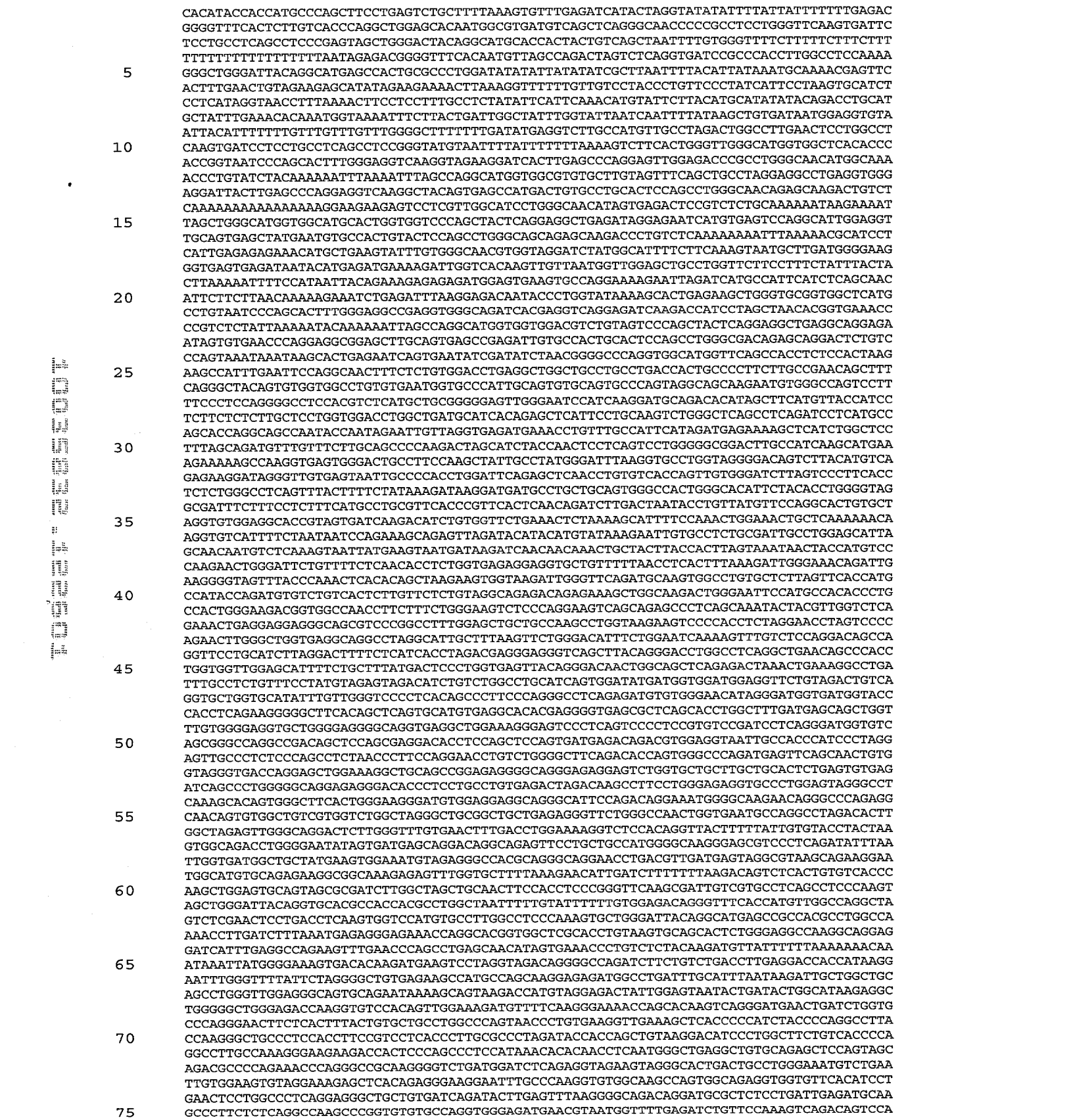
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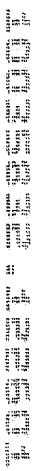
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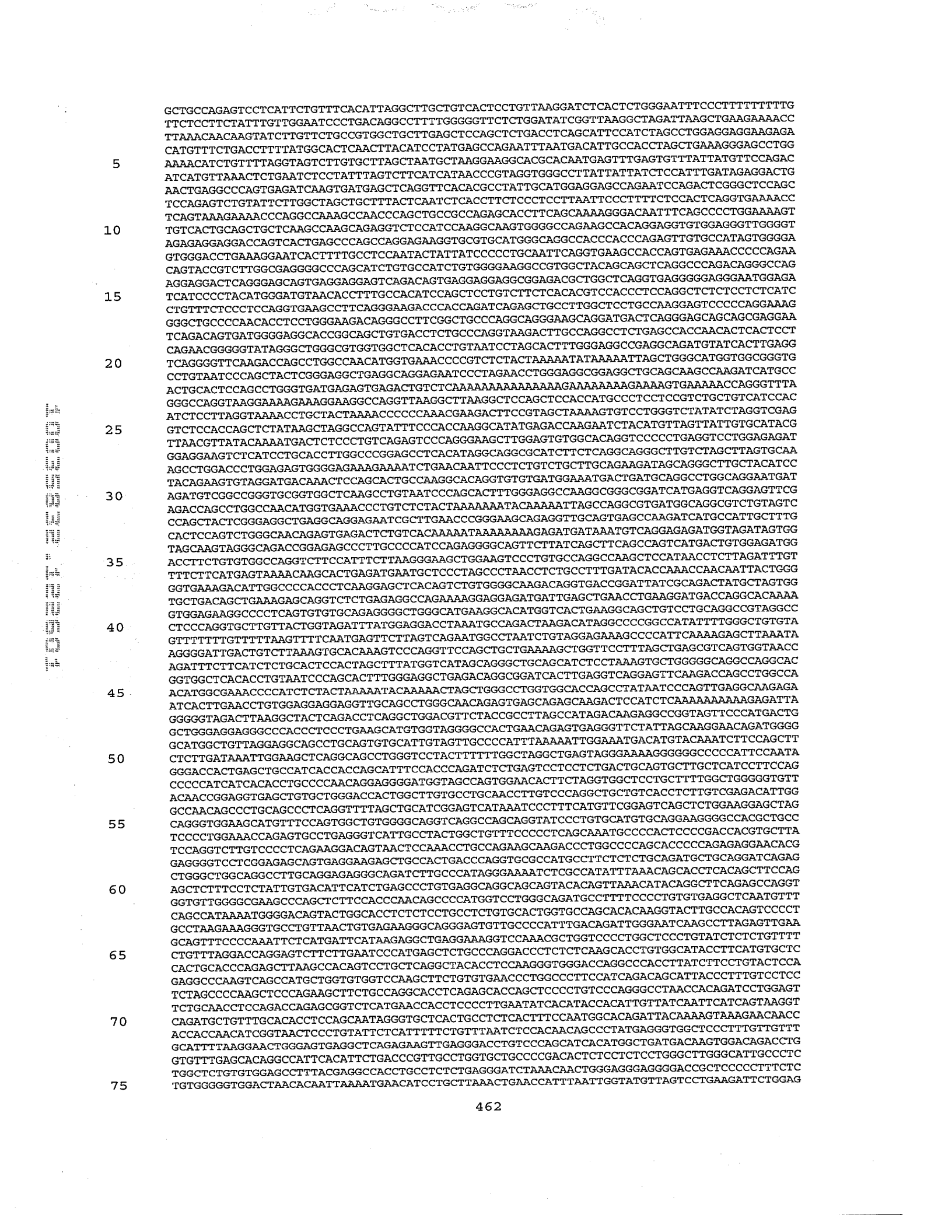


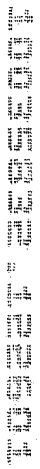
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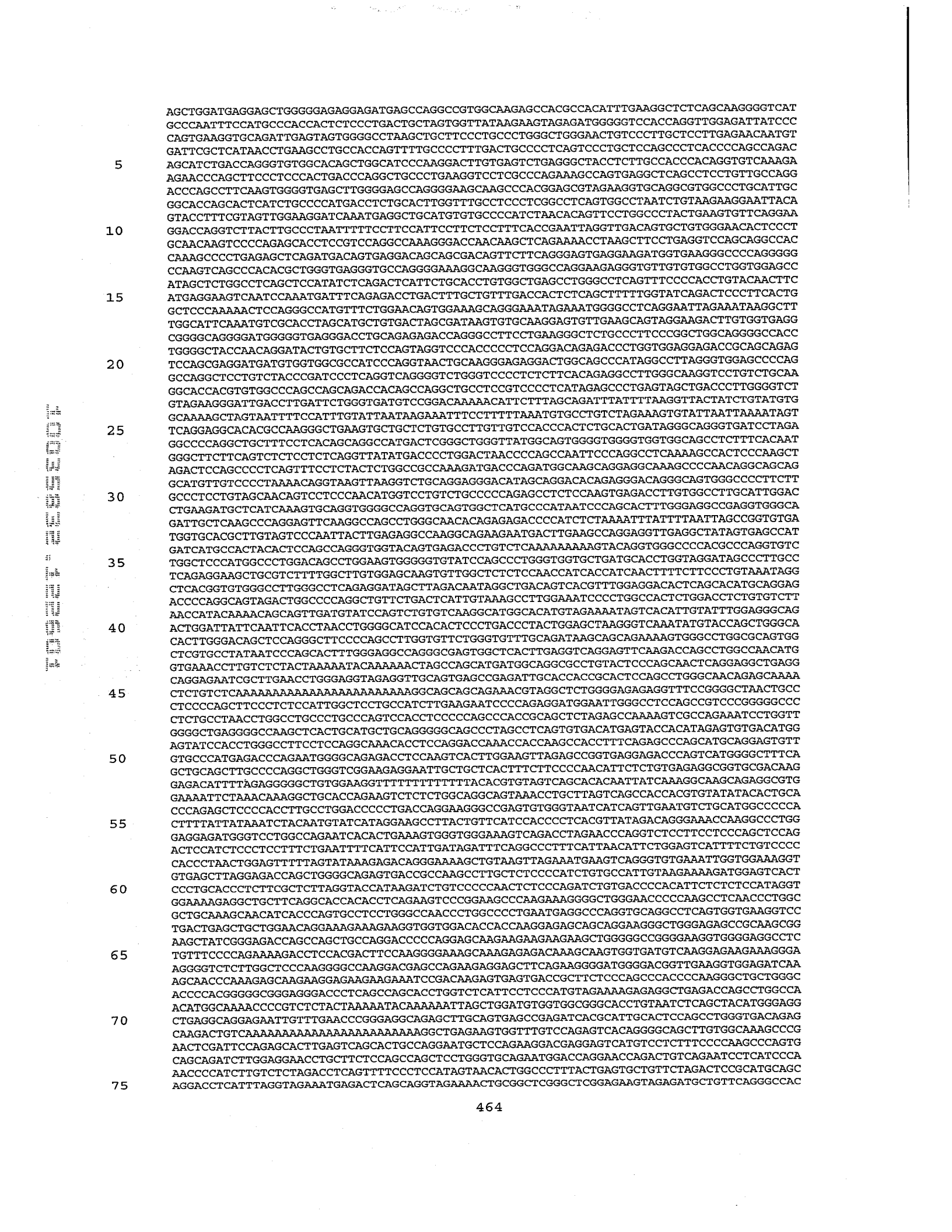


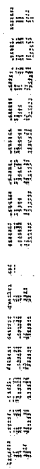
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Replacement Sheet

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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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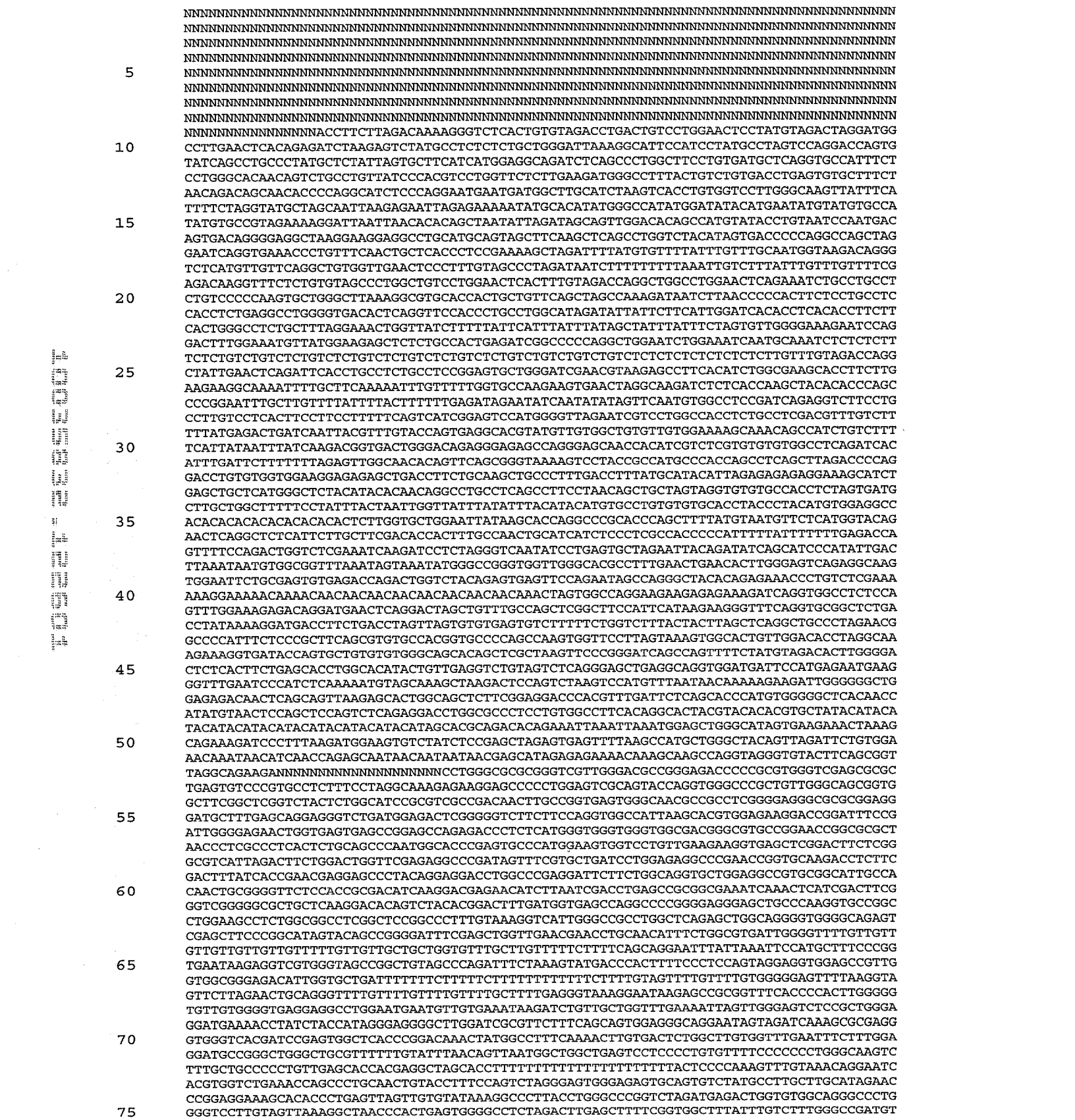
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Table 21

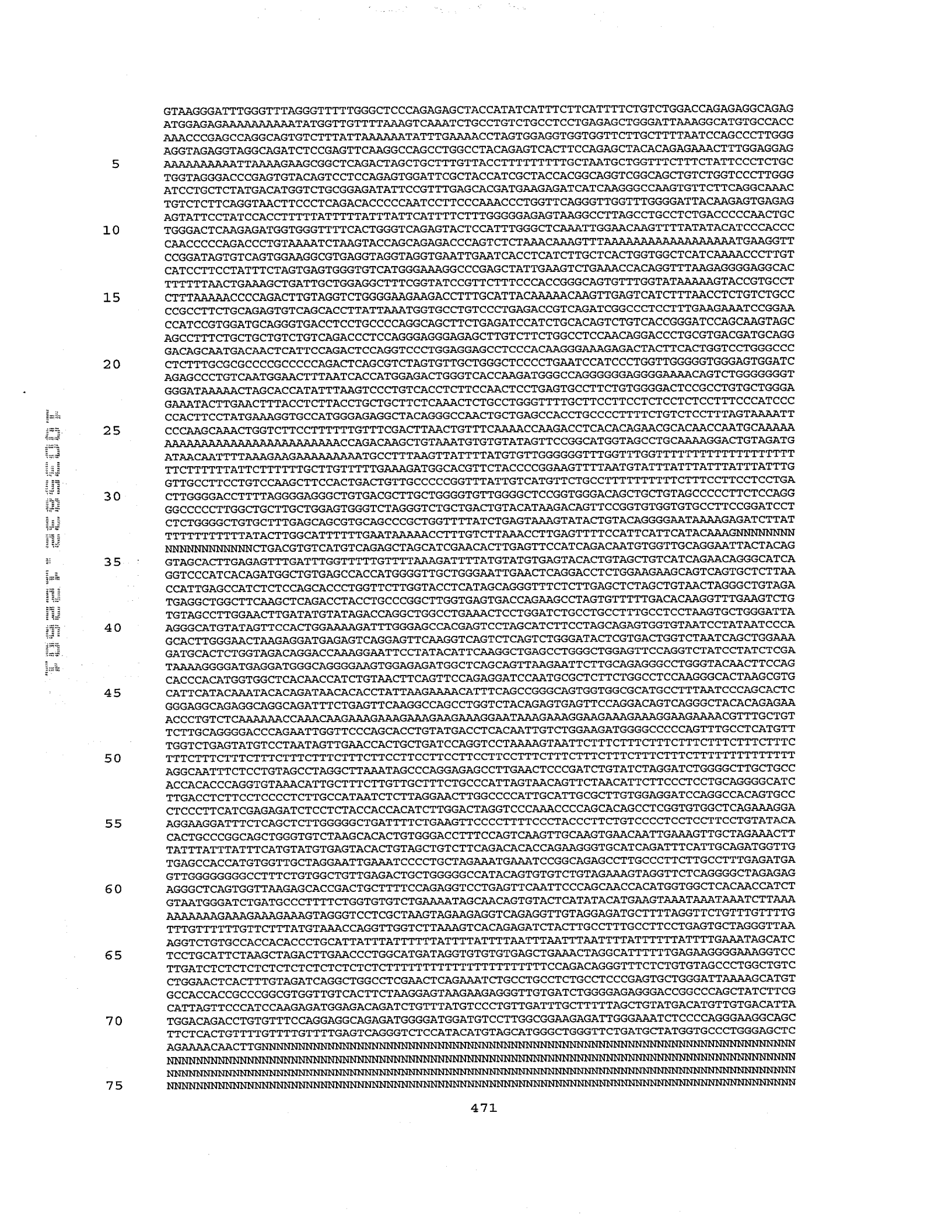
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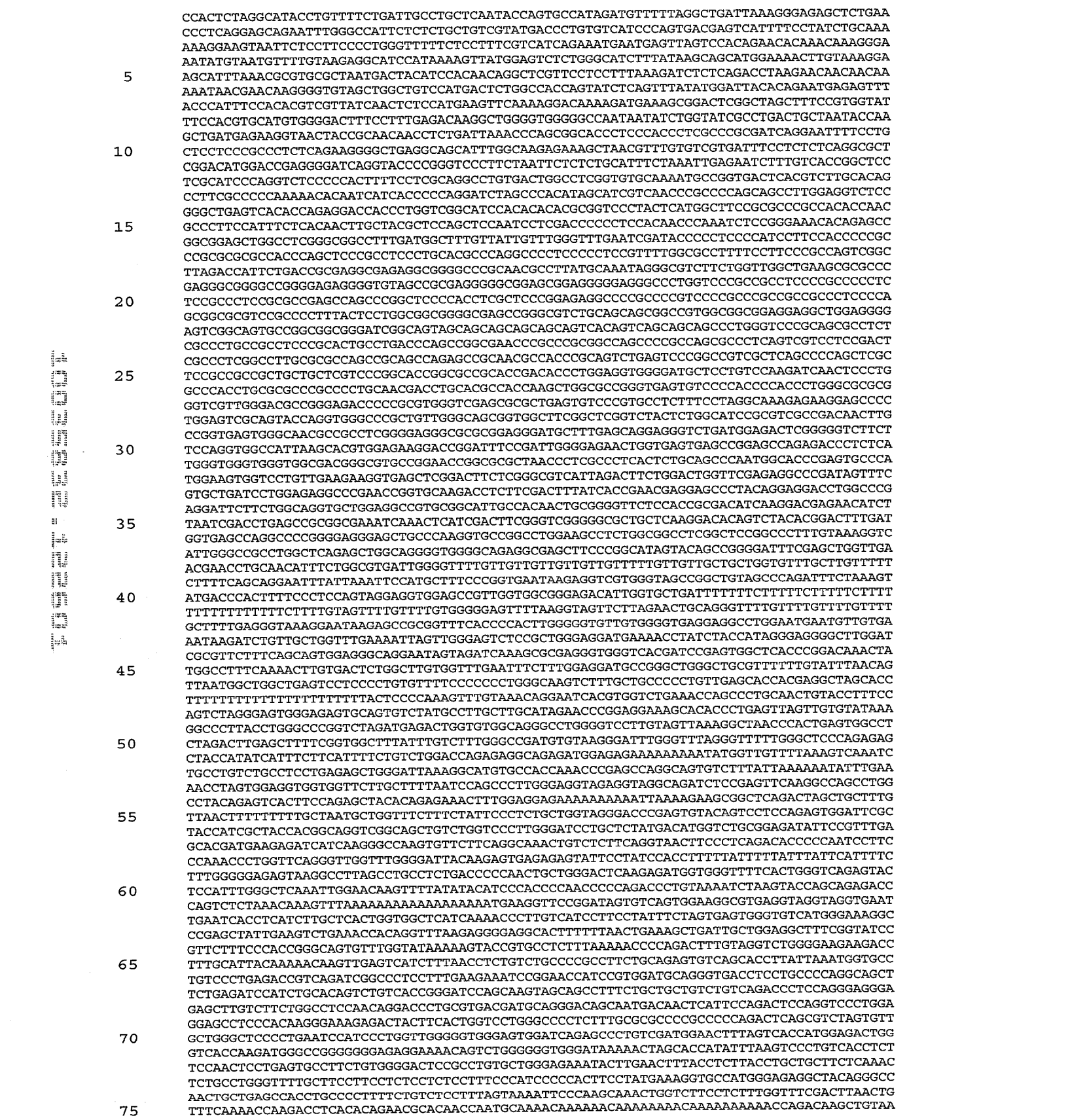


Replacement Sheet



Feb 22, 2005 11:38 AM

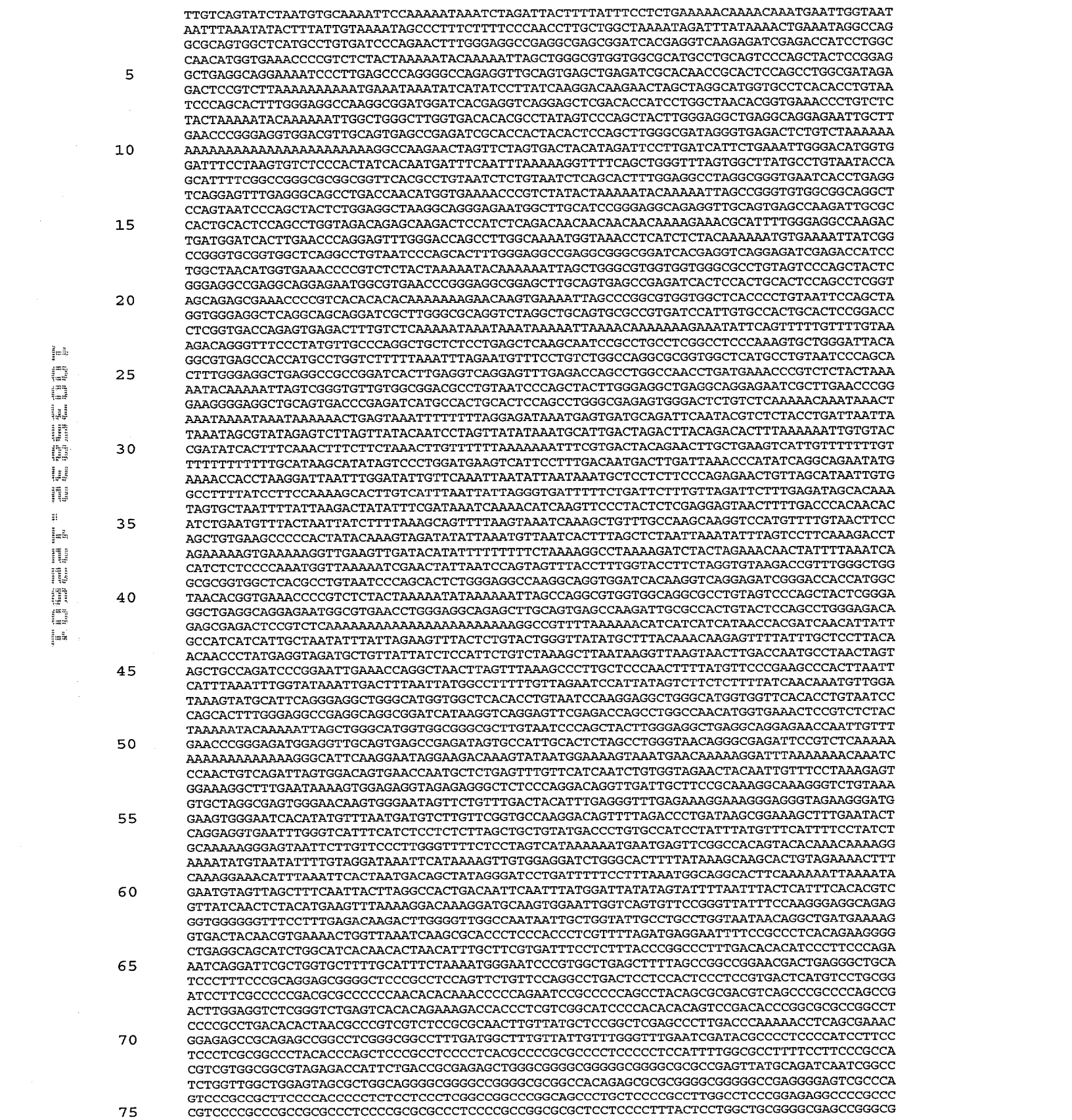
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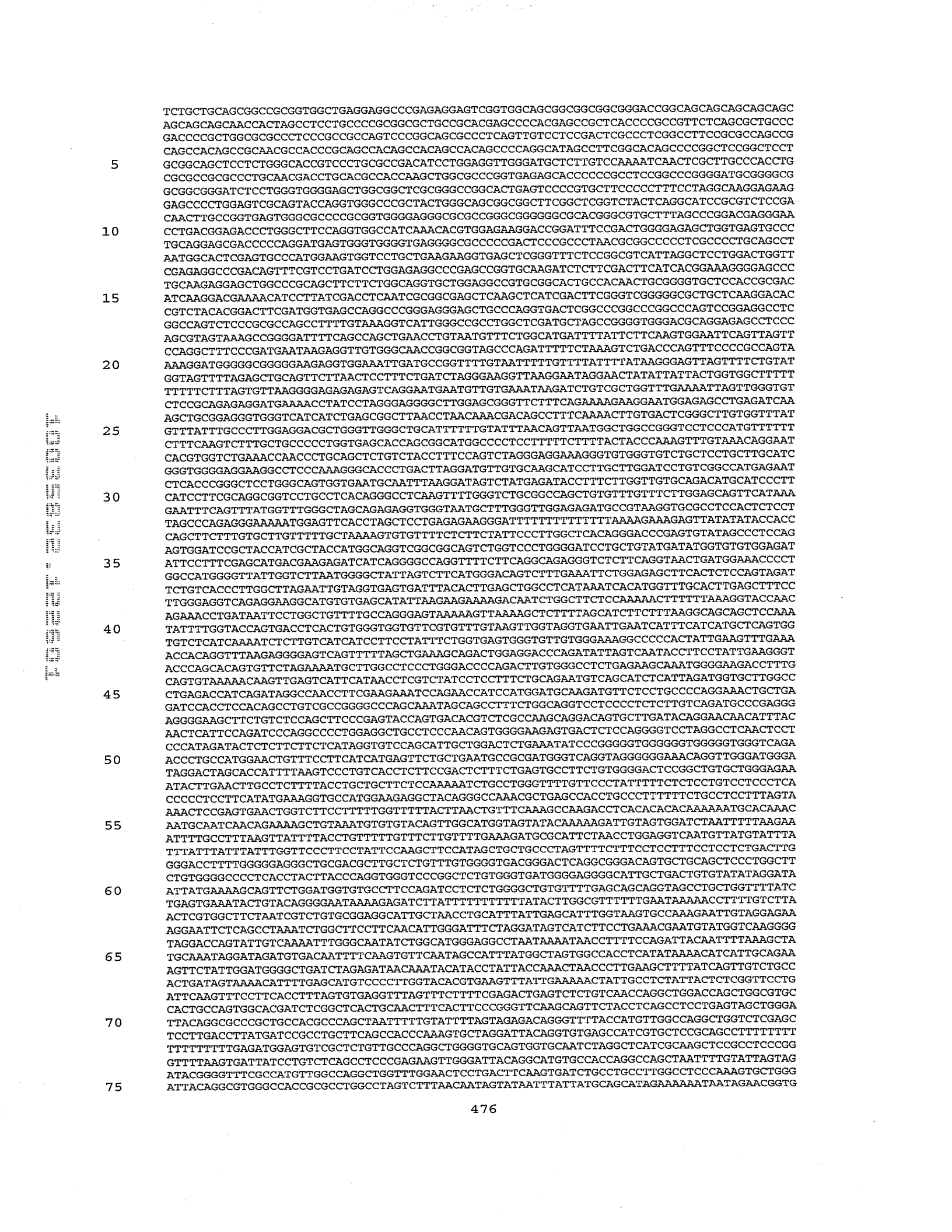


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HUMAN SEQUENCE - mRNA
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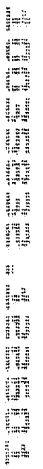
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Table 22

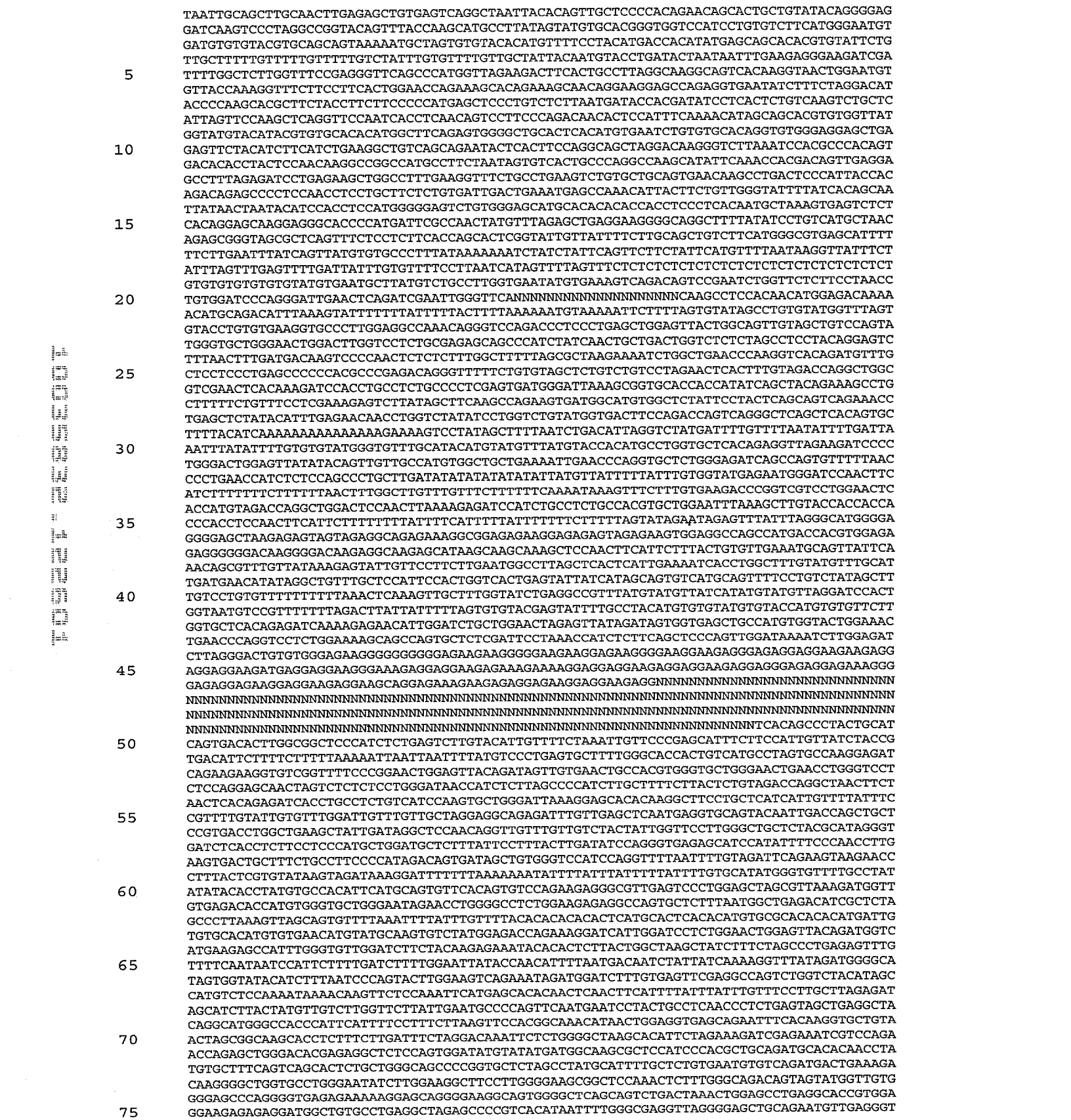
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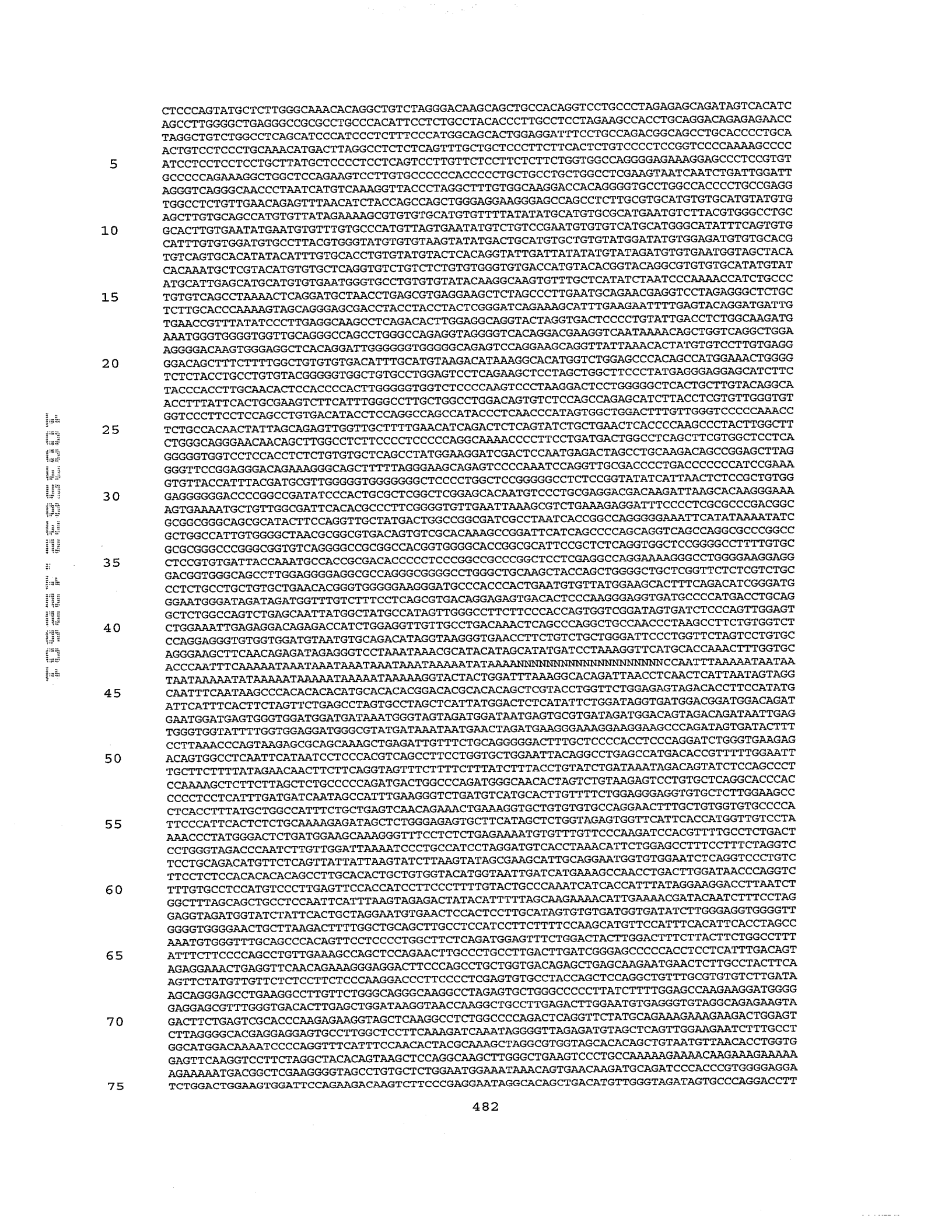
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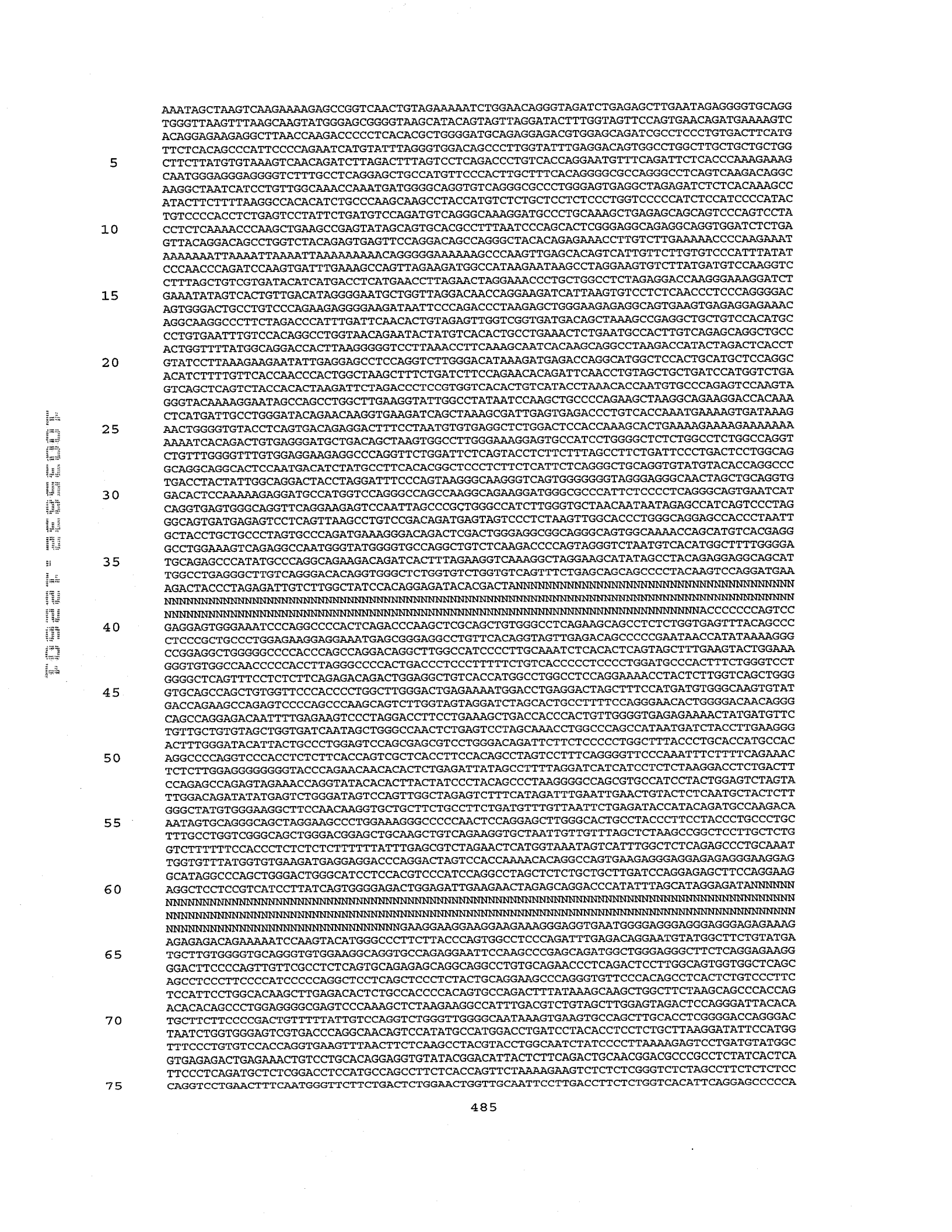




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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING

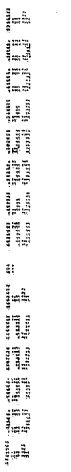
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HUMAN SEQUENCE - GENOMIC

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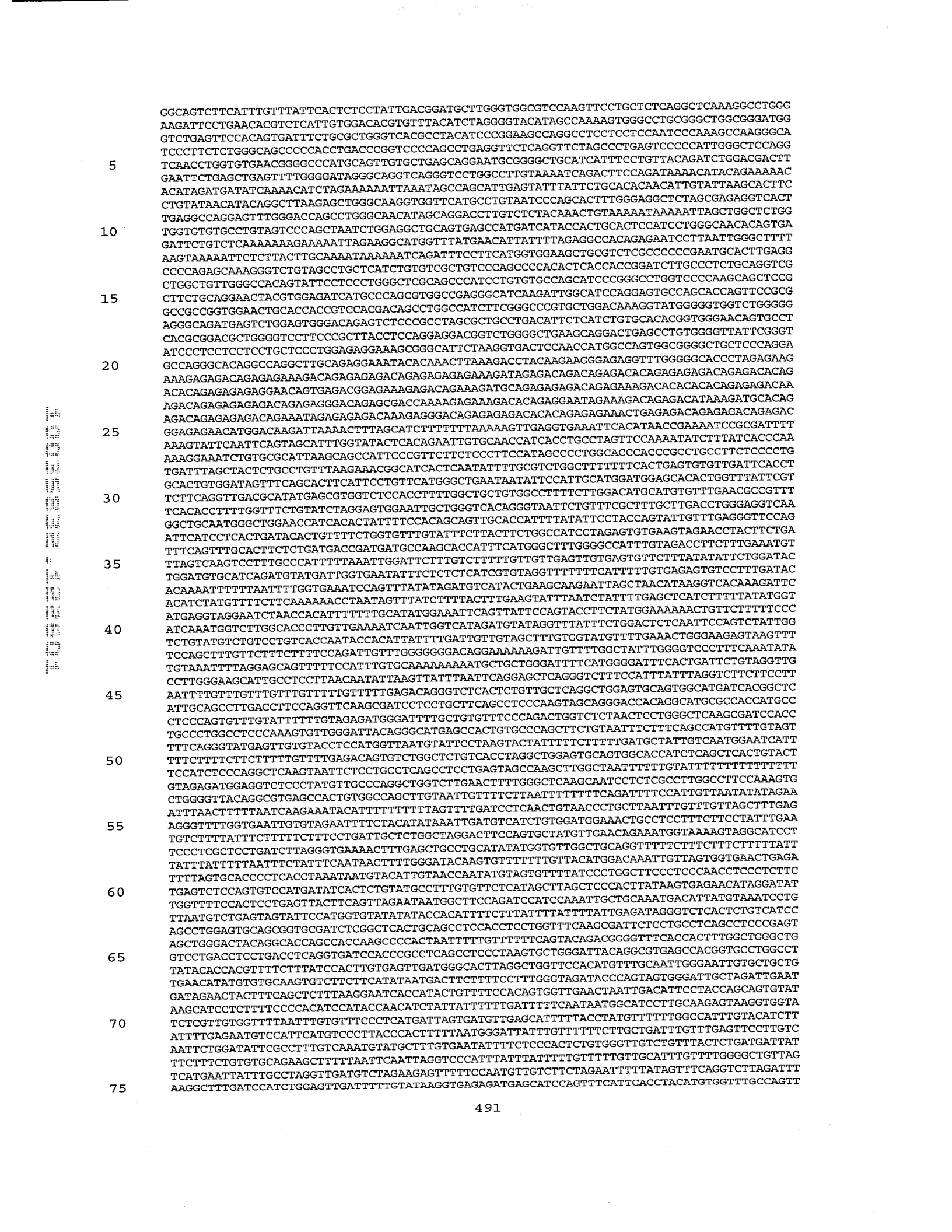
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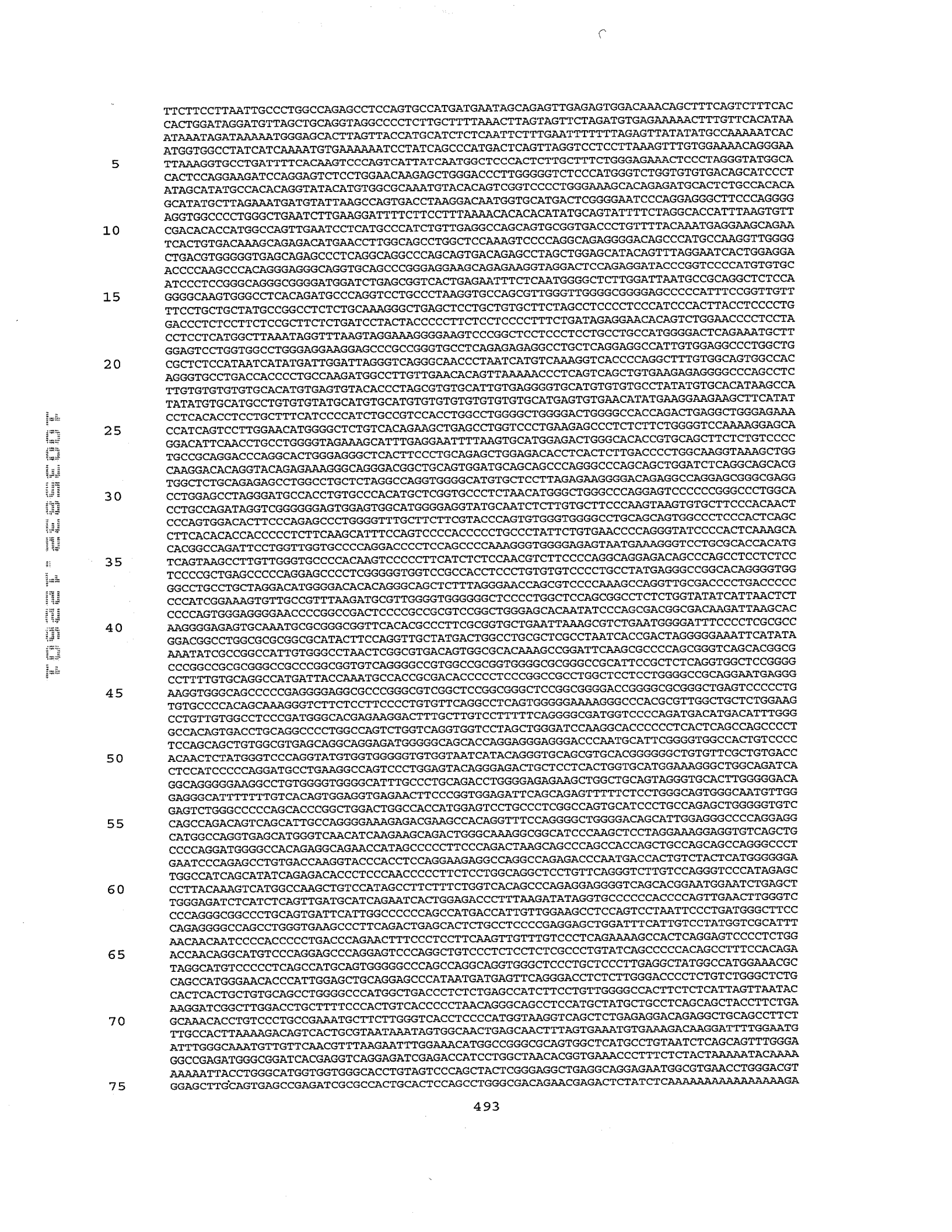
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Art Unit: 1635

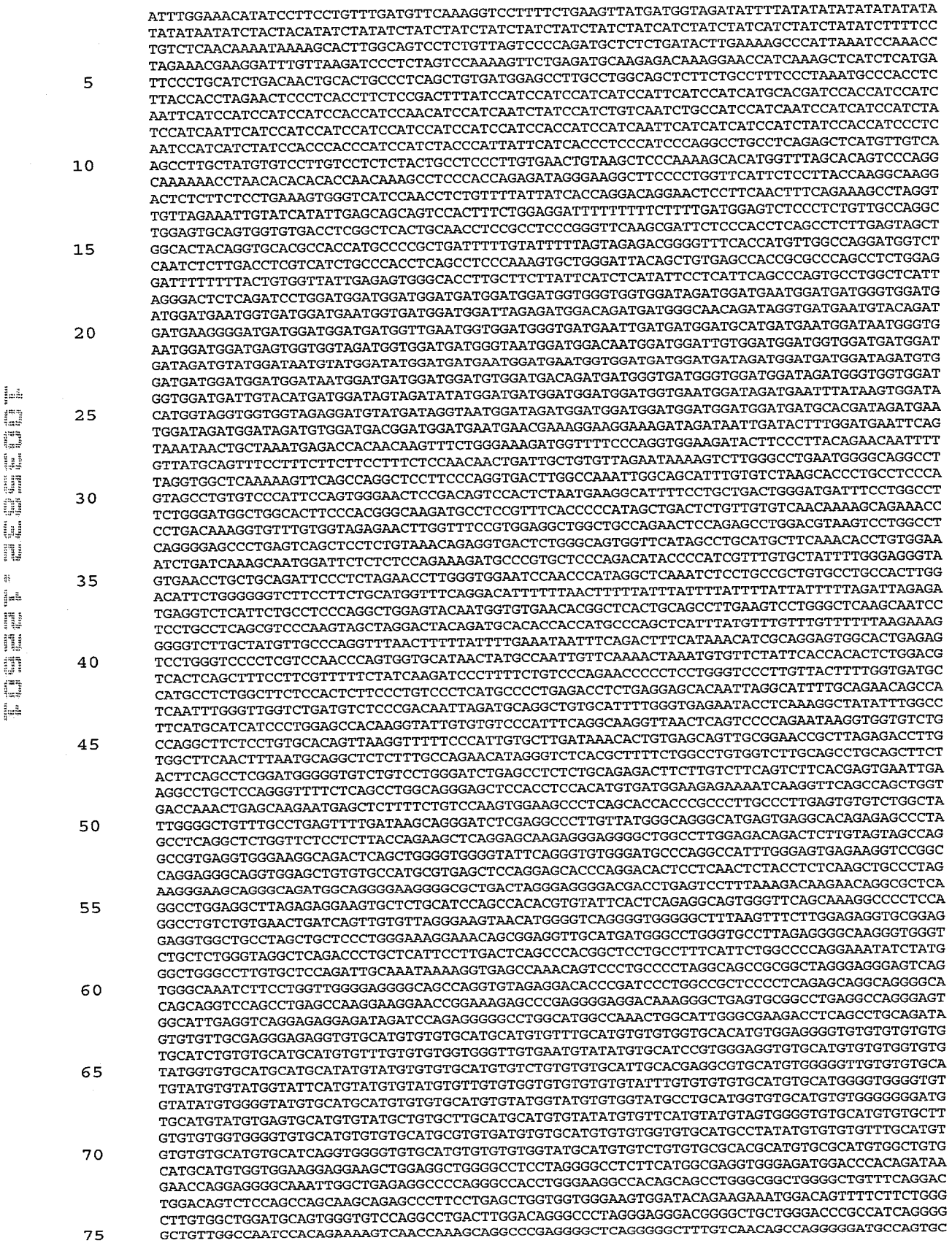


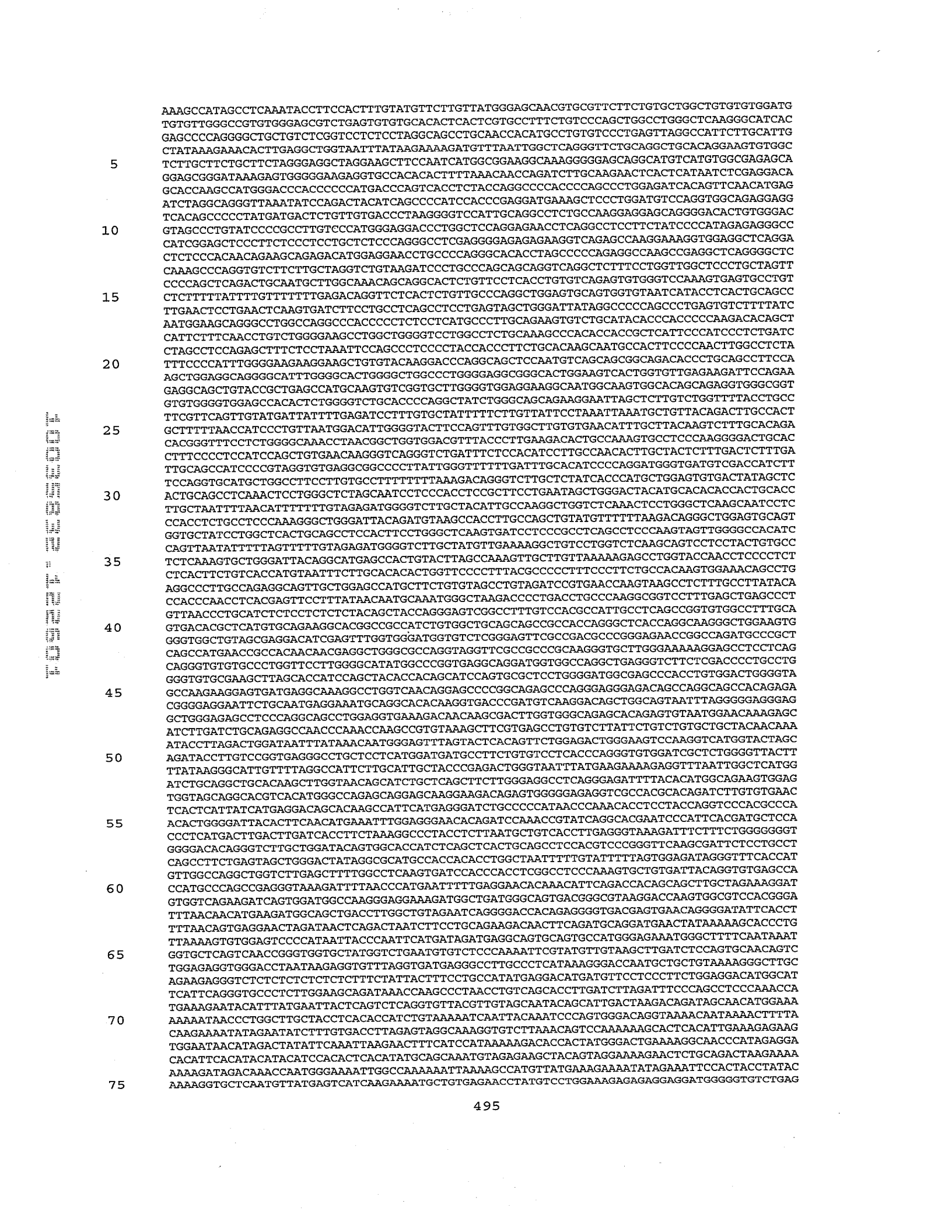
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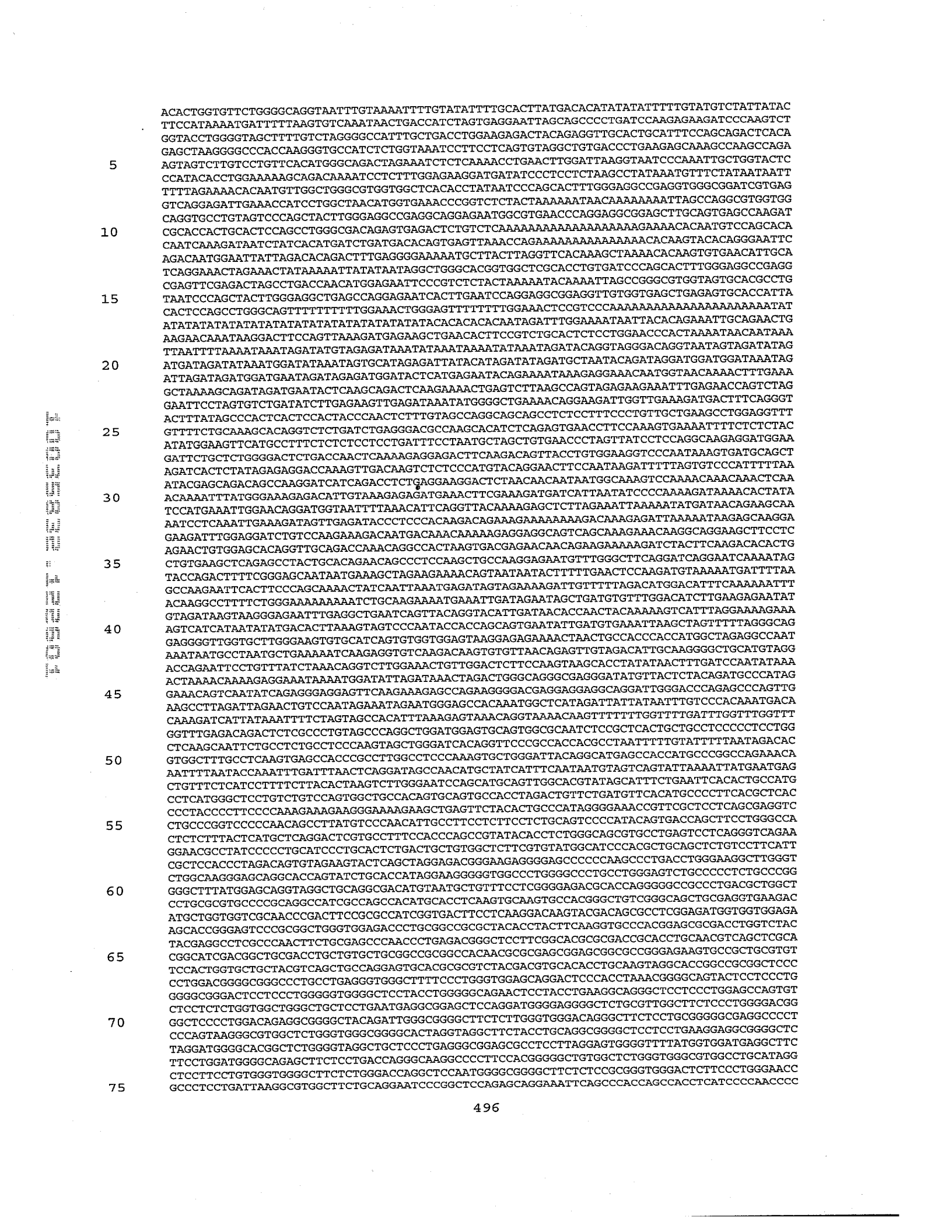
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CAAAGATCATTATAAATTTTCTAGTAGCCACATTTAAAGAGTAAACAGGTAAAACAAGTTTTTTTGGTTTTGATTTGGTTTGGTTT
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CTCAAGCAATTCTGCCTCTGCCTCCCAAGTAGCTGGGATCACAGGTTCCCGCCACCACGCCTAATTTTTGTATTTTTAATAGACAC
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CCCTACCCCTTCCCCAAAGAAAGAAGGGAAAAGAAGCTGAGTTCTACACTGCCCATAGGGGAAACCGTTCGCTCCTCAGCGAGGTC
CTGCCCGGTCCCCCAACAGCCTTATGTCCCAACATTGCCTTCCTCTTCCTCTGCAGTCCCCATACAGTGACCAGCTTCCTGGGCCA
CTCTCTTTACTCATGCTCAGGACTCGTGCCTTTCCACCCAGCCGTATACACCTCTGGGCAGCGTGCCTGAGTCCTCAGGGTCAGAA
GGAACGCCTATCCCCCTGCATCCCTGCACTCTGACTGCTGTGGCTCTTCGTGTATGGCATCCCACGCTGCAGCTCTGTCCTTCATT
CGCTCCACCCTAGACAGTGTAGAAGTACTCAGCTAGGAGACGGGAAGAGGGGAGCCCCCCAAGCCCTGACCTGGGAAGGCTTGGGT
CTGGCAAGGGAGCAGGCACCAGTATCTGCACCATAGGAAGGGGGTGGCCCTGGGGCCCTGCCTGGGAGTCTGCCCCCTCTGCCCGG
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CCTGCGCGTGCCCCGCAGGCCATCGCCAGCCACATGCACCTCAAGTGCAAGTGCCACGGGCTGTCGGGCAGCTGCGAGGTGAAGAC
ATGCTGGTGGTCGCAACCCGACTTCCGCGCCATCGGTGACTTCCTCAAGGACAAGTACGACAGCGCCTCGGAGATGGTGGTGGAGA
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TACGAGGCCTCGCCCAACTTCTGCGAGCCCAACCCTGAGACGGGCTCCTTCGGCACGCGCGACCGCACCTGCAACGTCAGCTCGCA
CGGCATCGACGGCTGCGACCTGCTGTGCTGCGGCCGCGGCCACAACGCGCGAGCGGAGCGGCGCCGGGAGAAGTGCCGCTGCGTGT
TCCACTGGTGCTGCTACGTCAGCTGCCAGGAGTGCACGCGCGTCTACGACGTGCACACCTGCAAGTAGGCACCGGCCGCGGCTCCC
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GGGGCGGGACTCCTCCCTGGGGGTGGGGCTCCTACCTGGGGGCAGAACTCCTACCTGAAGGCAGGGCTCCTCCCTGGAGCCAGTGT
CTCCTCTCTGGTGGCTGGGCTGCTCCTGAATGAGGCGGAGCTCCAGGATGGGGAGGGGCTCTGCGTTGGCTTCTCCCTGGGGACGG
GGCTCCCCTGGACAGAGGCGGGGCTACAGATTGGGCGGGGCTTCTCTTGGGTGGGACAGGGCTTCTCCTGCGGGGGCGAGGCCCCT
CCCAGTAAGGGCGTGGCTCTGGGTGGGCGGGGCACTAGGTAGGCTTCTACCTGCAGGCGGGGCTCCTCCTGAAGGAGGCGGGGCTC
TAGGATGGGGCACGGCTCTGGGGTAGGCTGCTCCCTGAGGGCGGAGCGCCTCCTTAGGAGTGGGGTTTTATGGTGGATGAGGCTTC
TTCCTGGATGGGGCAGAGCTTCTCCTGACCAGGGCAAGGCCCCTTCCACGGGGGCTGTGGCTCTGGGTGGGCGTGGCCTGCATAGG
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GTCCACAGCCCCTTAAGGGAAAGGTAGGAAGAGAGGTCCAGCCCCCCAGGCTGCCCAGAGCTGCTGGTCTCATTTGGGGGCGTTCG
GGAGGTTTGGGGGGCATCAACCCCCCGACTGTGCTGCTCGCGAAGGTCCCACAGCCCTGAGATGGGCCGGCCCCCTTCCTGGCCCC
TCATGGCGGGACTGGAGAAATGGTCCGCTTTCCTGGAGCCAATGGCCCGGCCCCTCCTGACTCATCCGCCTGGCCCGGGAATGAAT
GGGGAGGCCGCTGAACCCACCCGGCCCATATCCCTGGTTGCCTCATGGCCAGCGCCCCTCAGCCTCTGCCACTGTGAACCGGCTCC
CACCCTCAAGGTGCGGGGAGAAGAAGCGGCCAGGCGGGGCGCCCCAAGAGCCCAAAAGAGGGCACACCGCCATCCTCTGCCTCAAA
TTCTGCGTTTTTGGTTTTAATGTTATATCTGATGCTGCTATATCCACTGTCCAACGGAGTTAGACGAATAGATGTGTTGTGTTTTTT
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CACTCAGAGCCTGGCATCATCAGAGTGGGGGACCCAGGTCCCCGAGCCCAGGGCGGGGCTTGGTGGGTGGACTGTCCATCCTGCAC
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AGGTCAGTGTTCCTCCCTGCAGAACTGGACTGCTGTCAGTGGCTGCCTTCGGGATCATCTGGGAGGGCTTCCAGGAGGAGGTGAGC
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GGTGCTAATTGCTGTTTAGCTCCAAGCTGACTCCTTGCTCTCTTTTTGTCTCTCTCTCTCTCTCTTTTTTTTTTTTTACTTGAGC
CTCTAGAGCACACAGTAAACAGTCATTTGGCTCTTGGGGCCCTGCAAATTGGTGTTTATGGTGCGAAGATGAGGAGGATTTGTCCA
CCCAAACACAGGCTGGCTGGAGGGAGGAAGCAGGGGTGGGACATCCCATCCAGGCCCAGCTCGGGGAAGCCTCCTTCAGACTGAG
GAGCTGTGGTCTCACAAGCAGGGGACTGTGATTAACCCAGGAGAGCTTCTAGGAAGAGGTGAGGCATCCGCGGCAAAAAGACCTCC
TCCAGGGGAAGCTGCAAAGGCTCCACCATACCCTCAGGTGCCCATGGGGAGCCCTGCCCTCCAGACCCAGCTGGGATCAGAGCTTC
TTGGCTGGGTCACAGCCTGGGTCTCCTTCCAACAGCACACCTCACCTGCCCACCCAGCAGCCAGCTGCAGAATTACAAACTGGAAT
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CCAAGGCACCGTGCTCAGTGTCCATGATGGTTTGTGTGCTTTGTGTCTGGAGCATCACGTGGGGACCCTGCAGACACAGAGTCCTG
GTCACCCTCCCTGTTTCTGTGTCACTTGGCCTGCCTCAGGTGGAGGGTCAGAGGTCAGTGTGTTCCCCGTTAGTGTGGGCACTTTC
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CTGAAT

HUMAN SEQUENCE - mRNA
CGGCGATGGCCCCACTCGGATACTTCTTACTCCTCTGCAGCCTGAAGCAGGCTCTGGGCAGCTACCCGATCTGGTGGTCGCTGGCT
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CGCGCGTCTACGACGTGCACACCTGCAAGTAGGCACCGGCCGCGGCTCCCCCTGGACGGGGCGGGCCCTGCCTGAGGGTGGGCTTT
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AGGTAGGCTTCTACCTGCAGGCGGGGCTCCTCCTGAAGGAGGCGGGGCTCTAGGATGGGGCACGGCTCTGGGGTAGGCTGCTCCCT
GAGGGCG

HUMAN SEQUENCE - CODING
ATGGCCCCACTCGGATACTTCTTACTCCTCTGCAGCCTGAAGCAGGCTCTGGGCAGCTACCCGATCTGGTGGTCGCTGGCTGTTGG
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Table 23

MOUSE NOMENCLATURE
ICSGNM Ly6e
Celera mCG2785

HUMAN NOMENCLATURE
HGNC LY6E
Celera hCG1765592

MOUSE SEQUENCE - GENOMIC

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Application/Control Number: 10/552,760
Art Unit: 1634

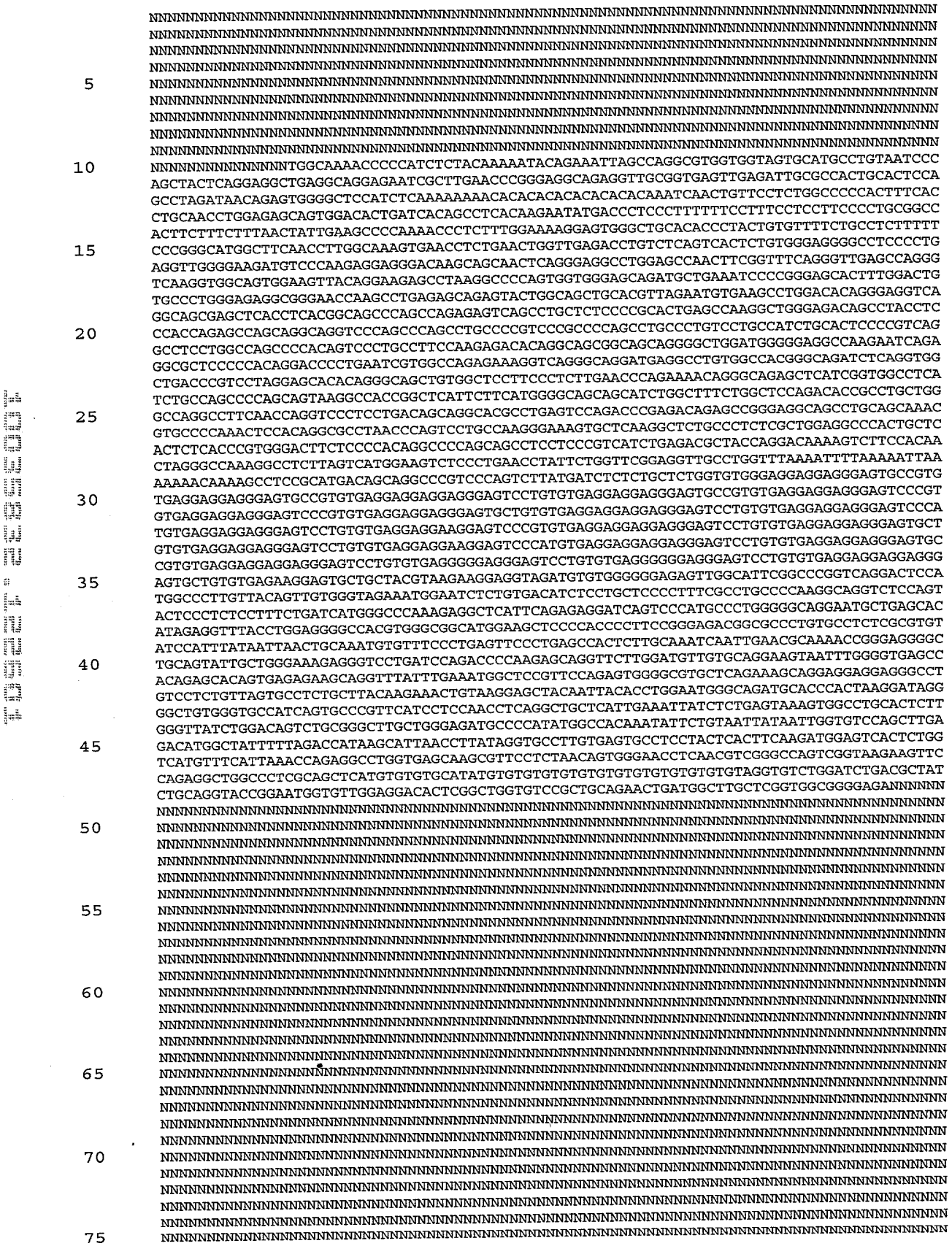
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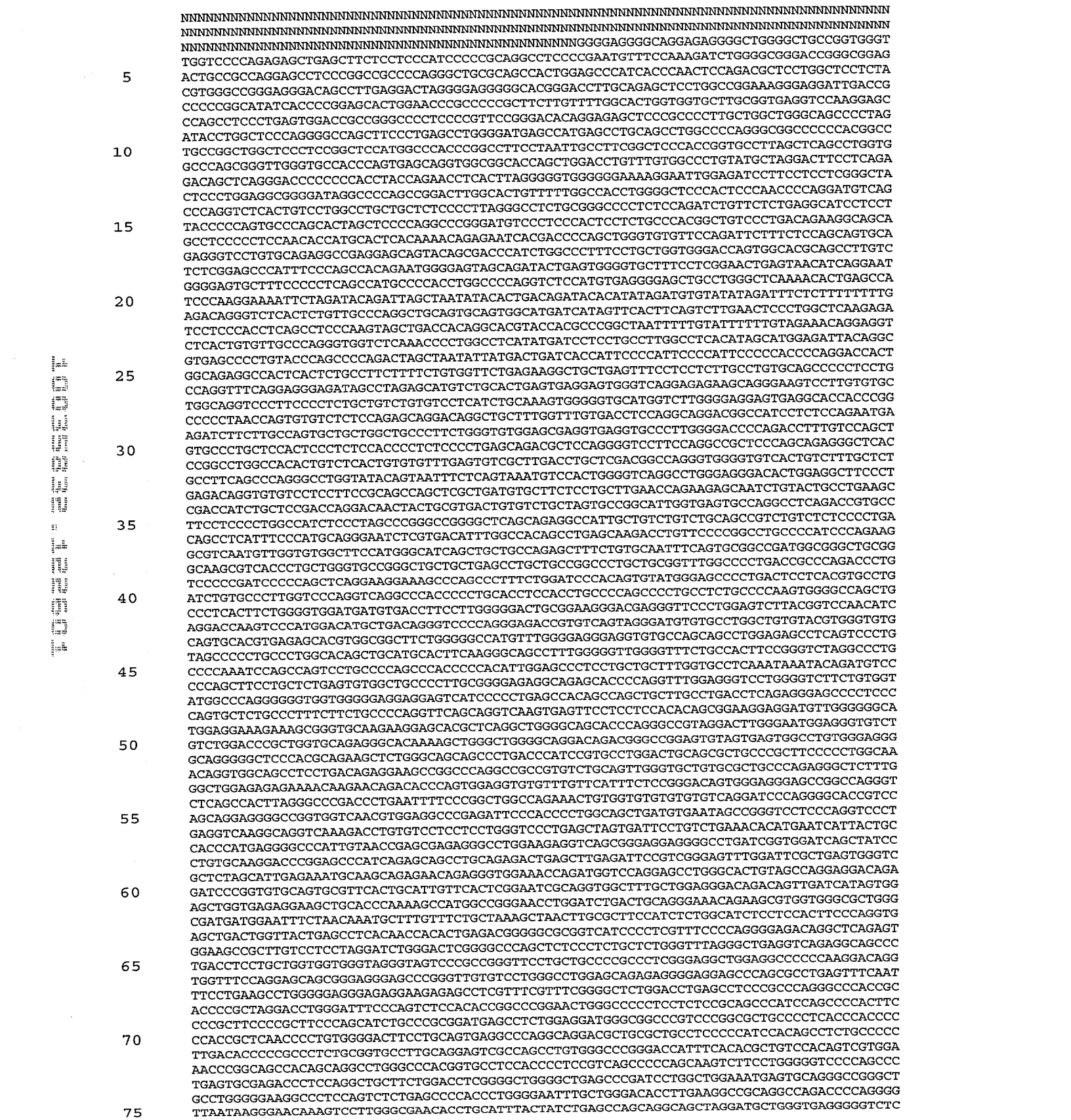
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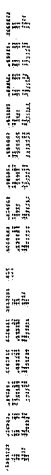
MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 24

MOUSE NOMENCLATURE

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Celera	mCG21645

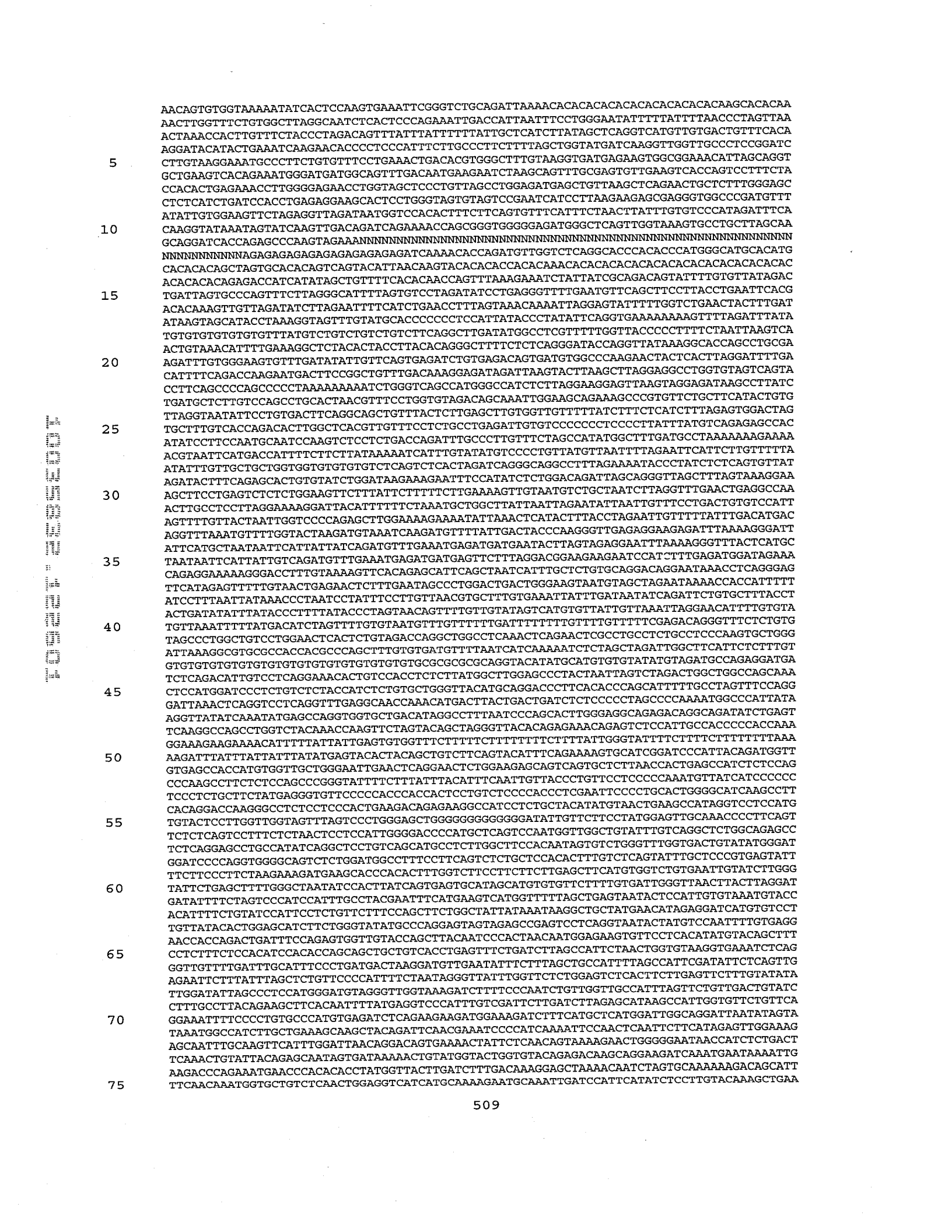
HUMAN NOMENCLATURE

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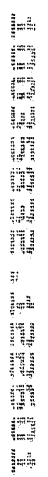
MOUSE SEQUENCE - GENOMIC

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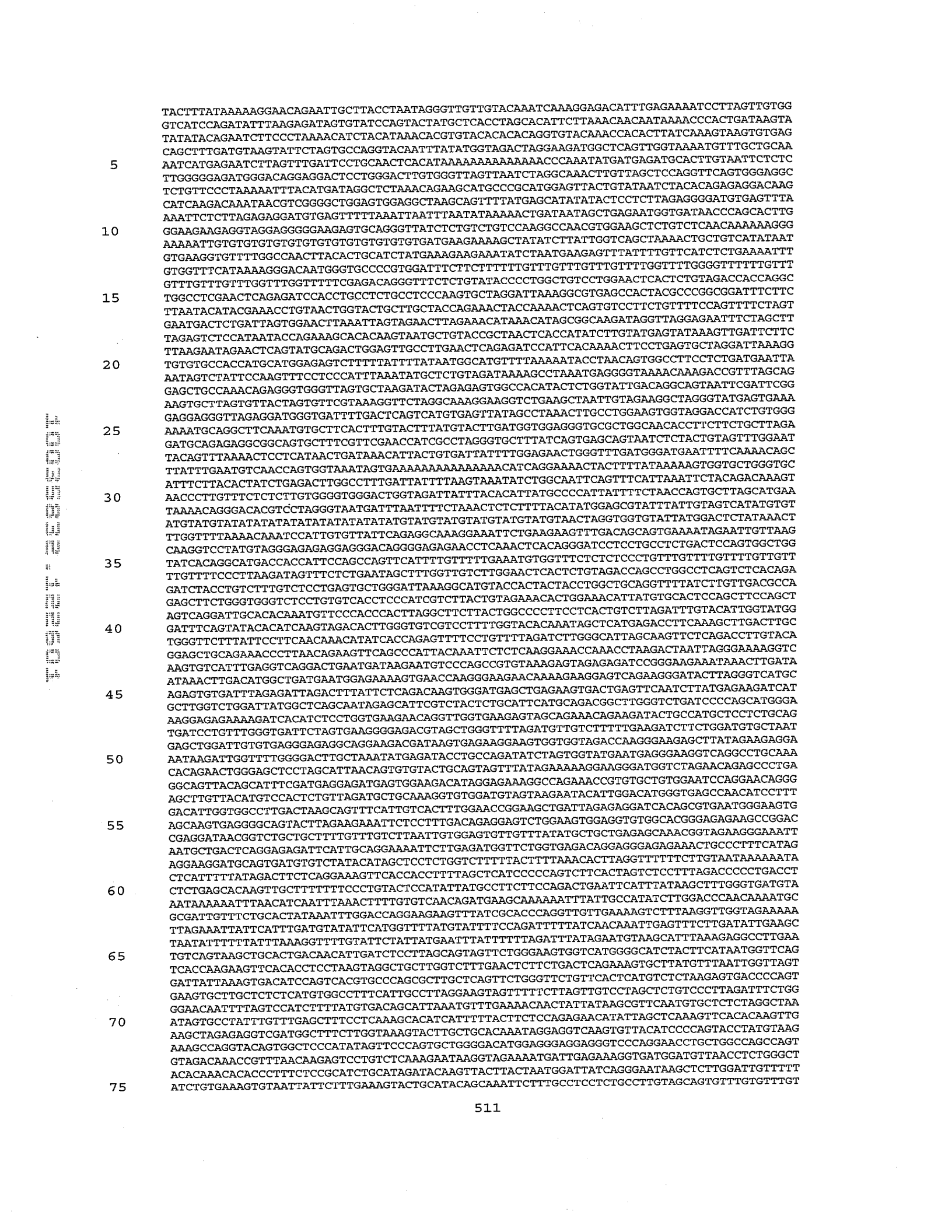
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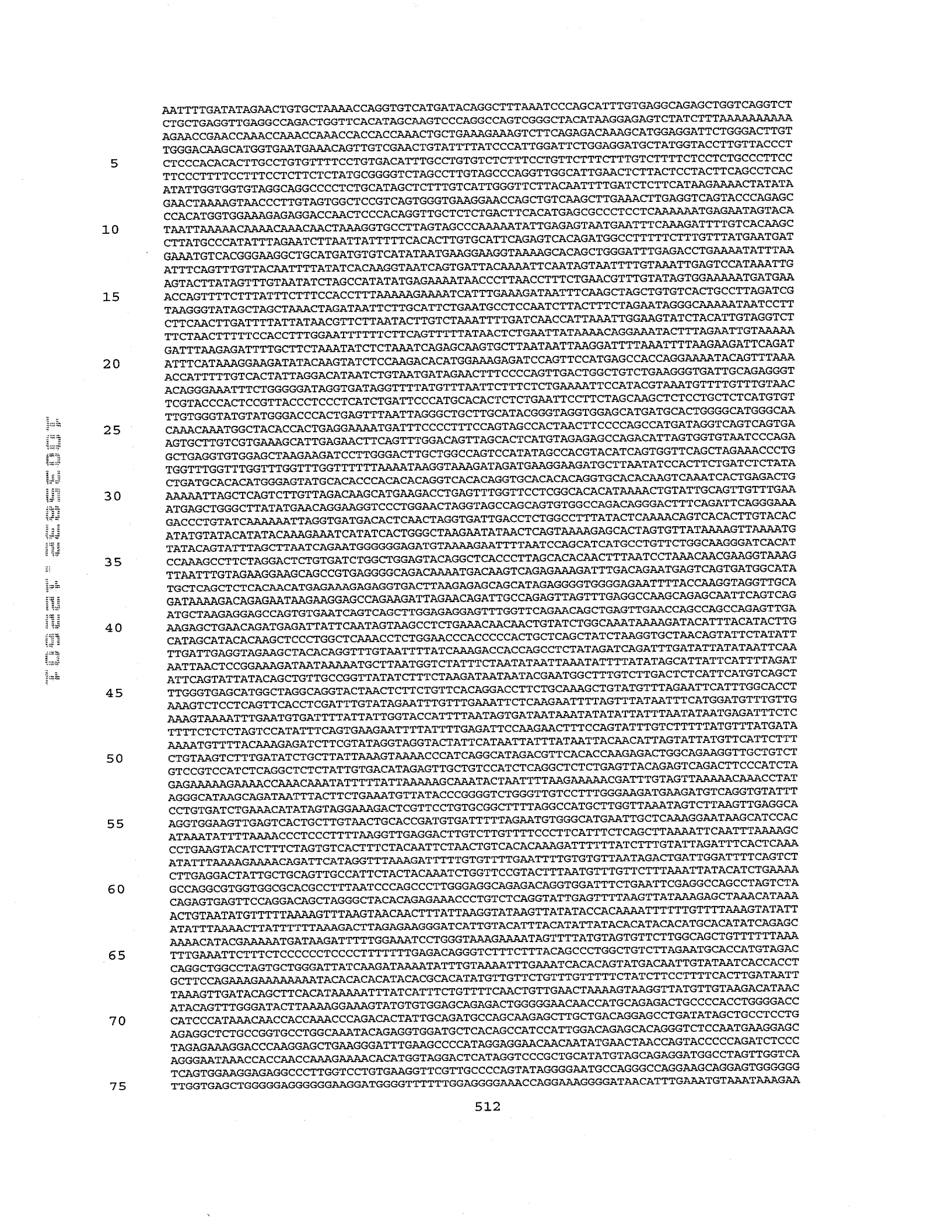


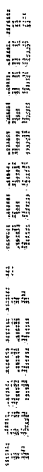
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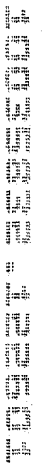




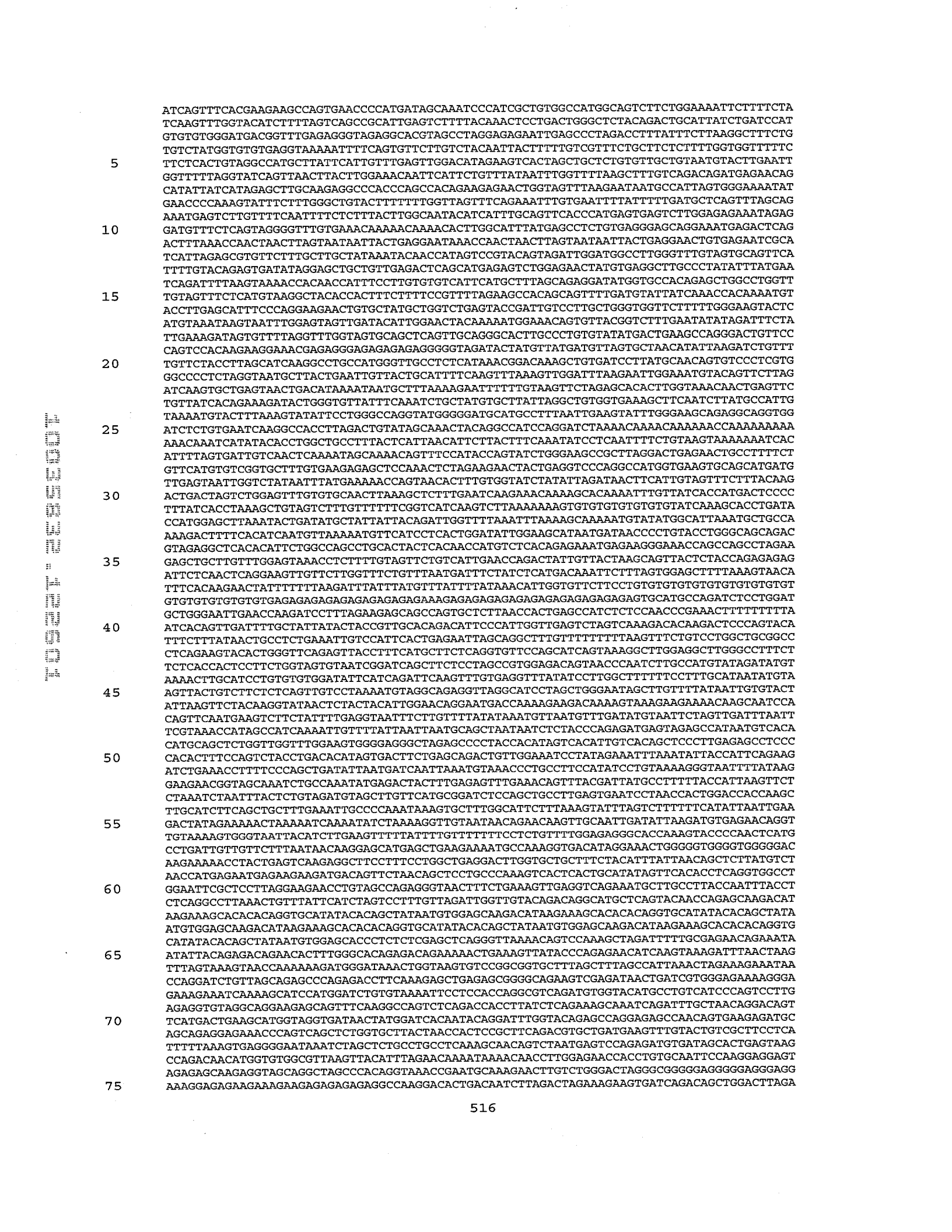
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FIGURE 2 - Sequence Listing

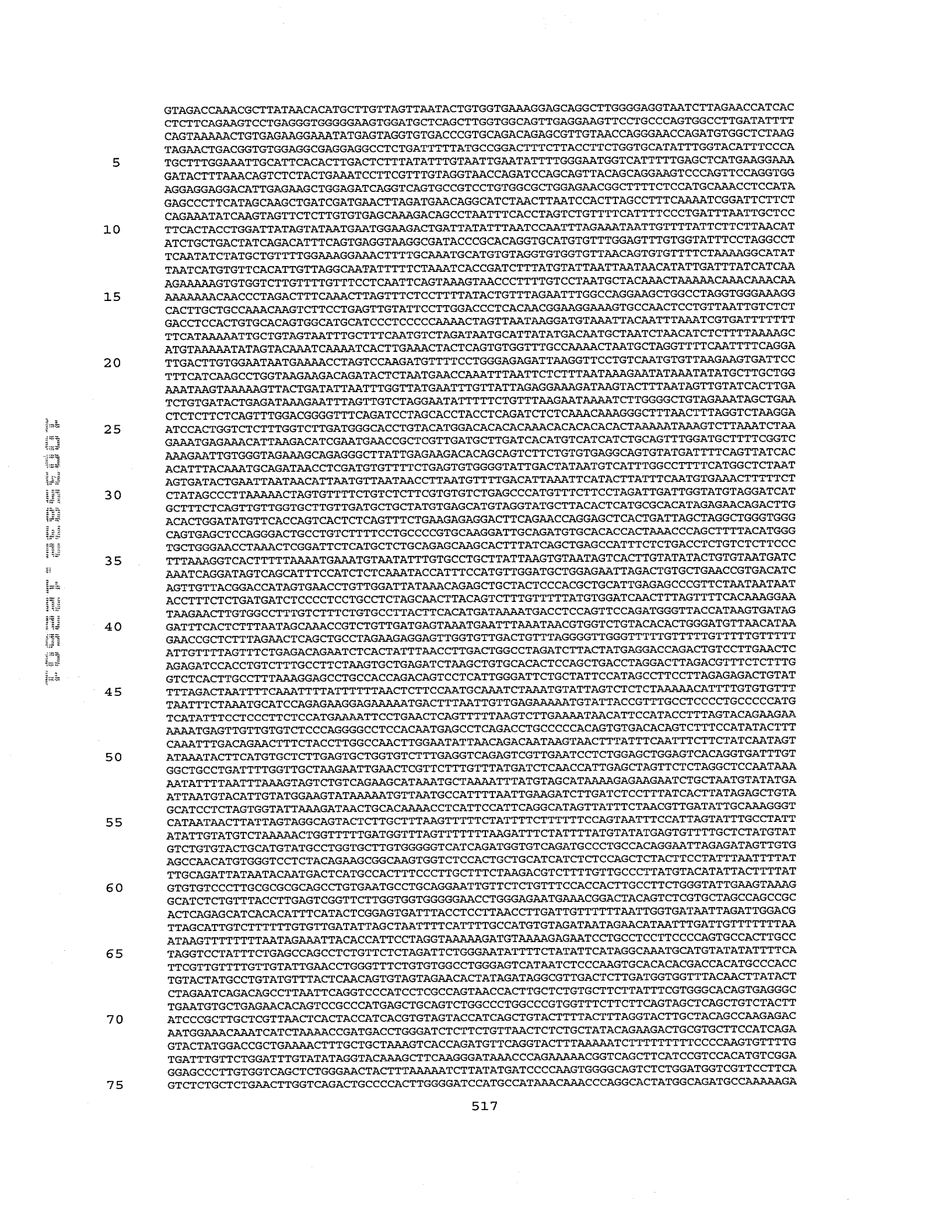
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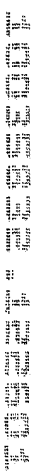


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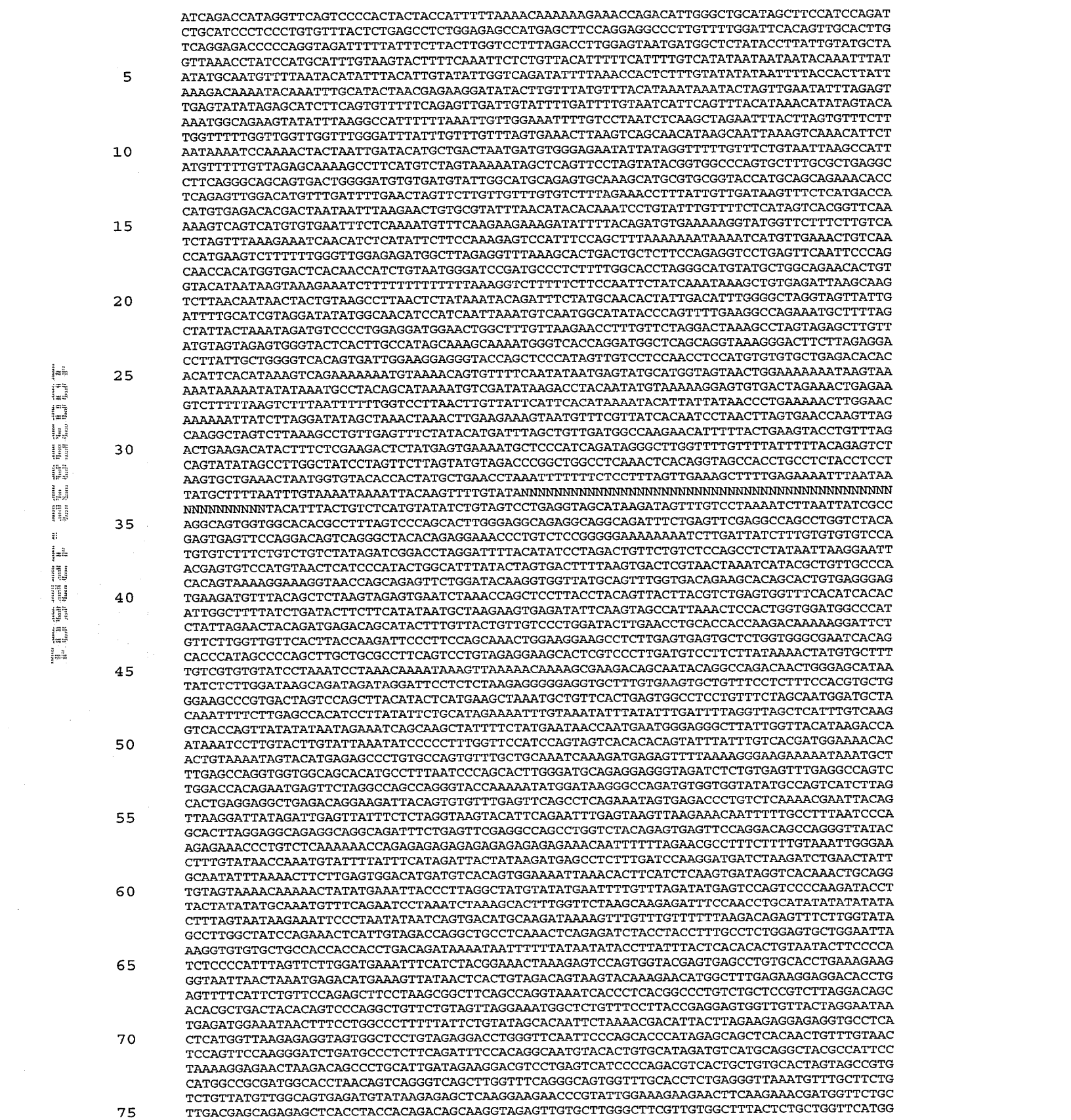
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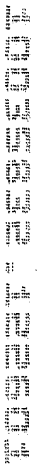
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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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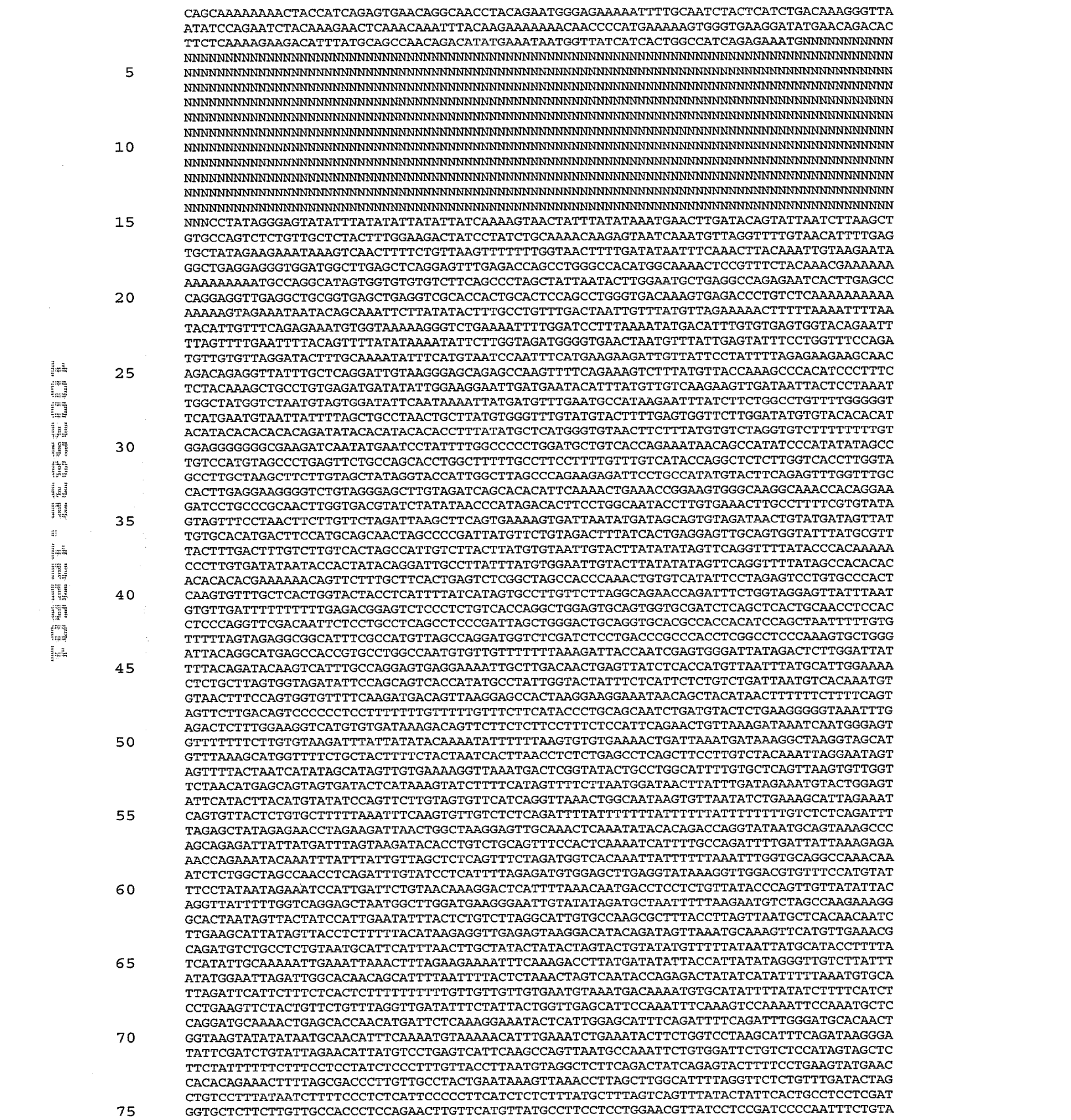
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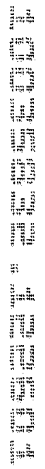


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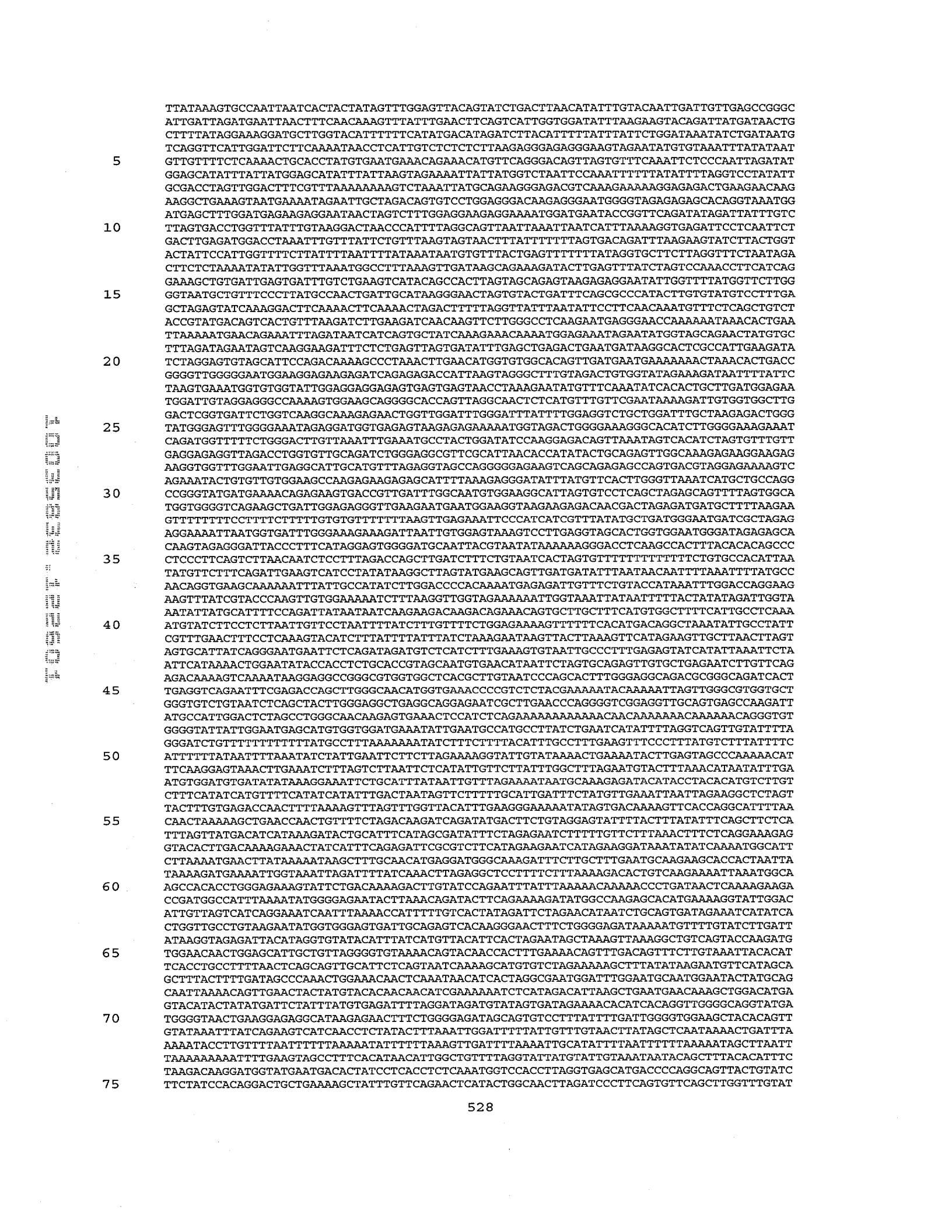
FIGURE 2 - SEQUENCE LISTING

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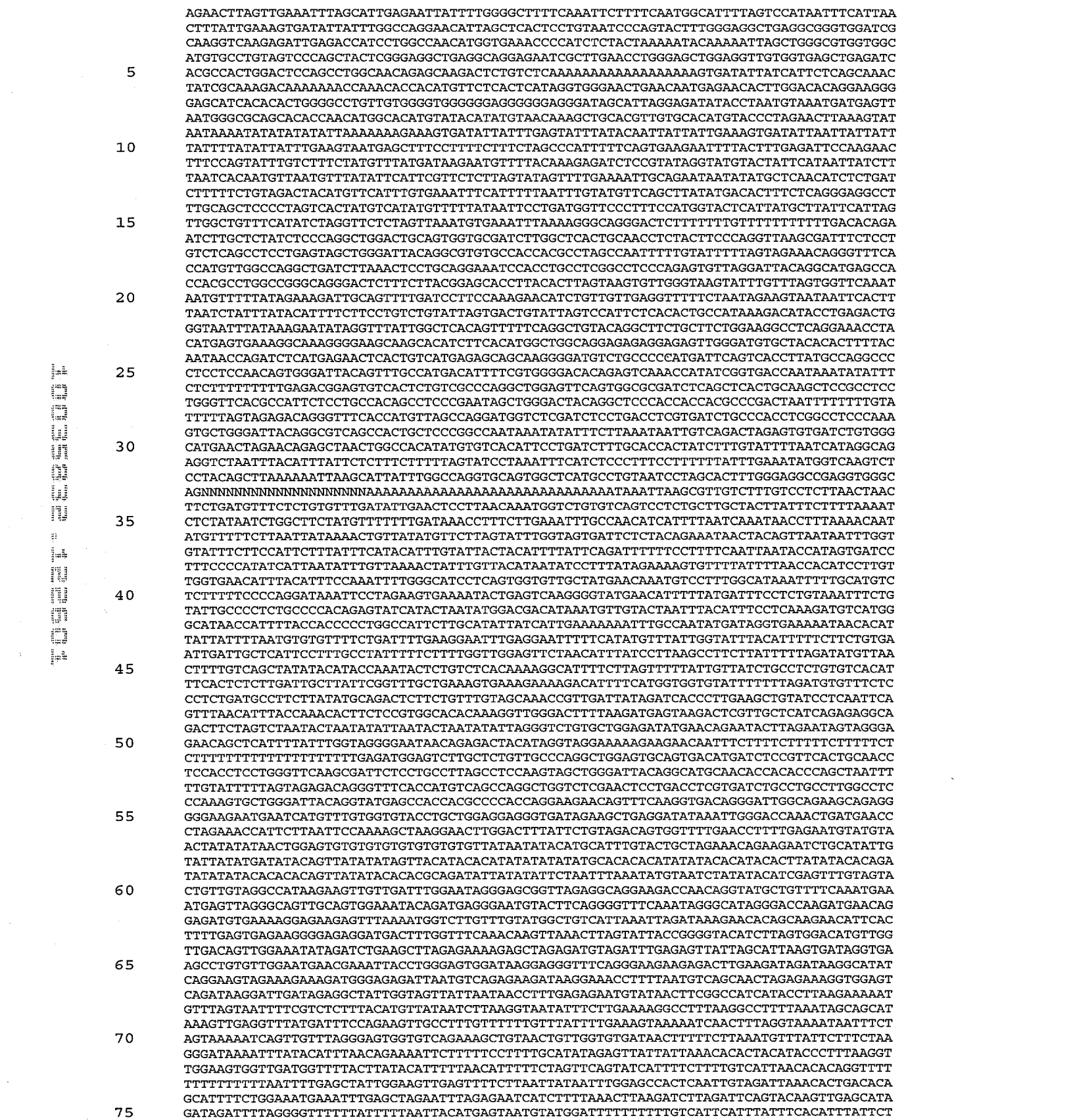


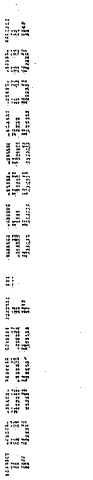


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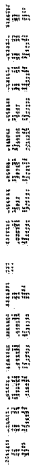


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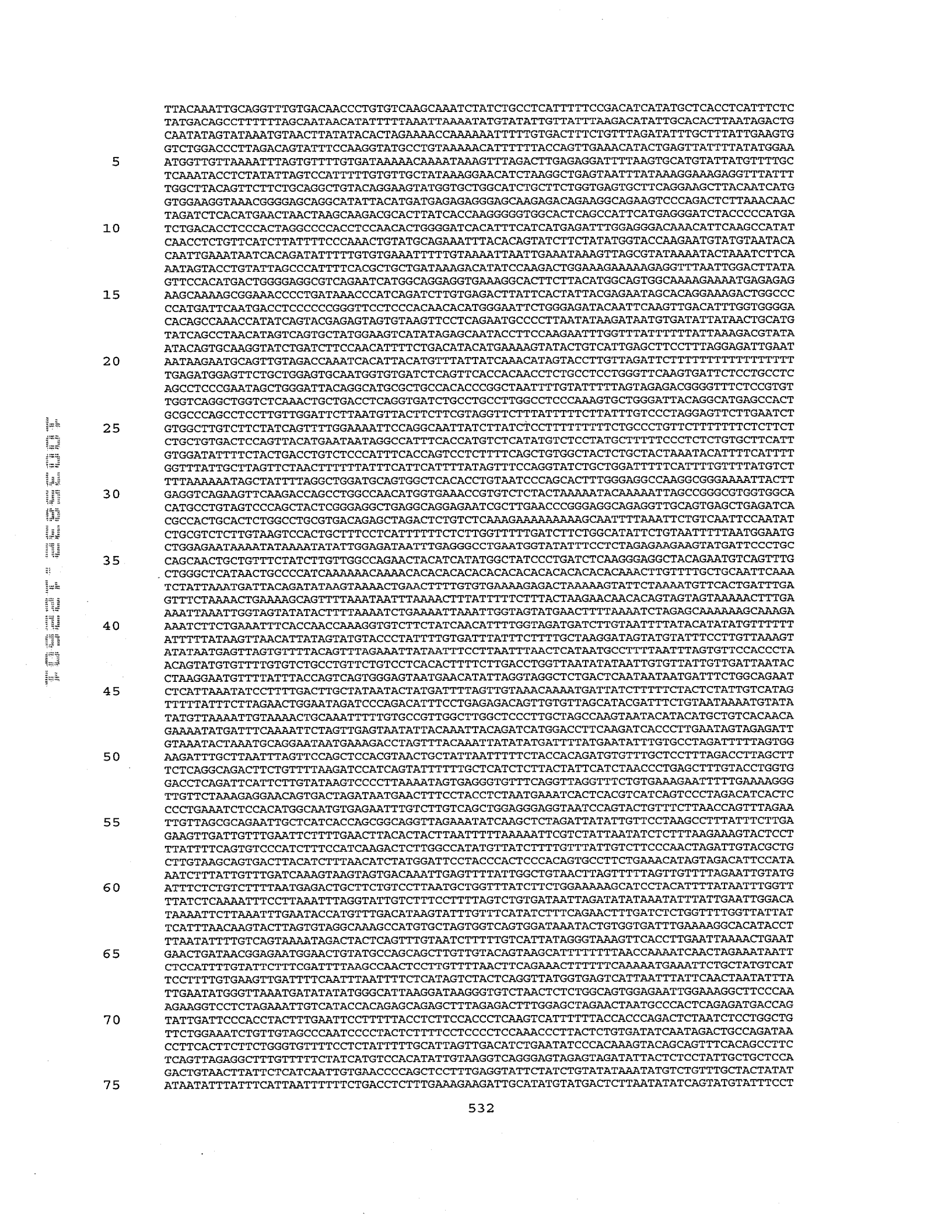




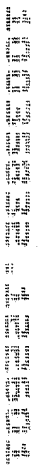
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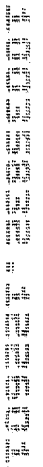
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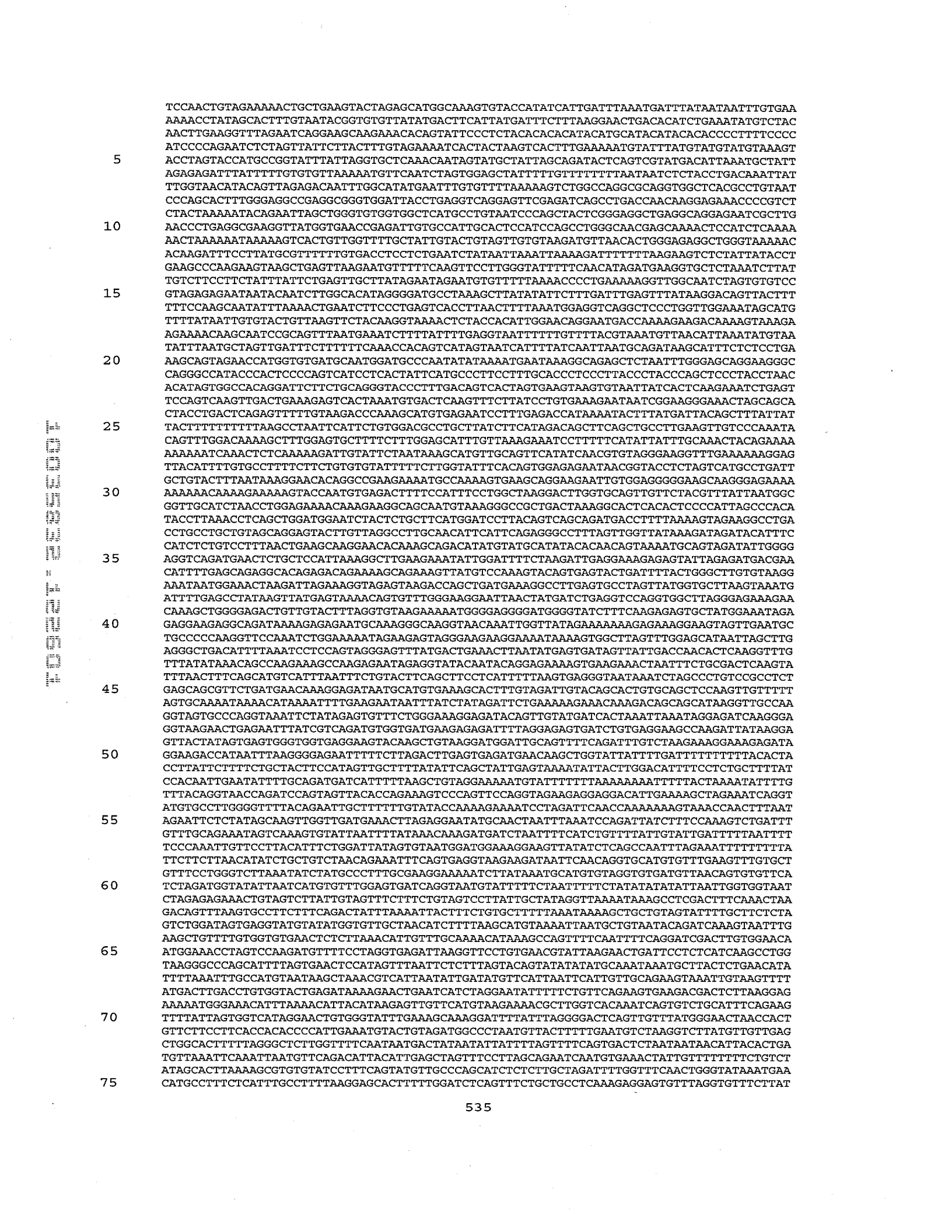
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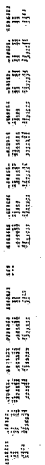
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

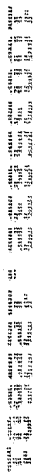
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CCAGTAGTGCAAAATATGGGAGCAAGGAAAATCCAATTGTTGGGAAAGCATCTTAG

Table 25

MOUSE NOMENCLATURE
ICSGNM Gata1
Celera mCG3964

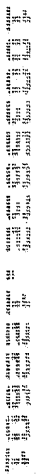
HUMAN NOMENCLATURE
HGNC GATA1
Celera hCT10890

MOUSE SEQUENCE - GENOMIC
TGCCTATAGTTTCAGAGGCTGAGTCCATTATCATTGTGGAAGCATAGCAGAAGGCAGACAGGAGTTGGGGCACTATCTGAGACCTT
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TACTGACCCCCCCCCCATAGAACAGGGAGGAACTAACGGGGCCCACAGTCTGCAGACACAAGTGAAGTGGGGGAGGGGATAAAGCC
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MOUSE SEQUENCE - mRNA

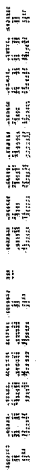
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - CODING

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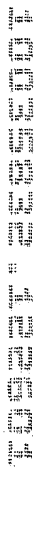
Table 26

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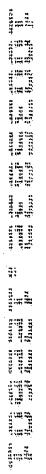
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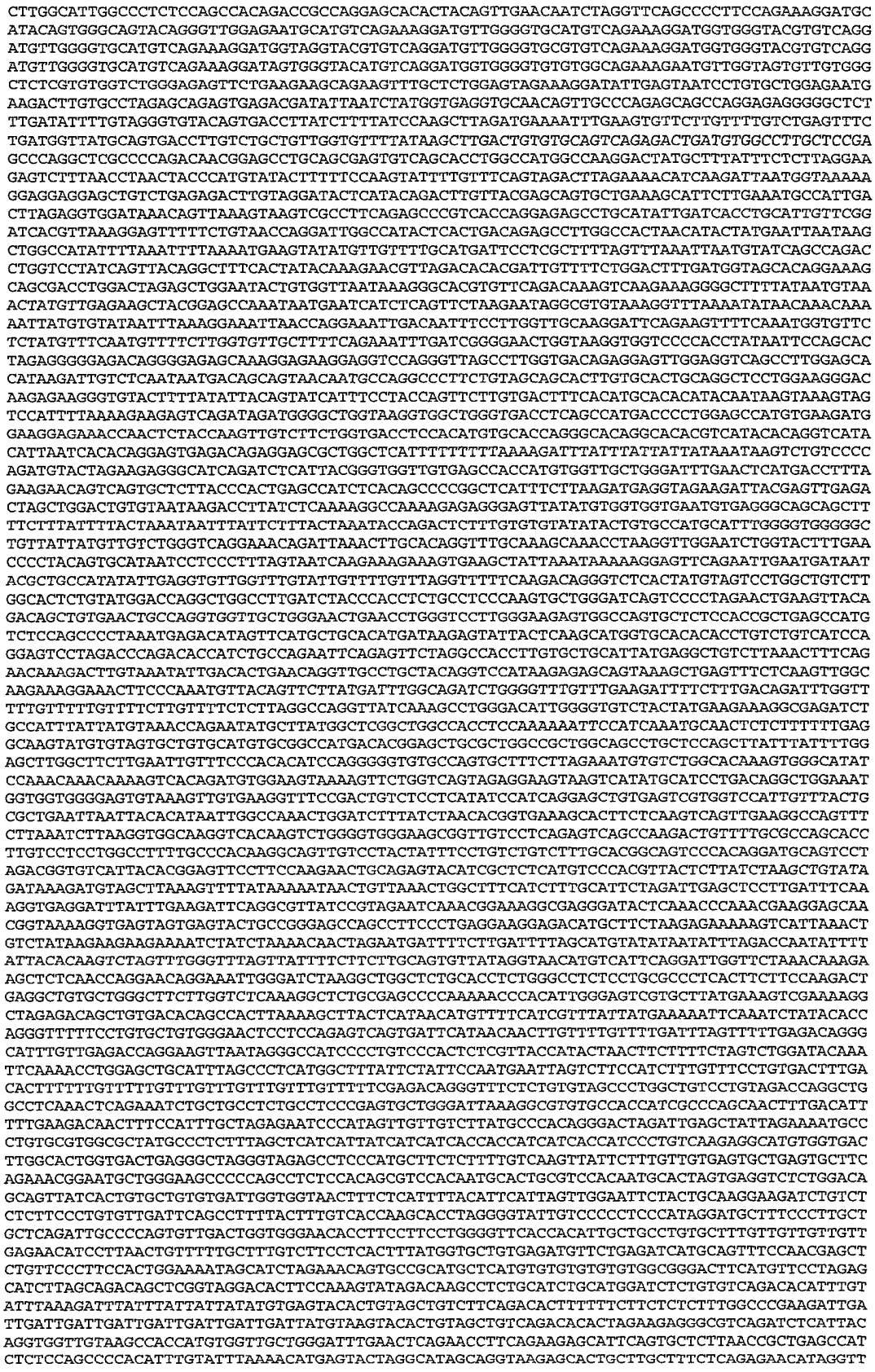
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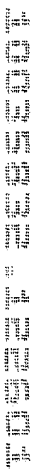


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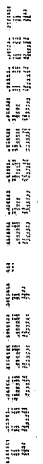
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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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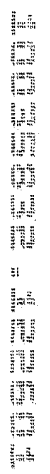
HUMAN SEQUENCE - GENOMIC

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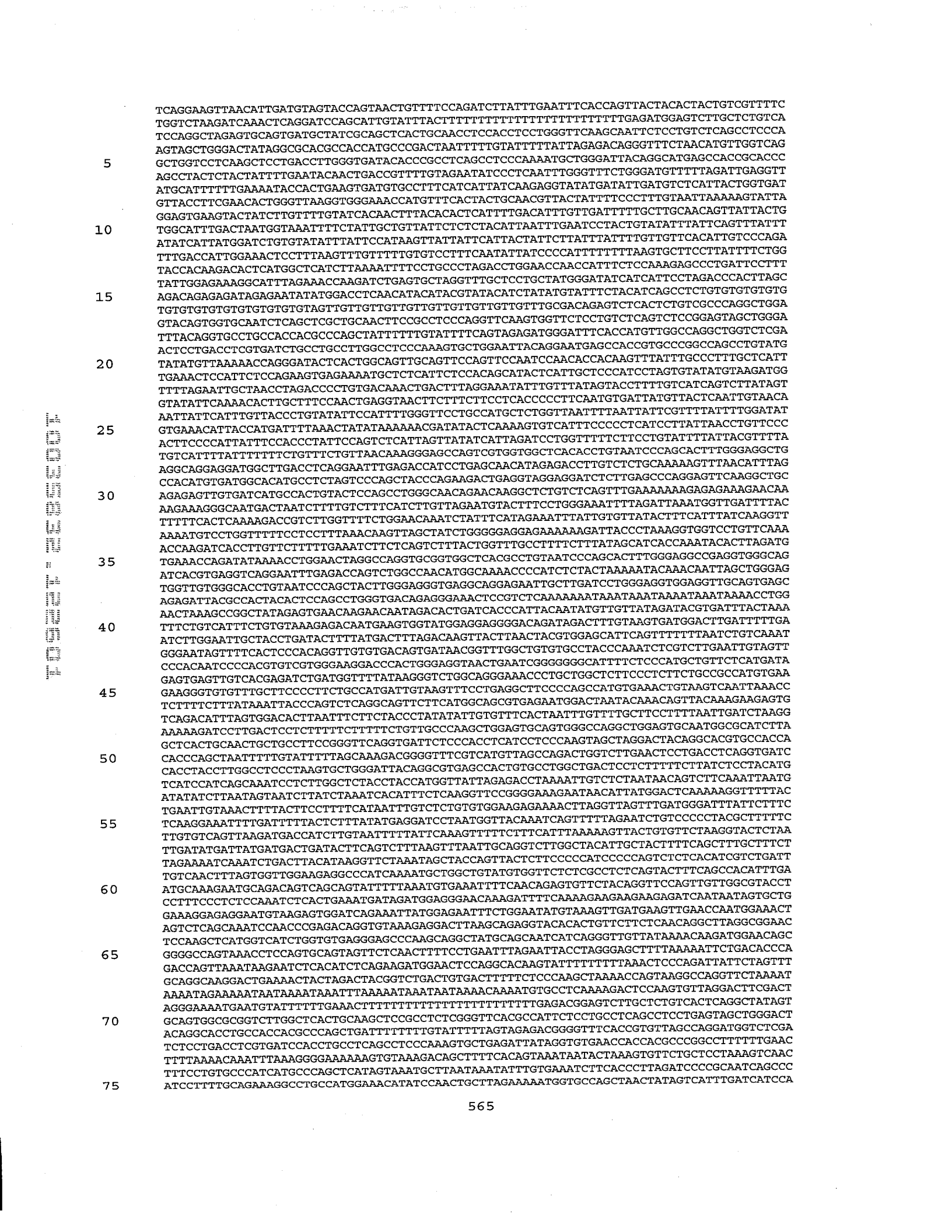
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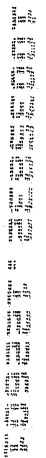
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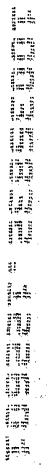
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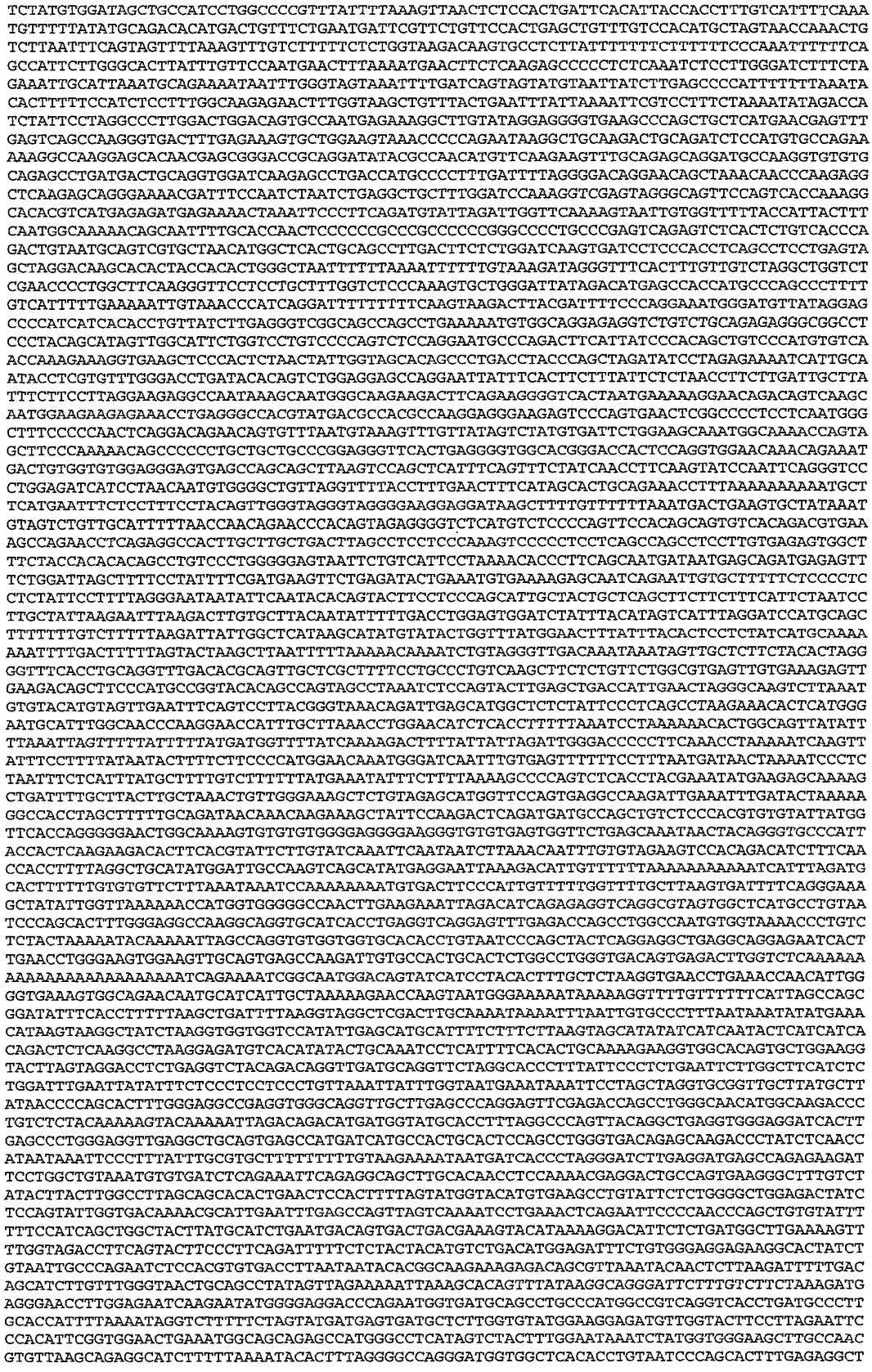
Application Number: 09/782,004

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Sequence Listing - 08/15/2005 10:59:05 AM



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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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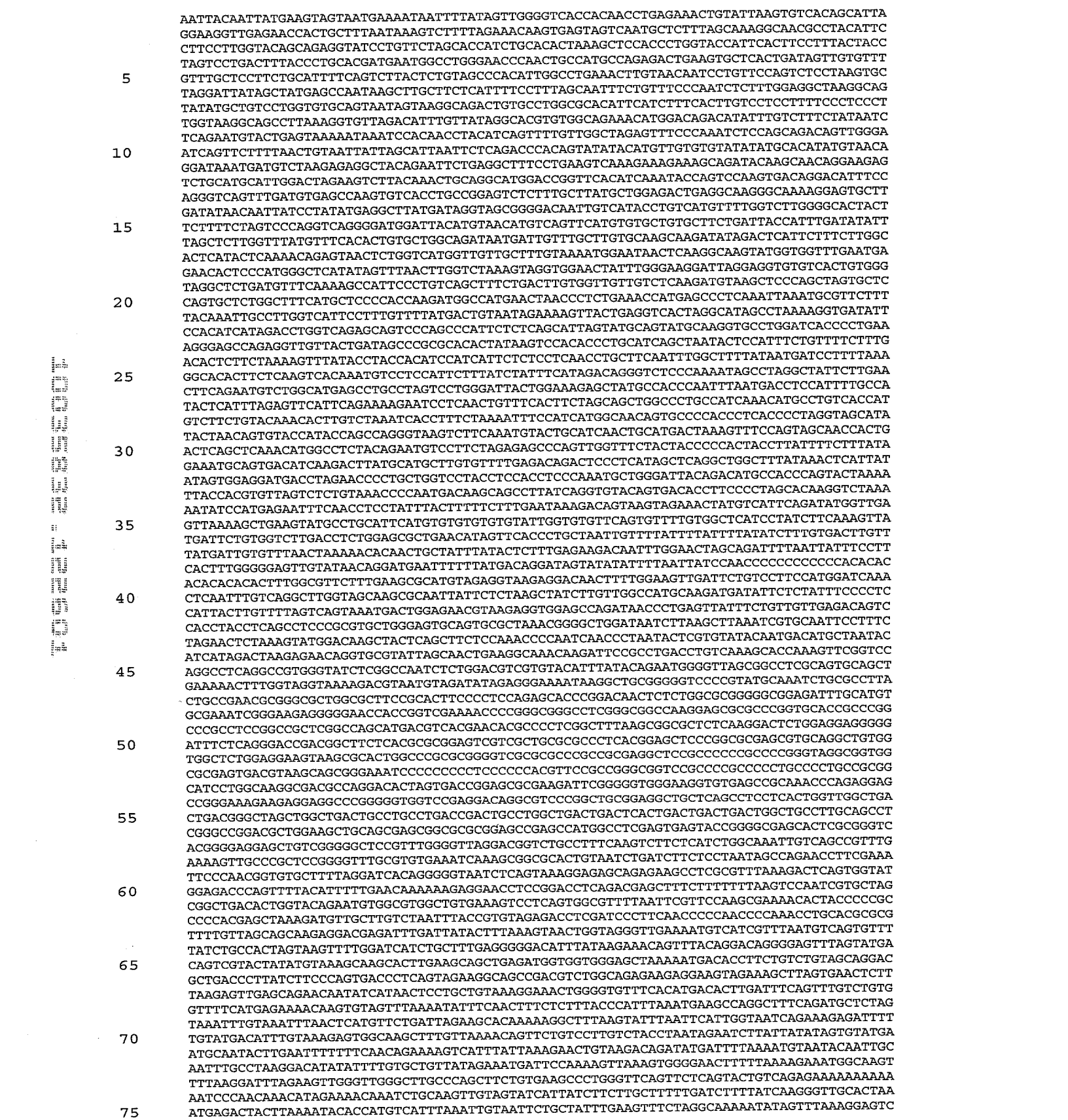
Table 27

MOUSE NOMENCLATURE
ICSGNM Rel
Celera mCG8770

HUMAN NOMENCLATURE
HGNC REL
Celera hCG15154

MOUSE SEQUENCE - GENOMIC

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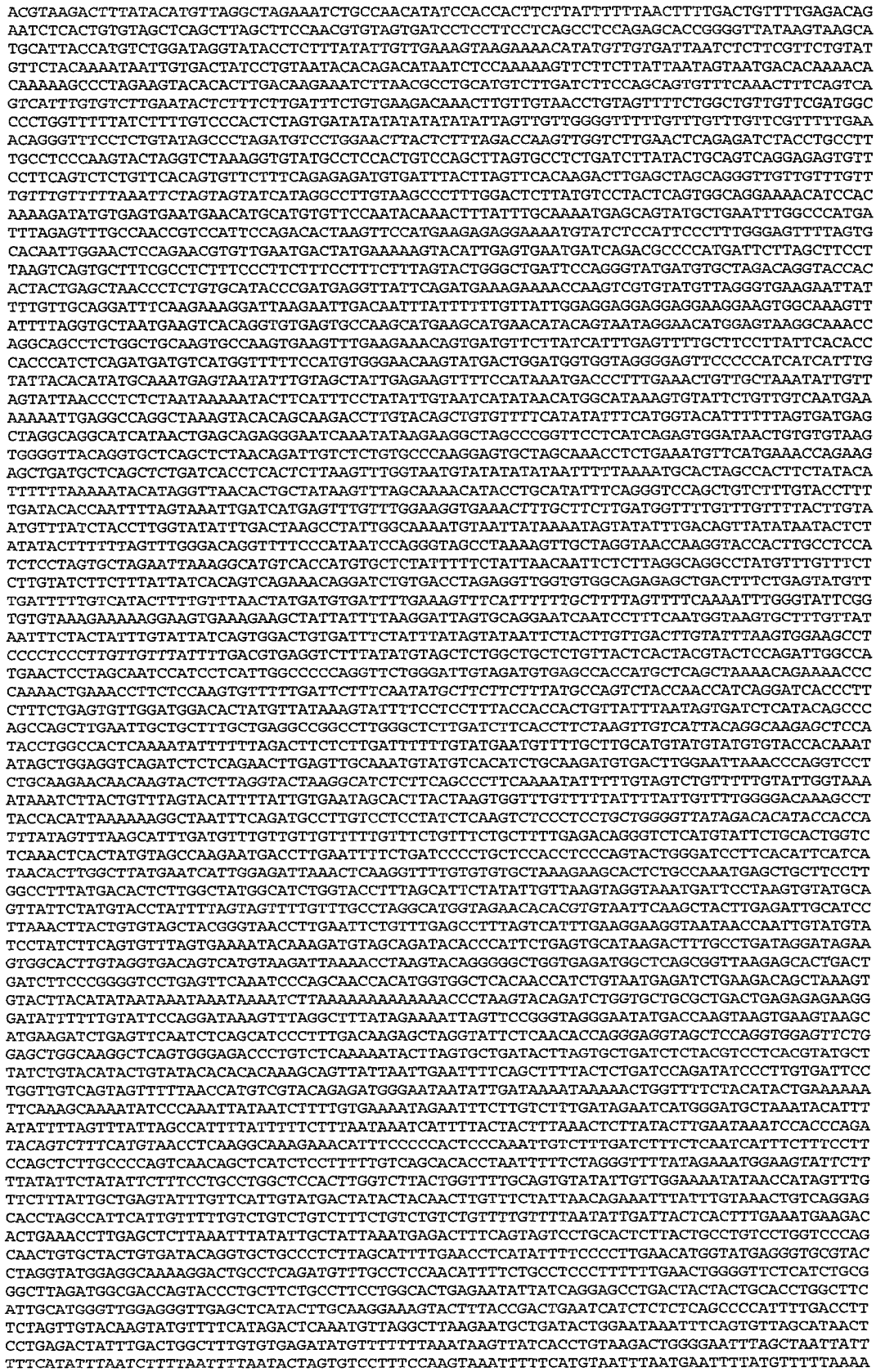


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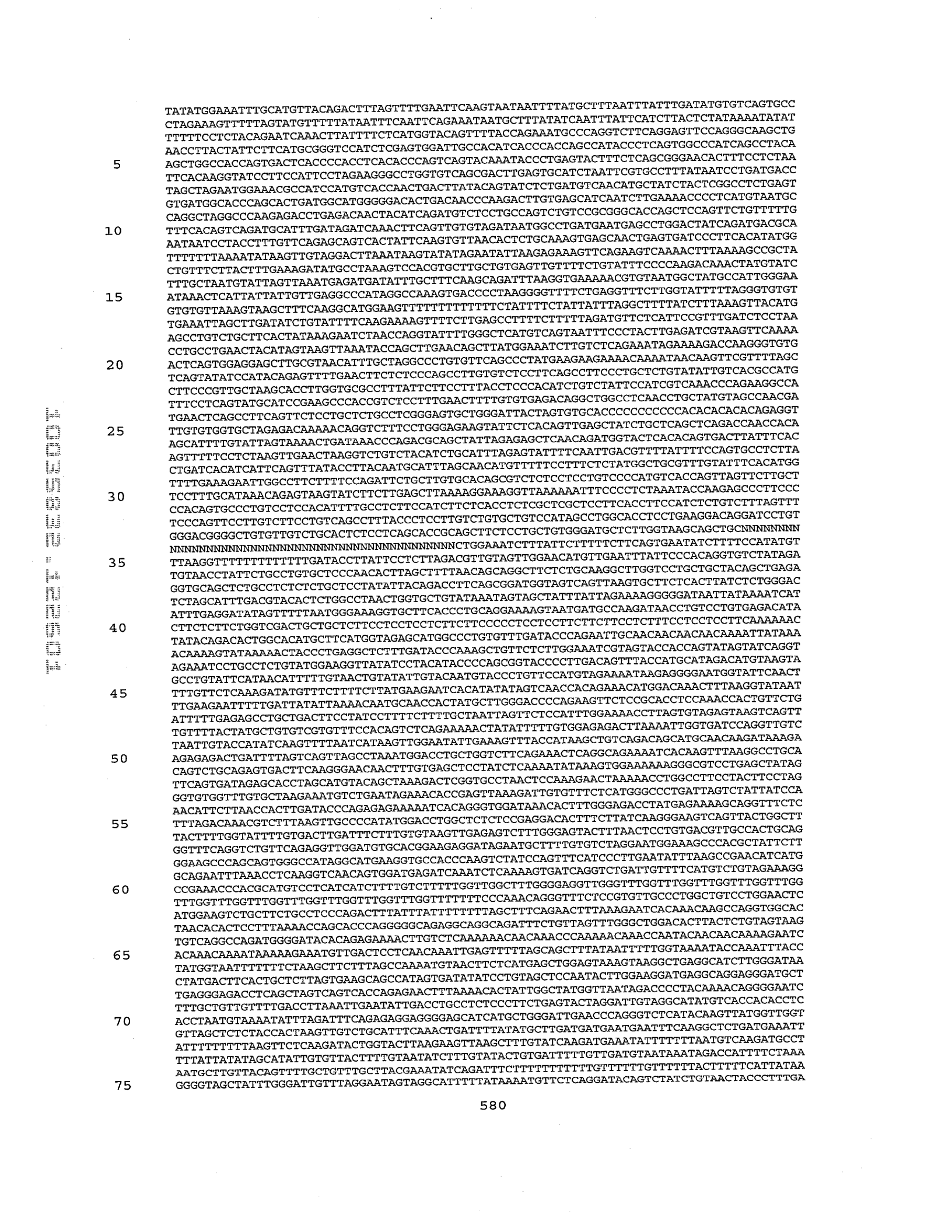
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MOUSE SEQUENCE - mRNA
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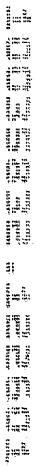
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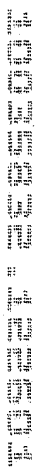
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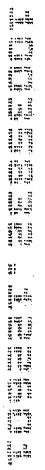




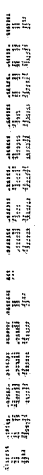
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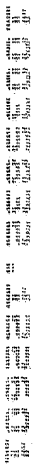
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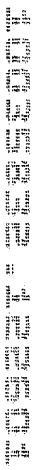


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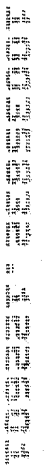


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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 28

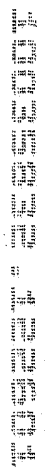
MOUSE NOMENCLATURE
ICSGNM Icsbp
Celera mCG21199

HUMAN NOMENCLATURE
HGNC ICSBP1
Celera hCG17046

MOUSE SEQUENCE - GENOMIC

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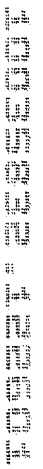


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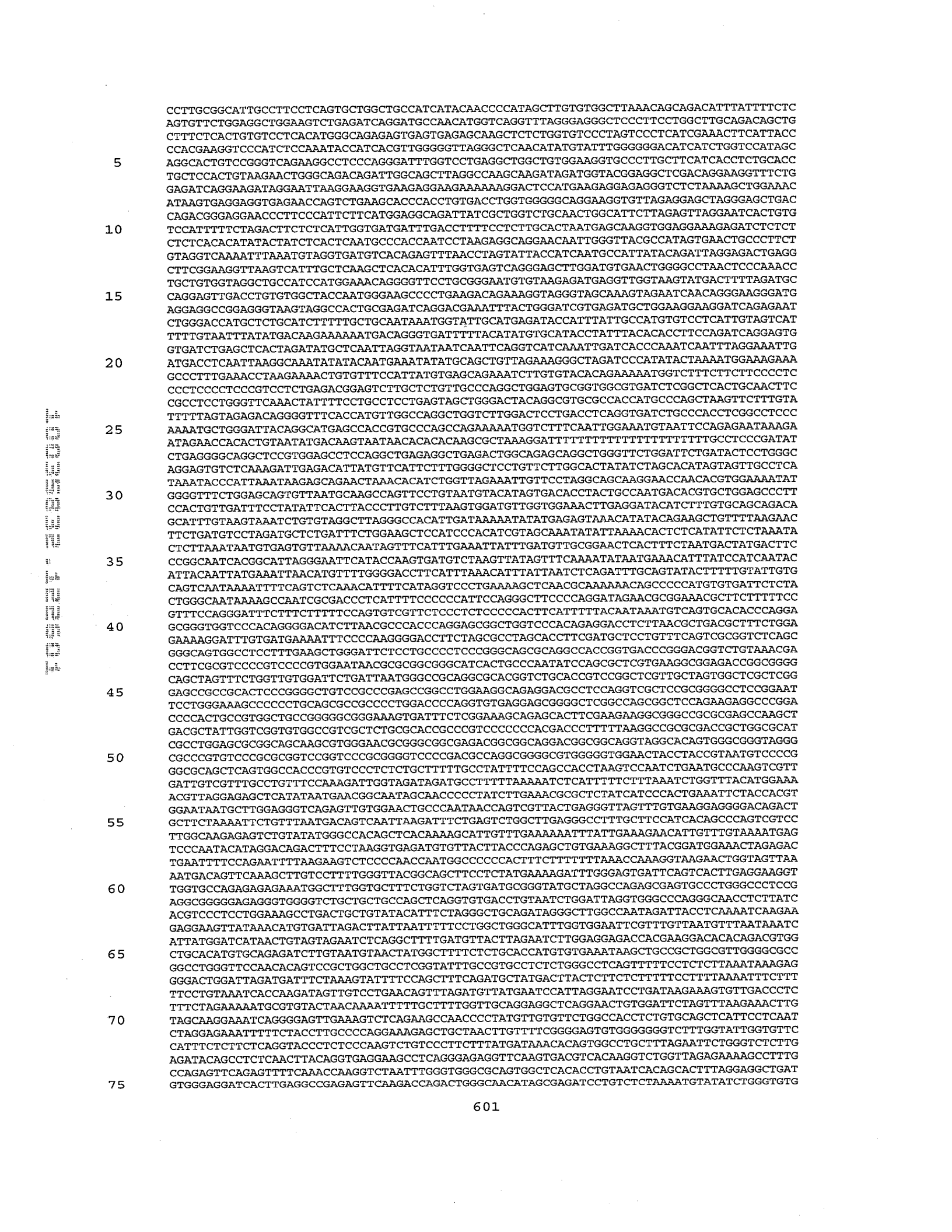
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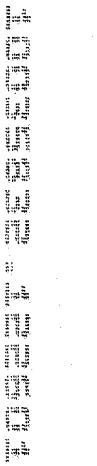
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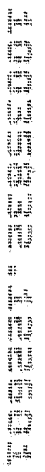


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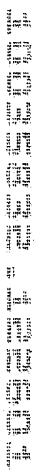
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HUMAN SEQUENCE - mRNA
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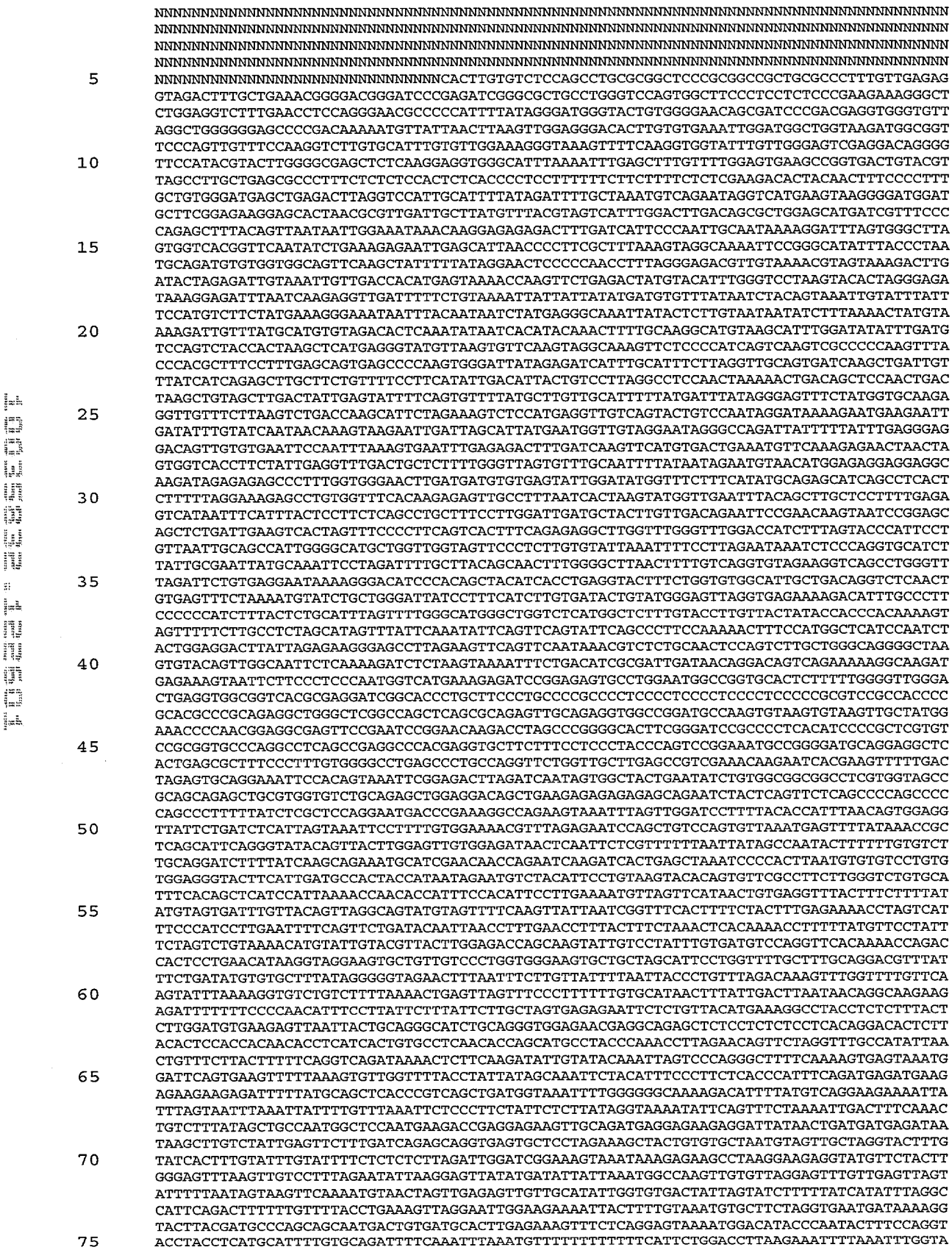
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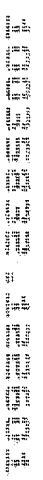
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Table 29
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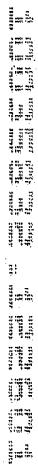
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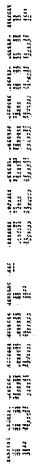


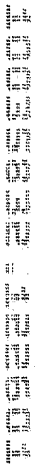
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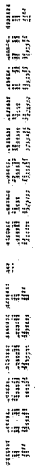
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HUMAN SEQUENCE - GENOMIC
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HUMAN SEQUENCE - mRNA

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Table 30

MOUSE NOMENCLATURE

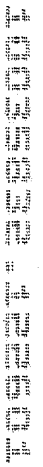
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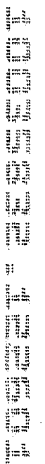
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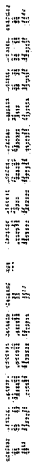
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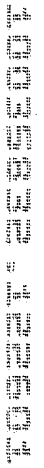


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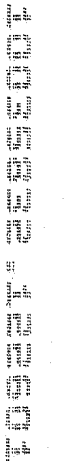


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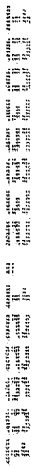
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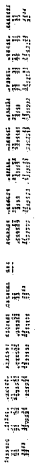
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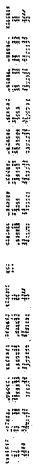
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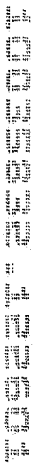
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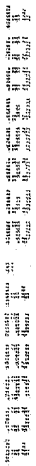
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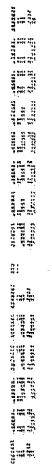
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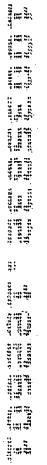
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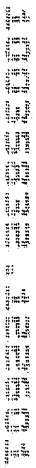
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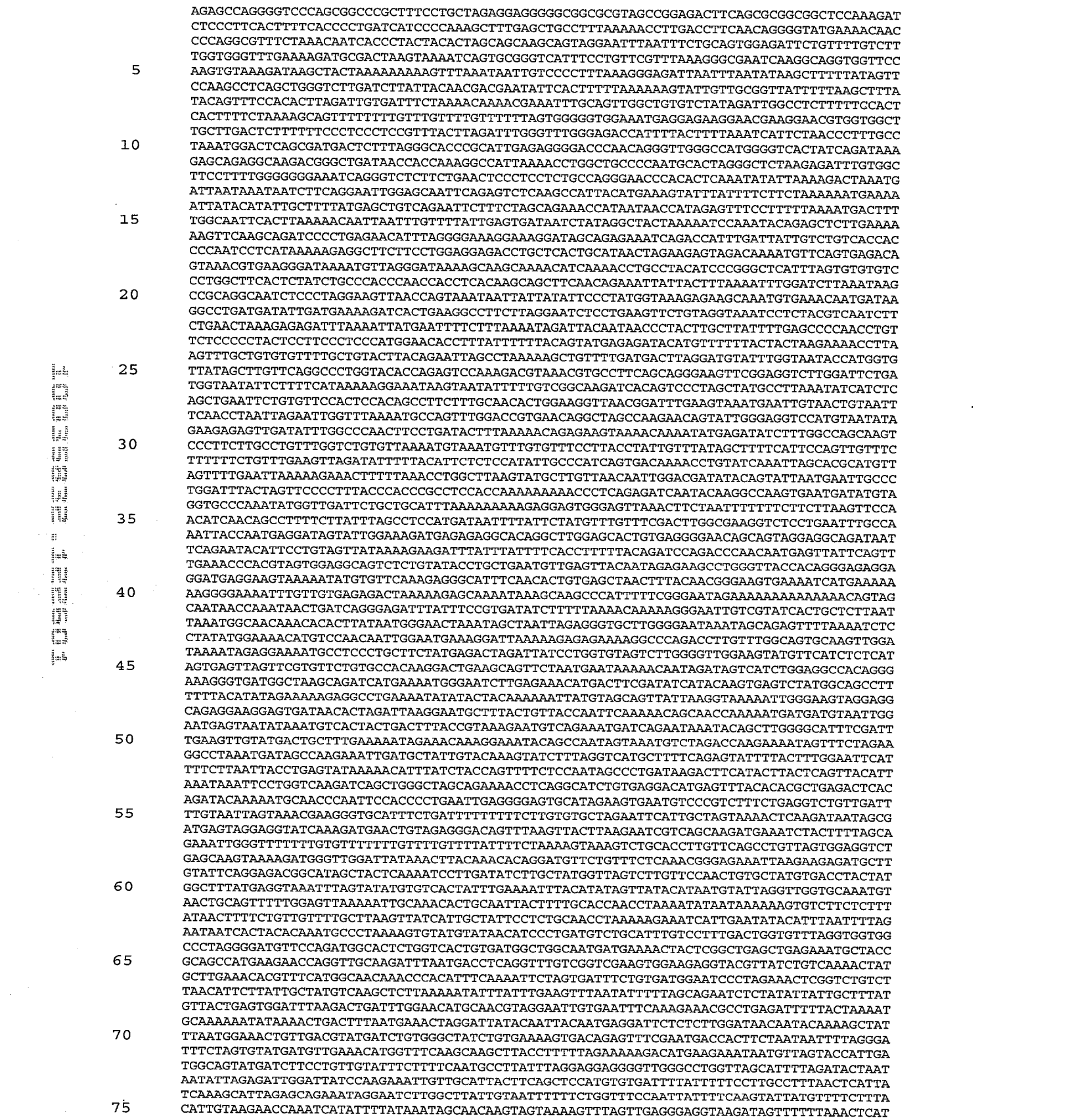
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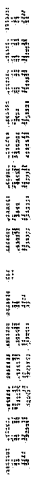
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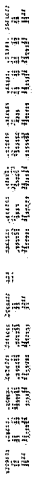


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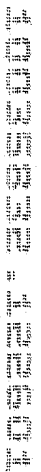
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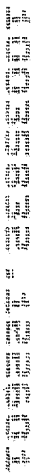
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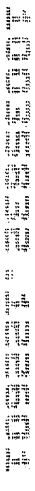
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 31

MOUSE NOMENCLATURE

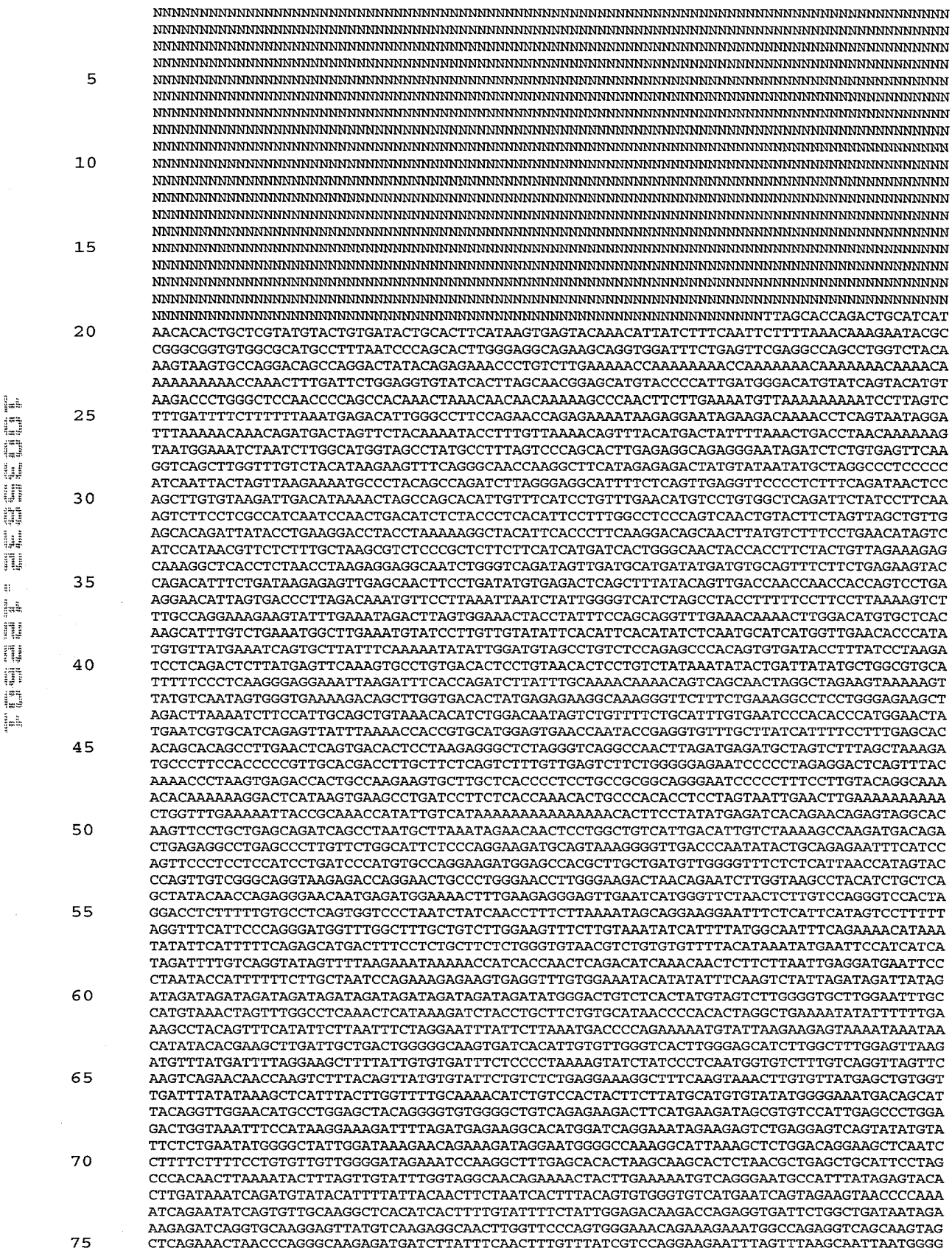
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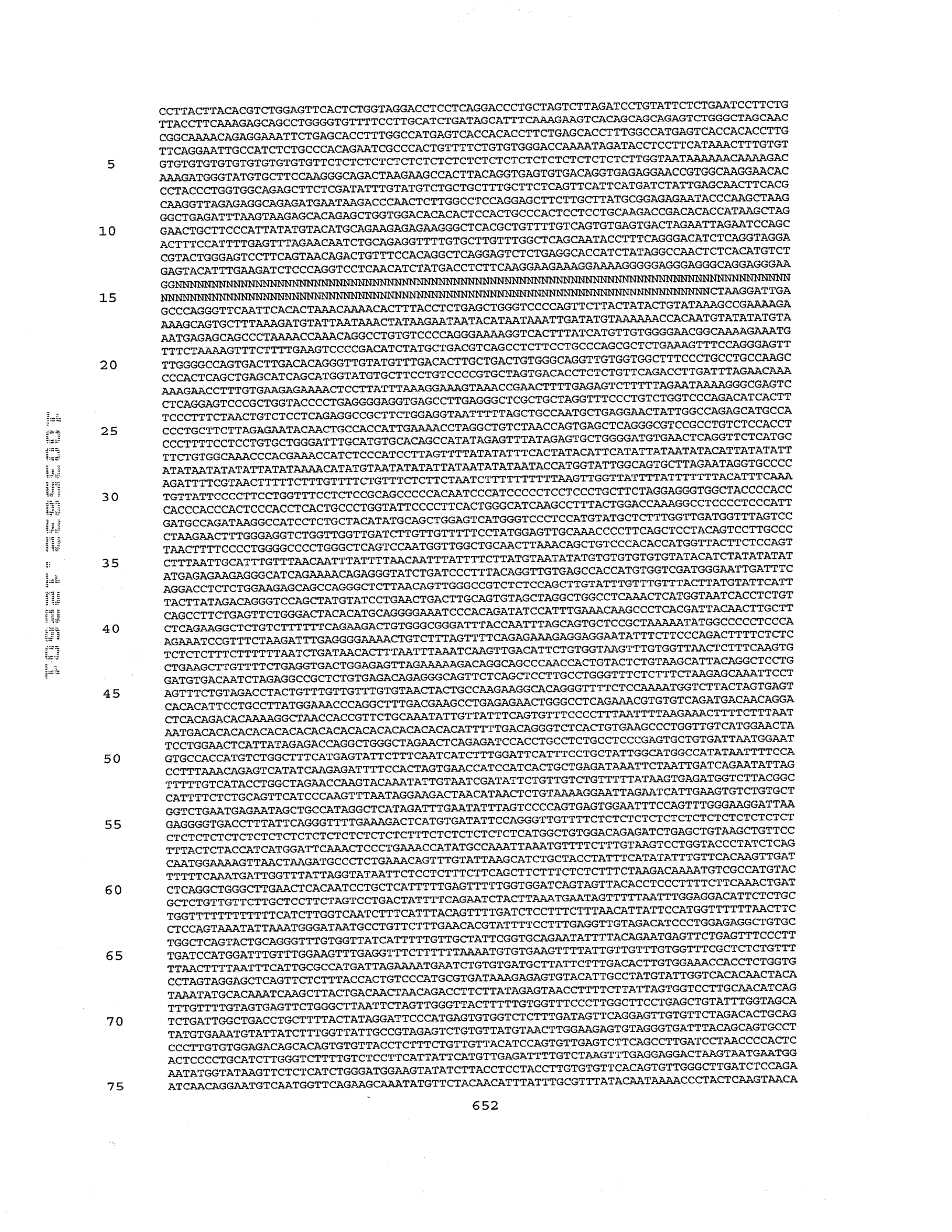
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MOUSE SEQUENCE - GENOMIC

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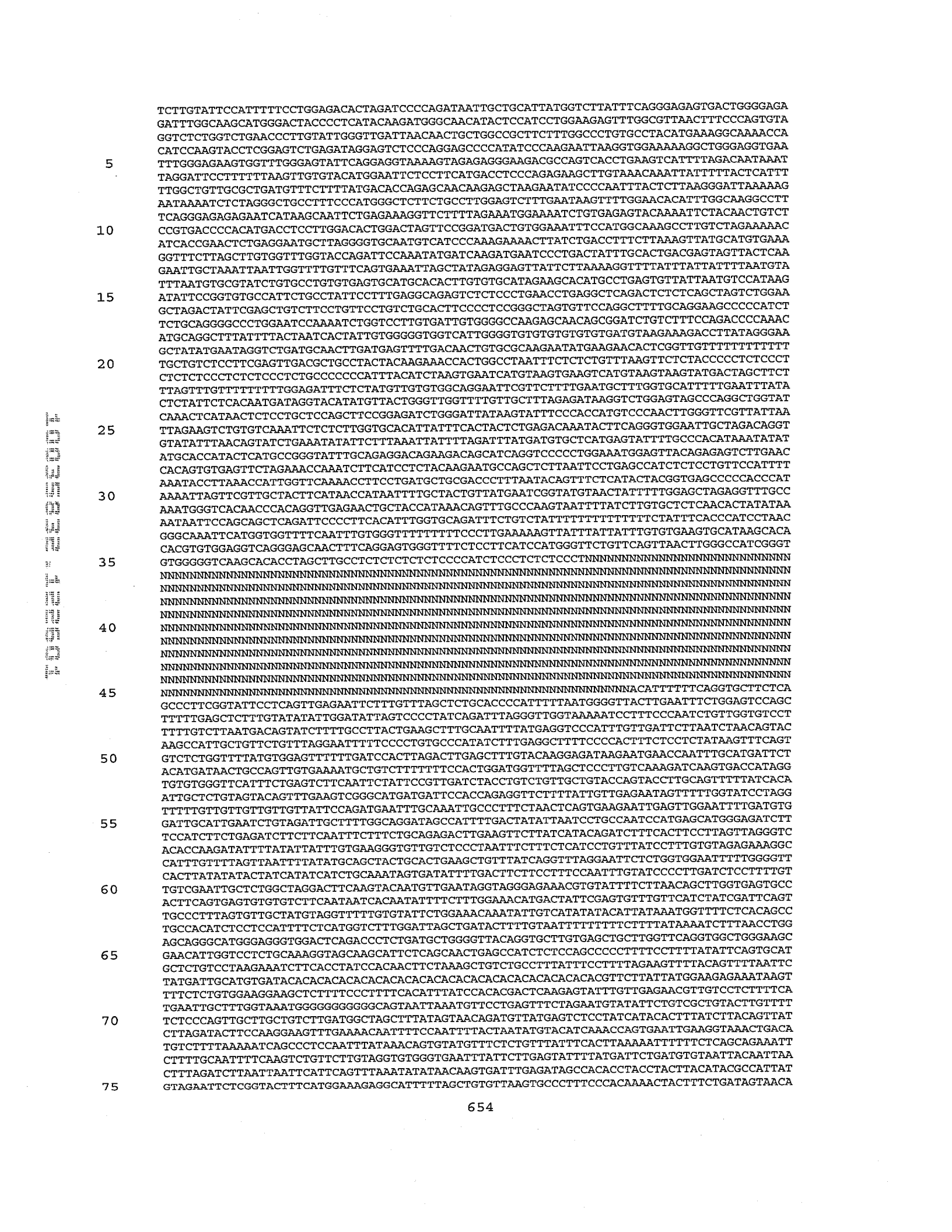


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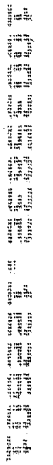
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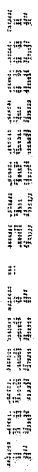


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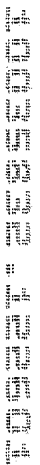
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MOUSE SEQUENCE - mRNA

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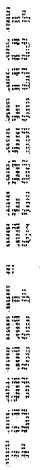
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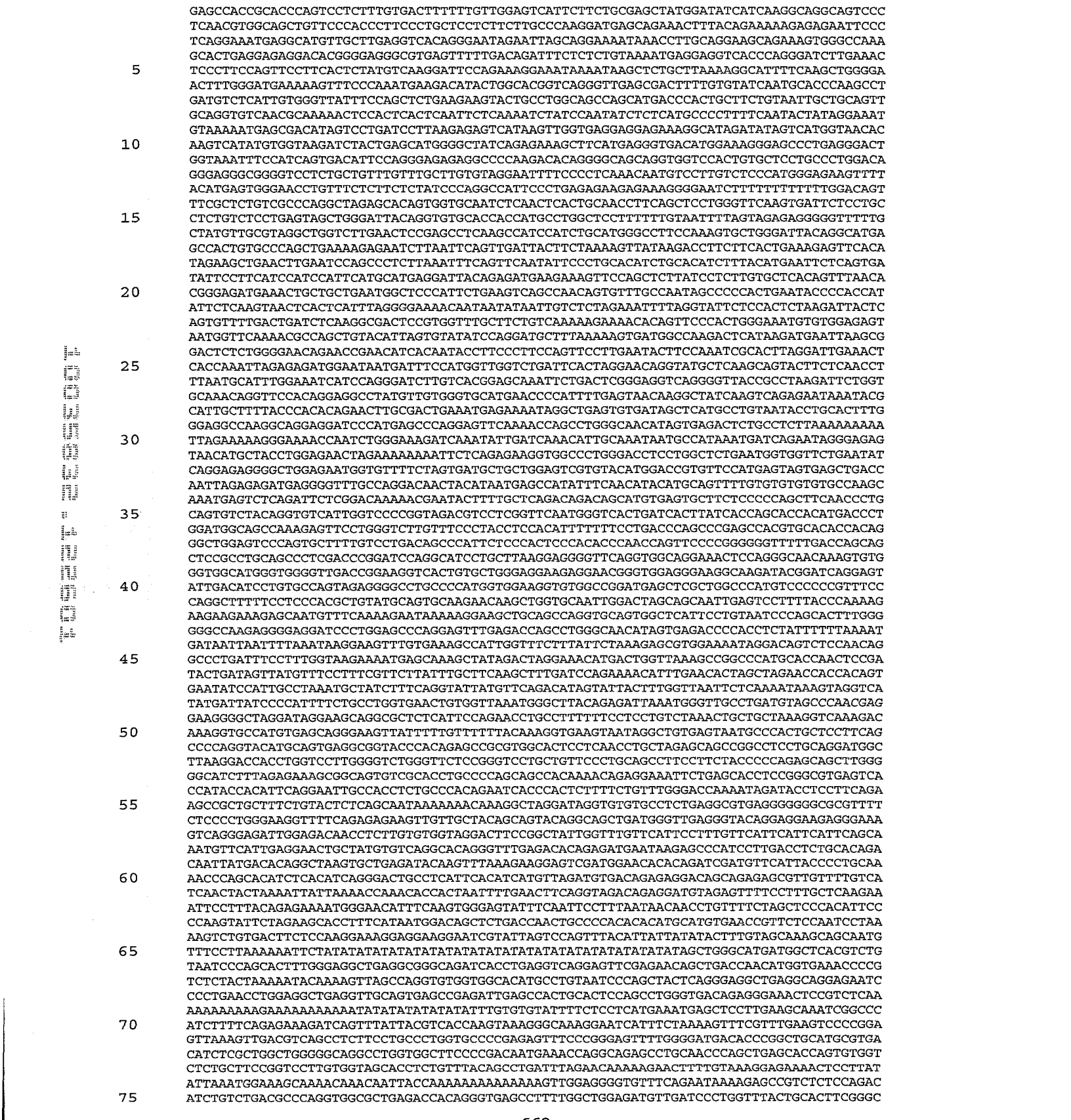
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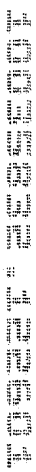
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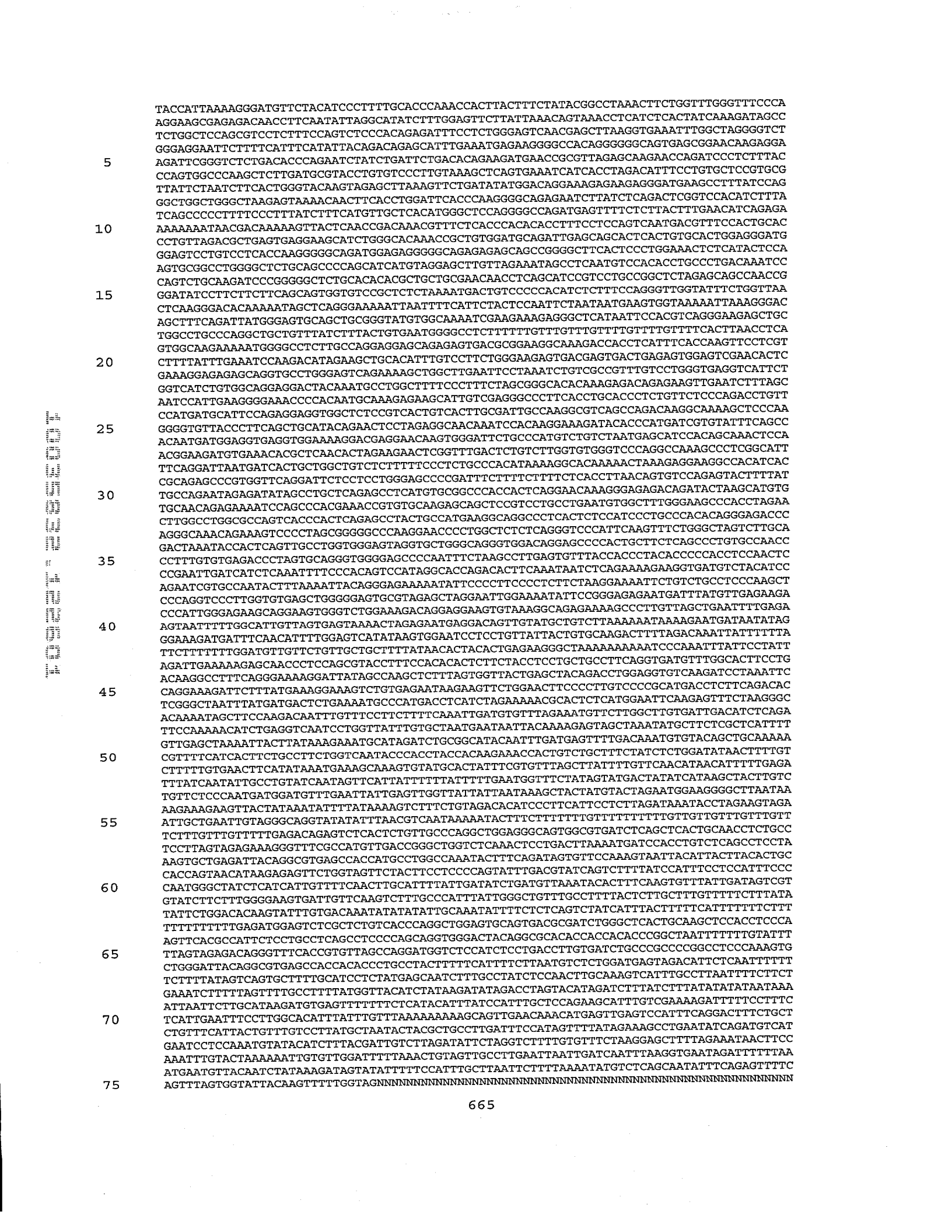
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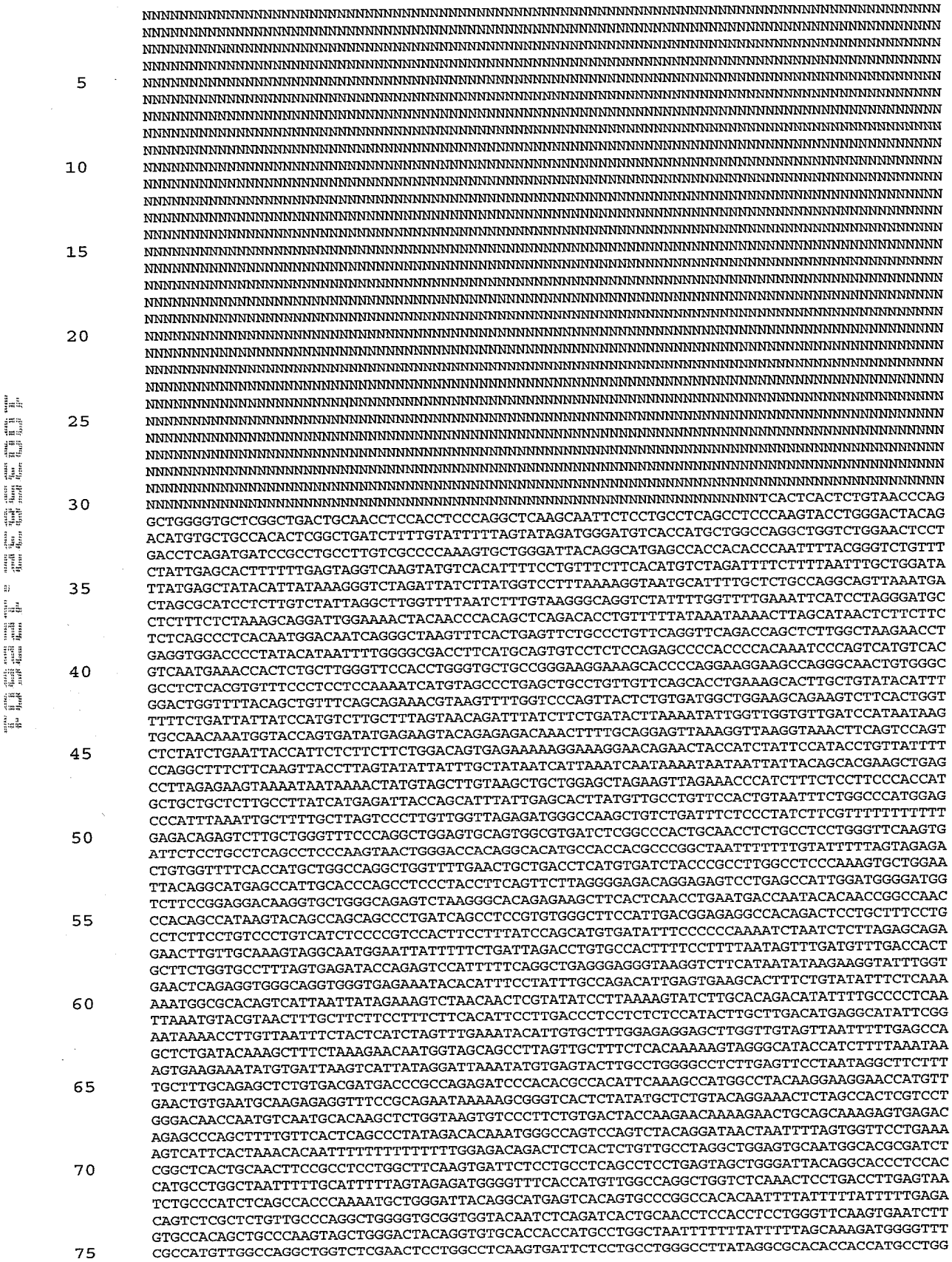
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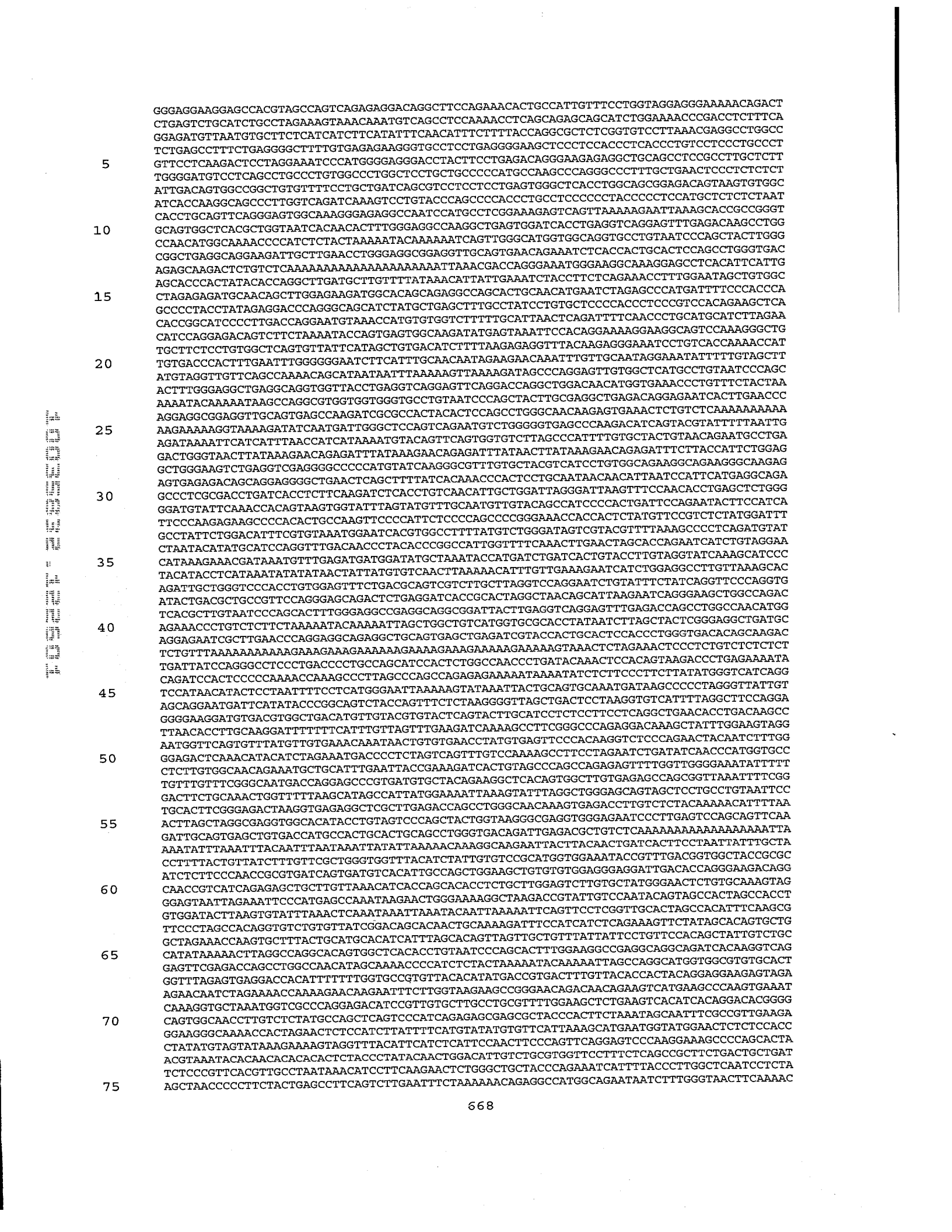
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HUMAN SEQUENCE - mRNA
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Table 32

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HUMAN NOMENCLATURE

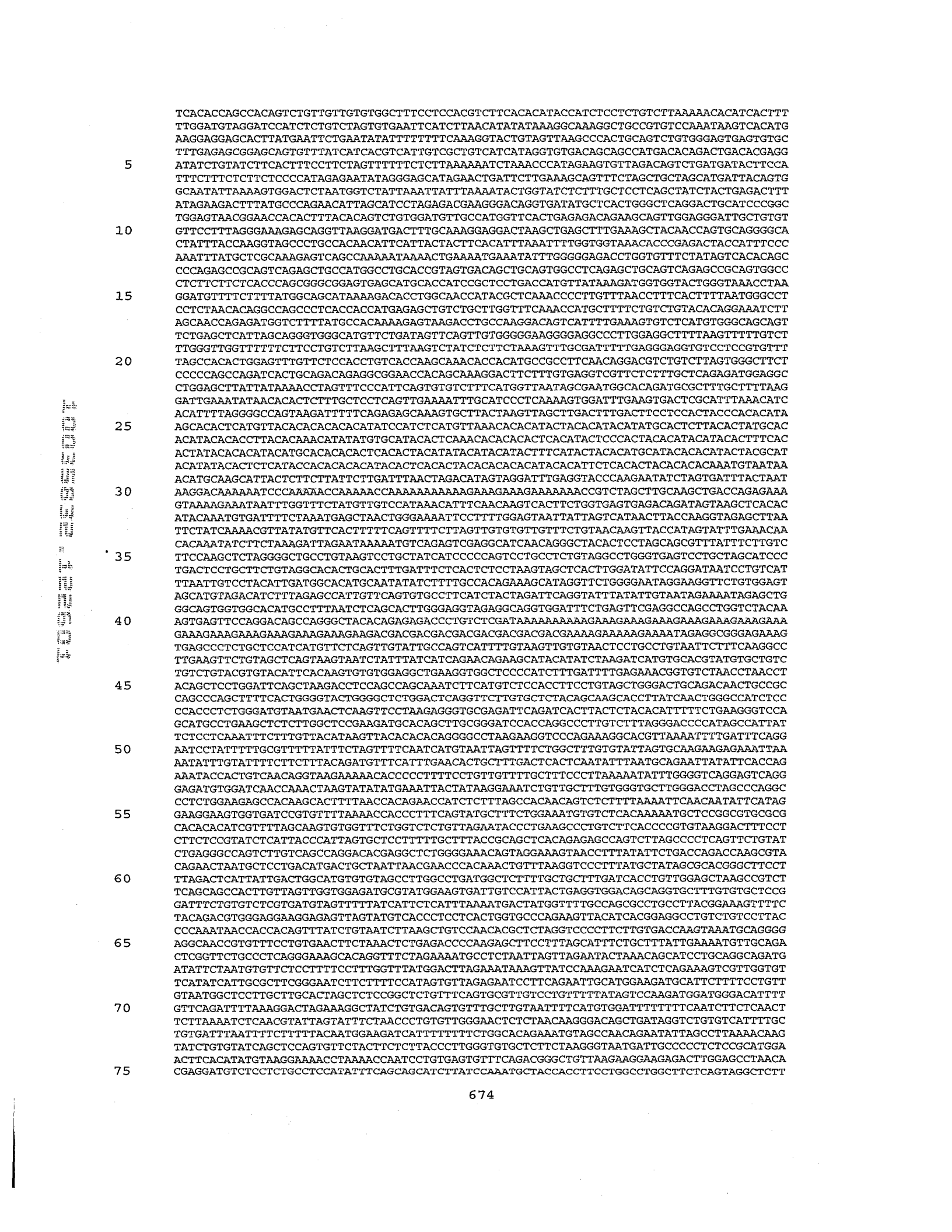
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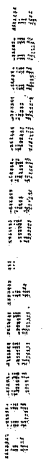
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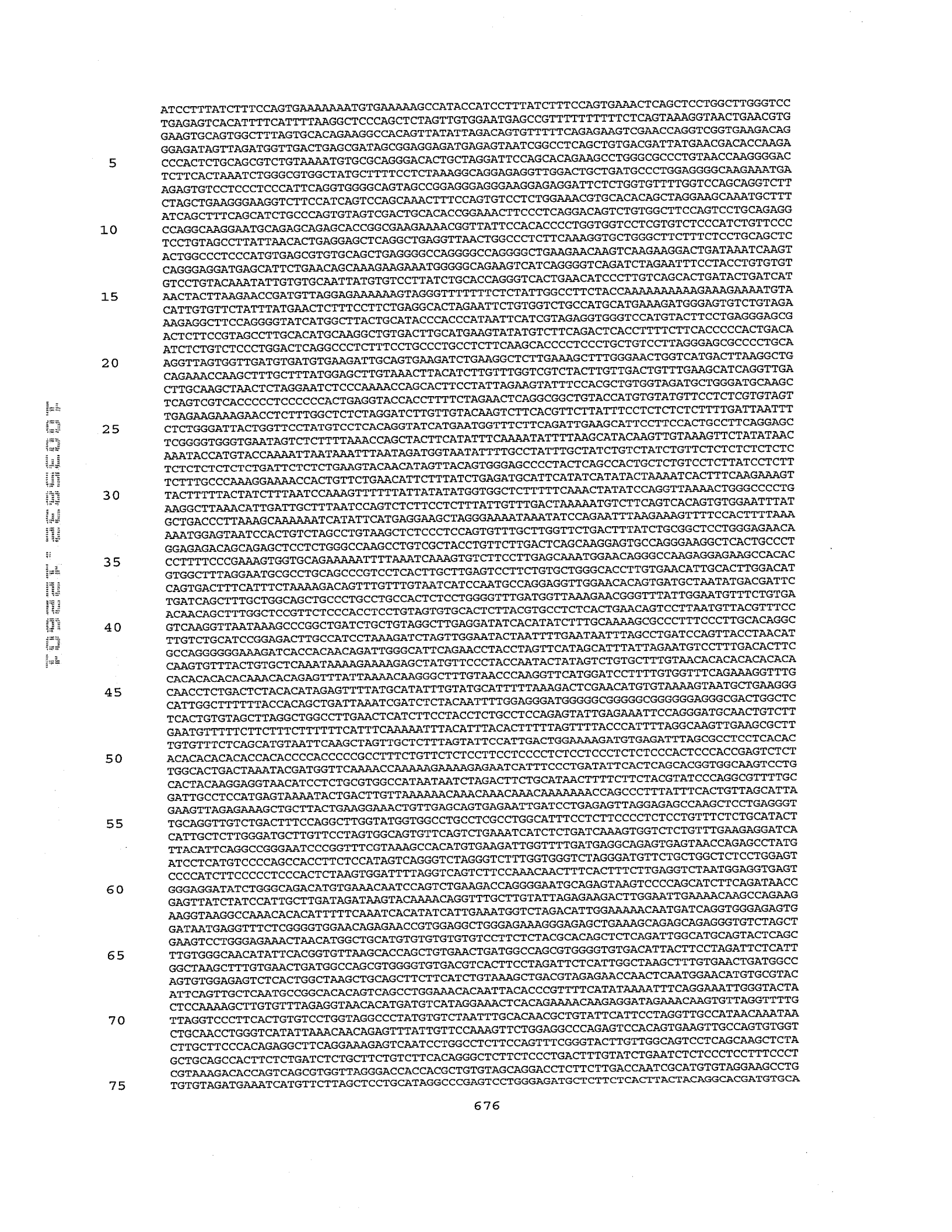


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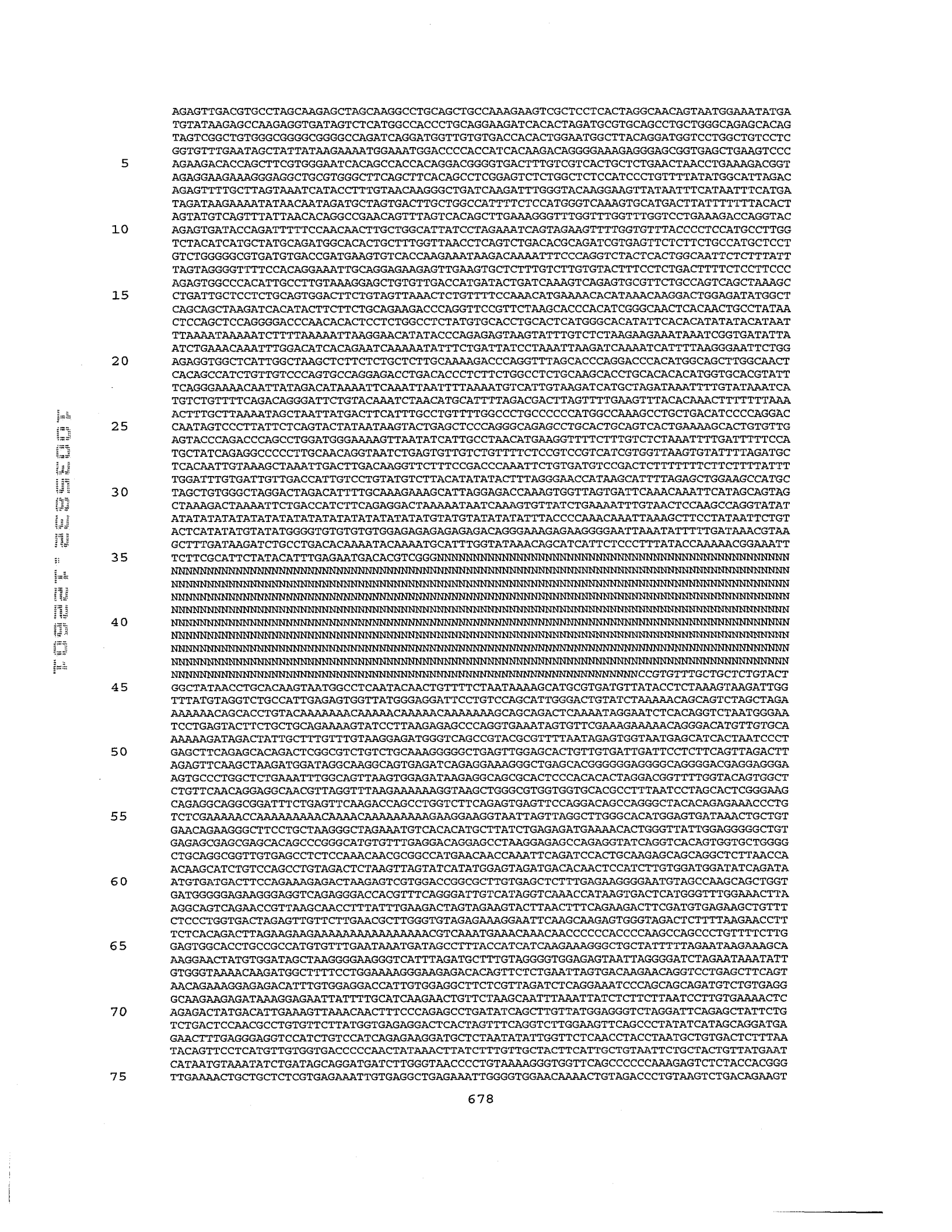


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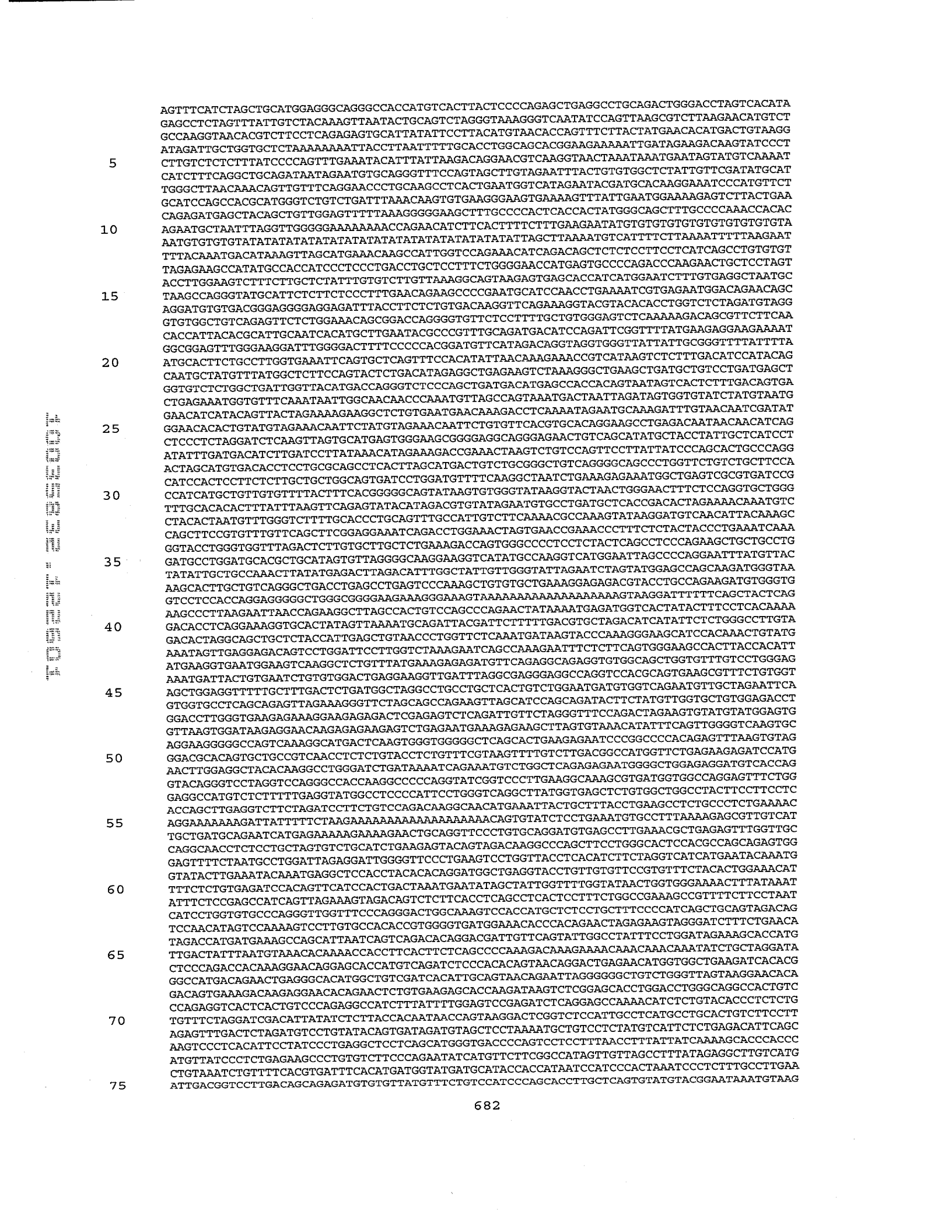


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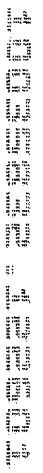
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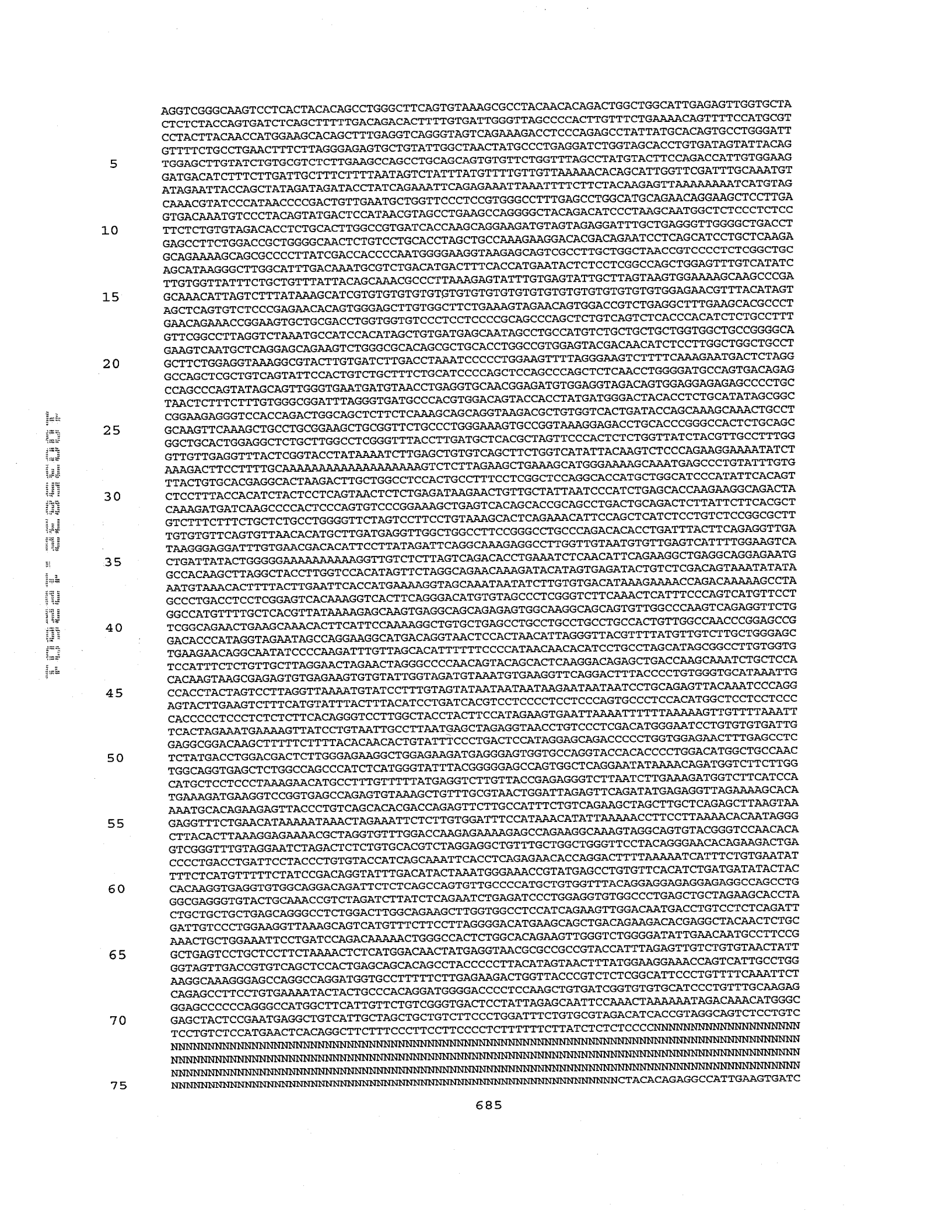
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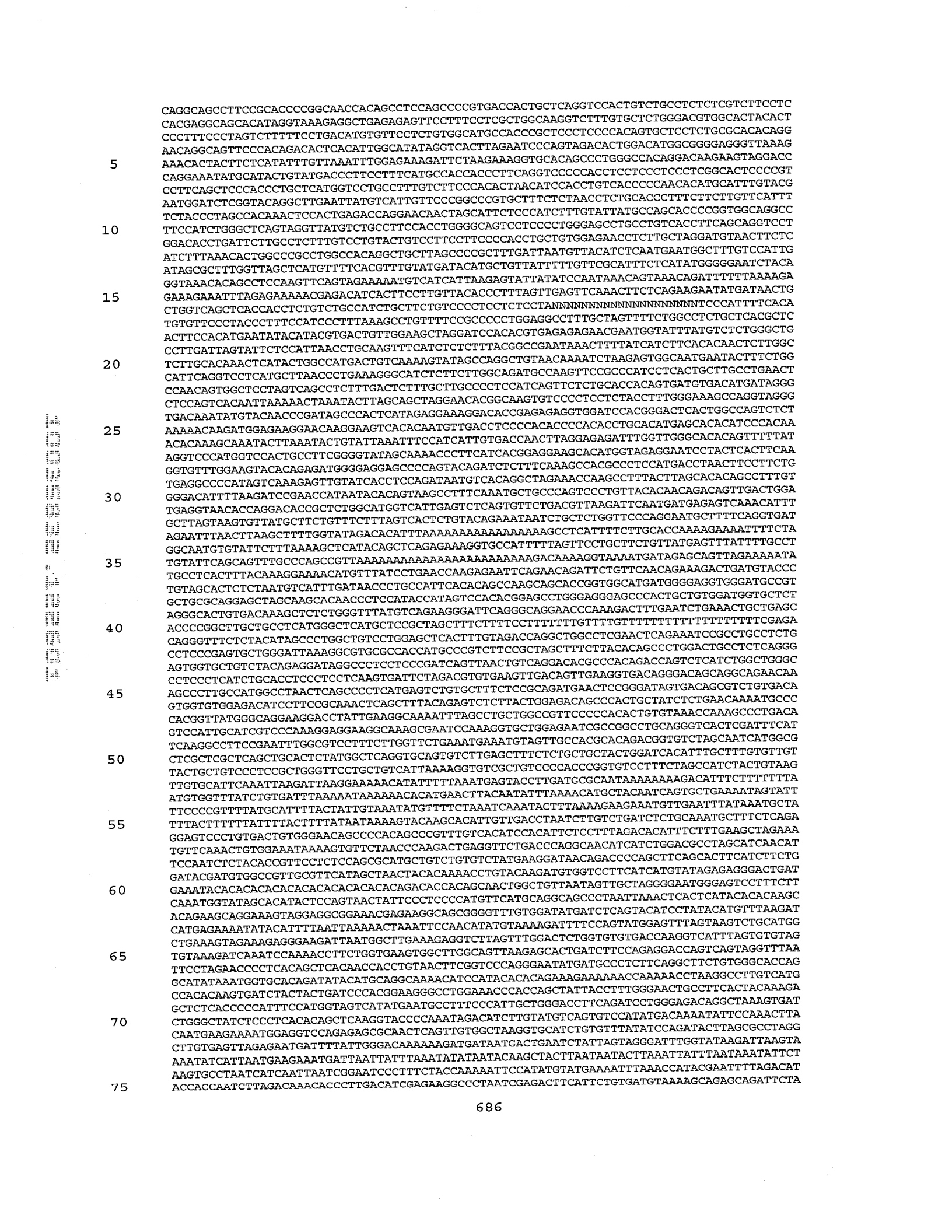


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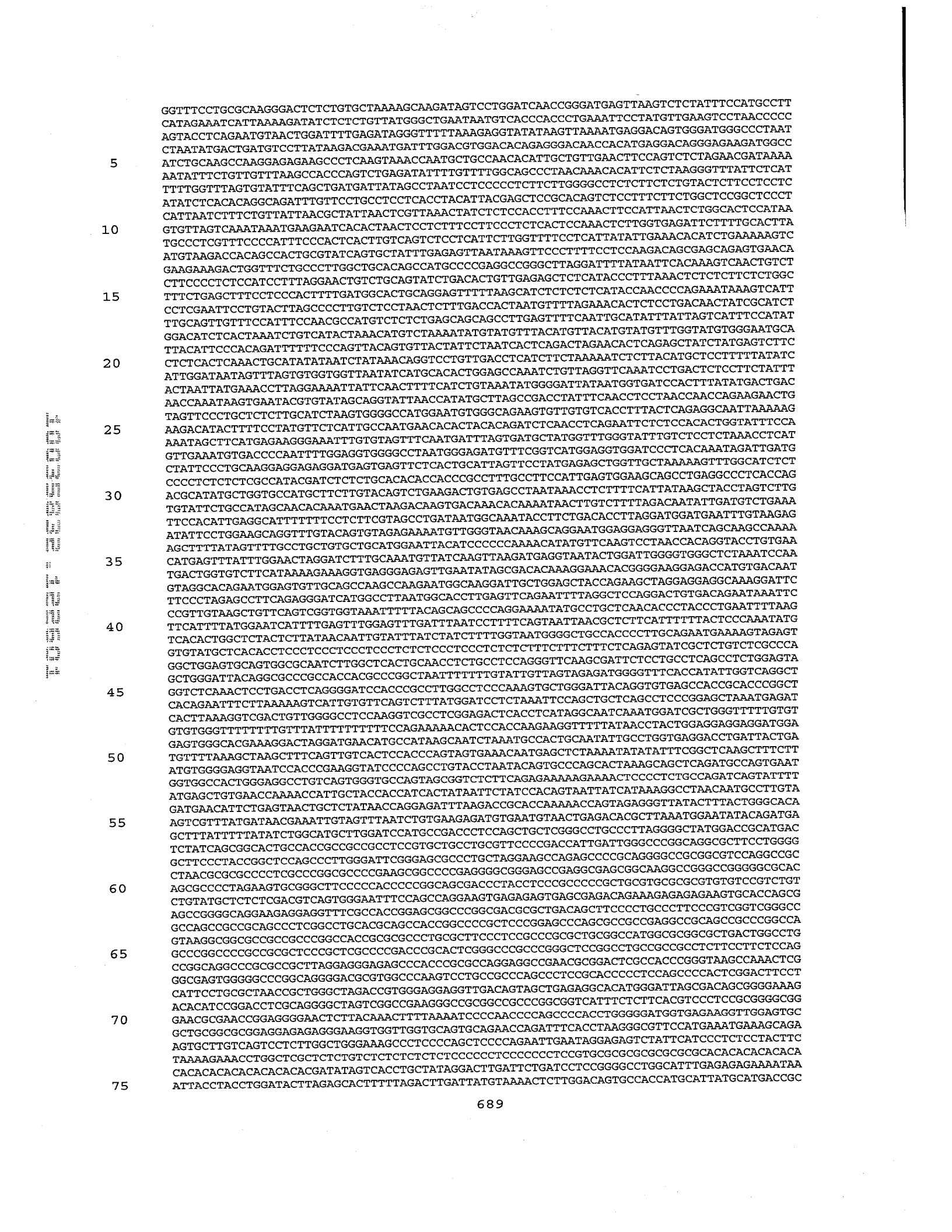
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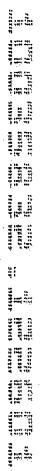
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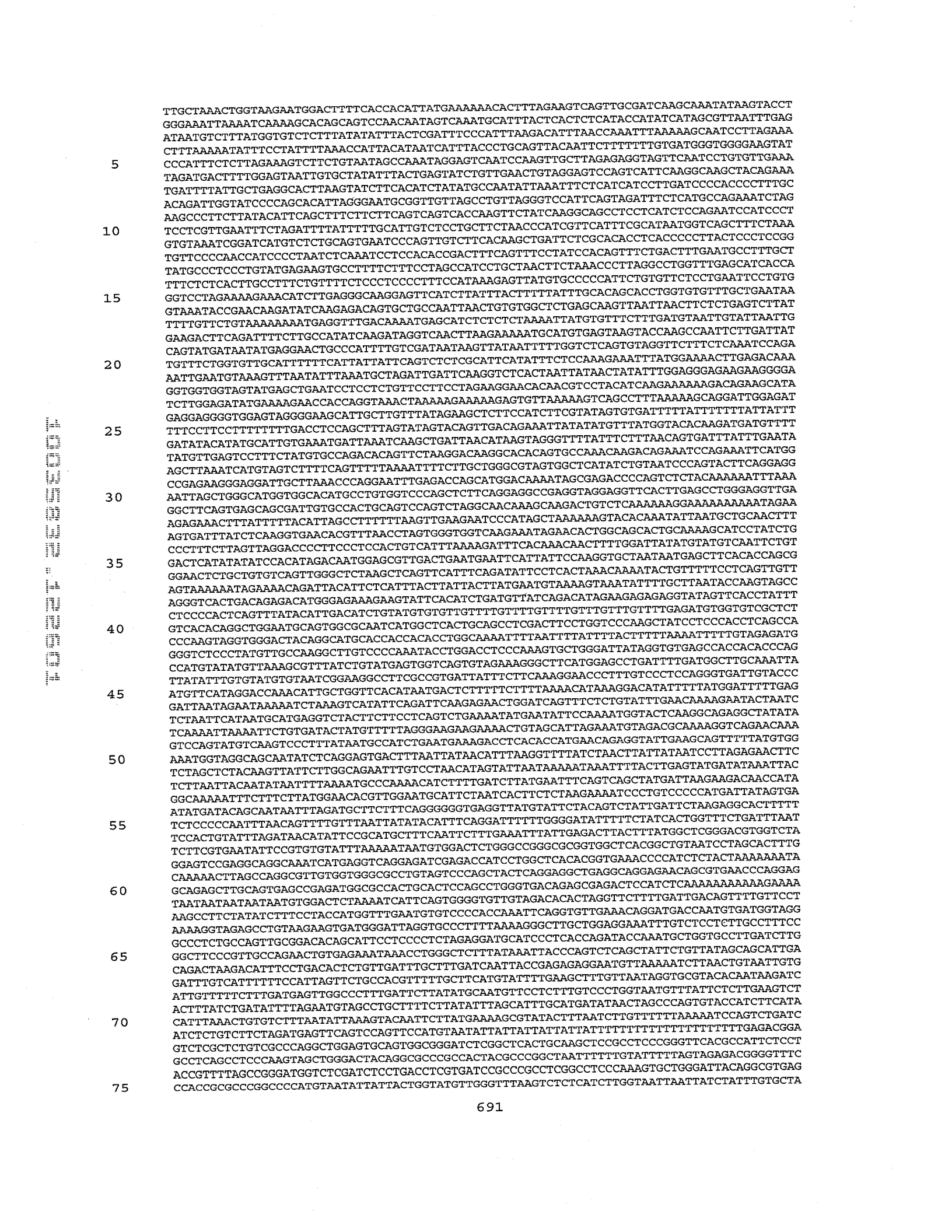
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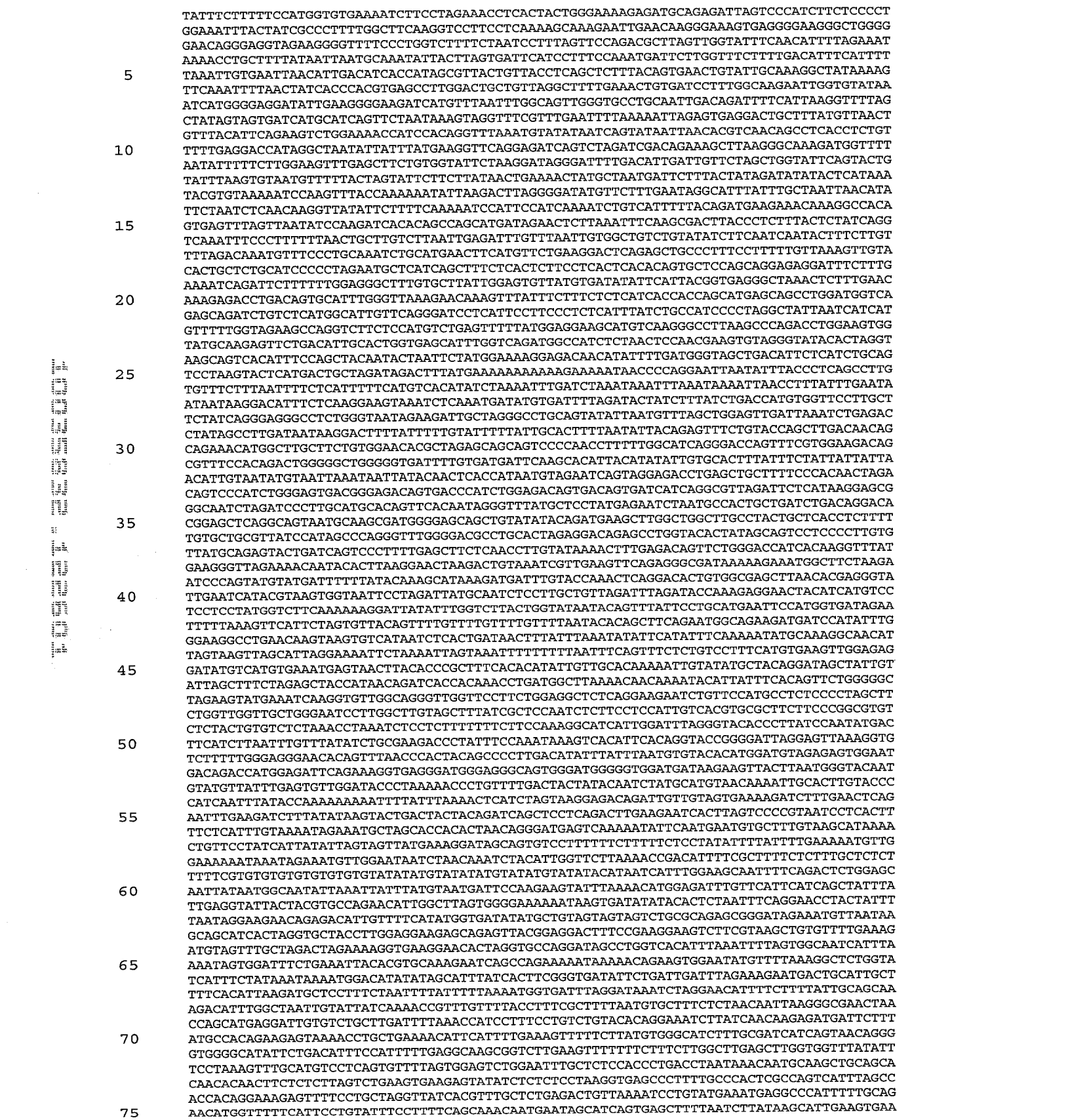


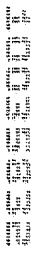
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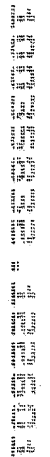
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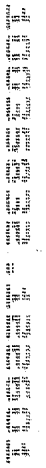




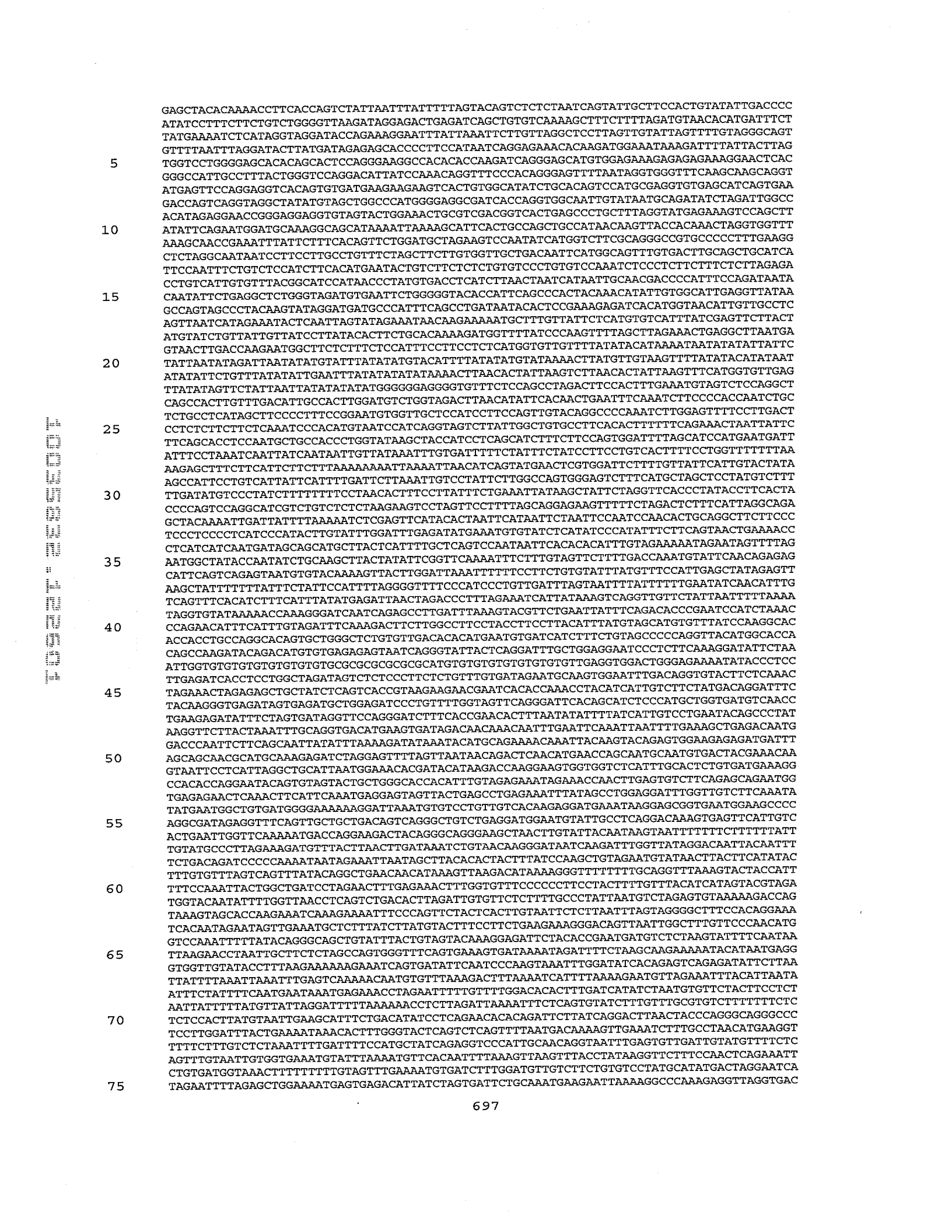
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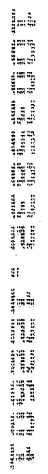
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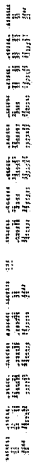
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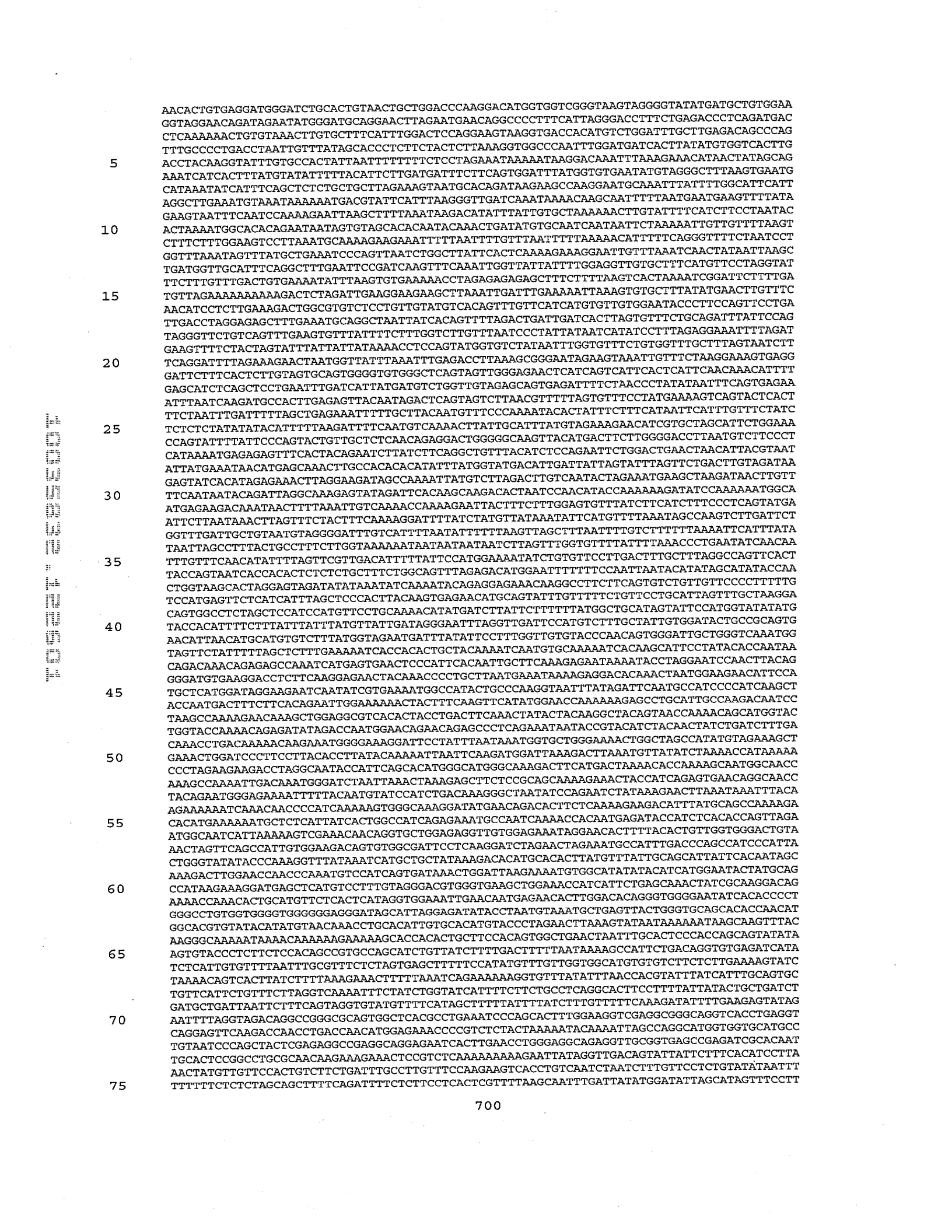
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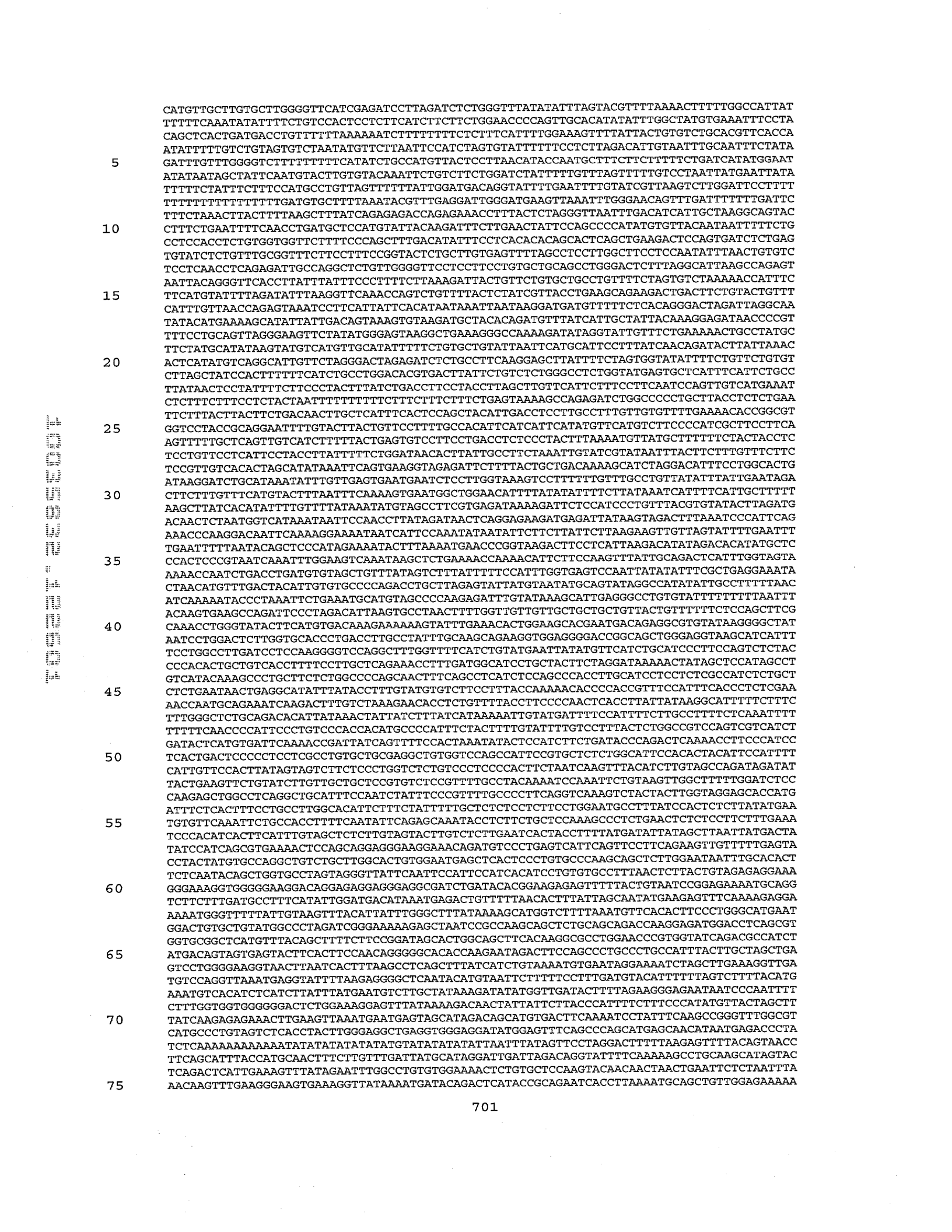
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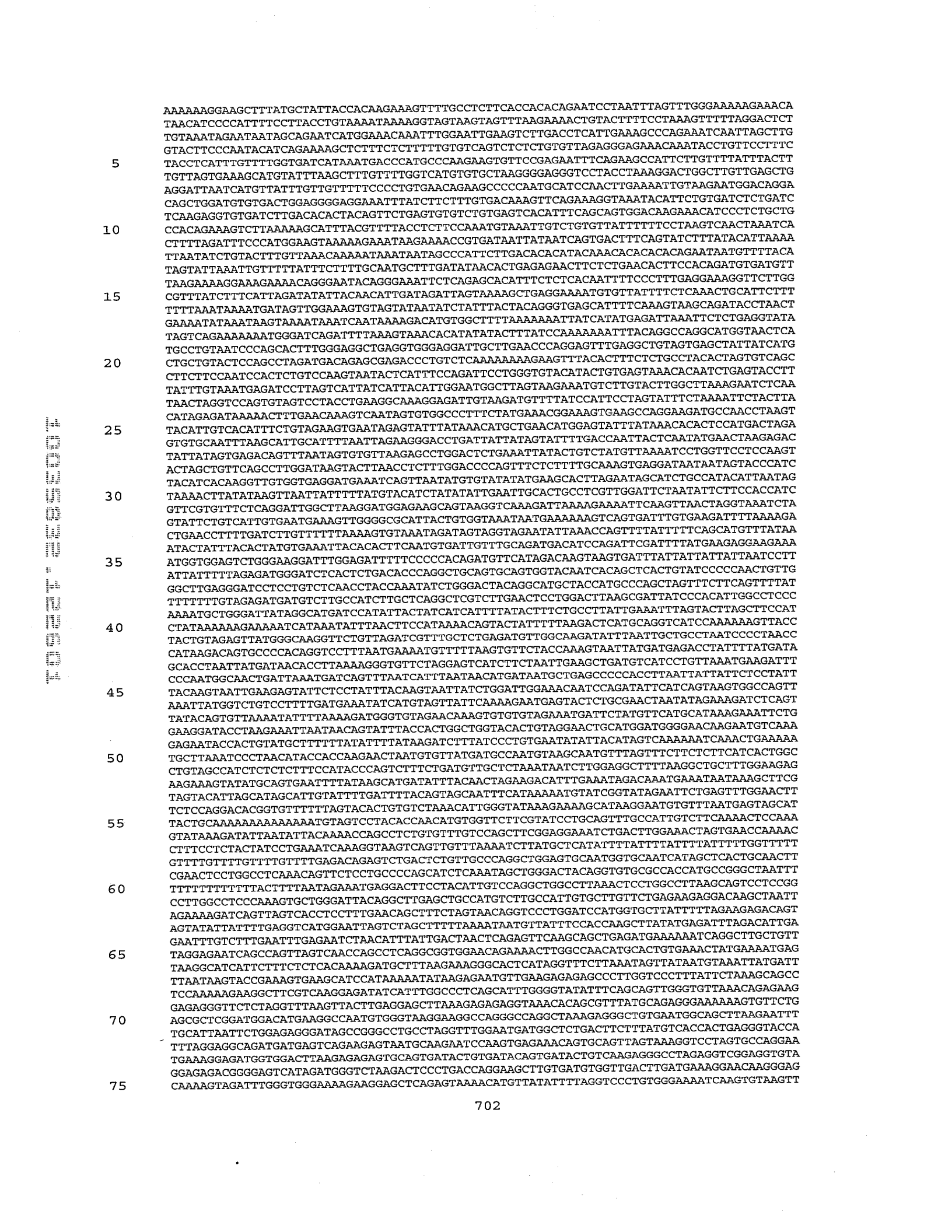
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 33

MOUSE NOMENCLATURE

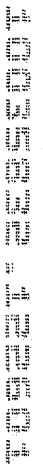
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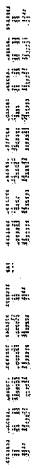
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MOUSE SEQUENCE - GENOMIC

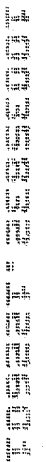
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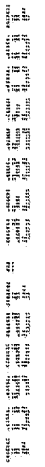
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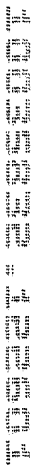
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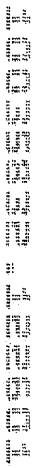


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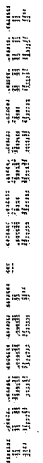


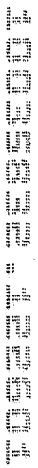
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MOUSE SEQUENCE - mRNA

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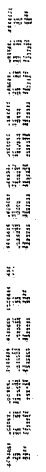
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MOUSE SEQUENCE - CODING
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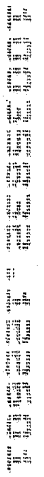
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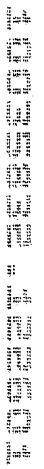
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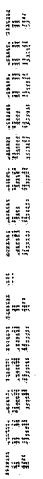
Application # 09/944,887 Filed: August 31, 2001

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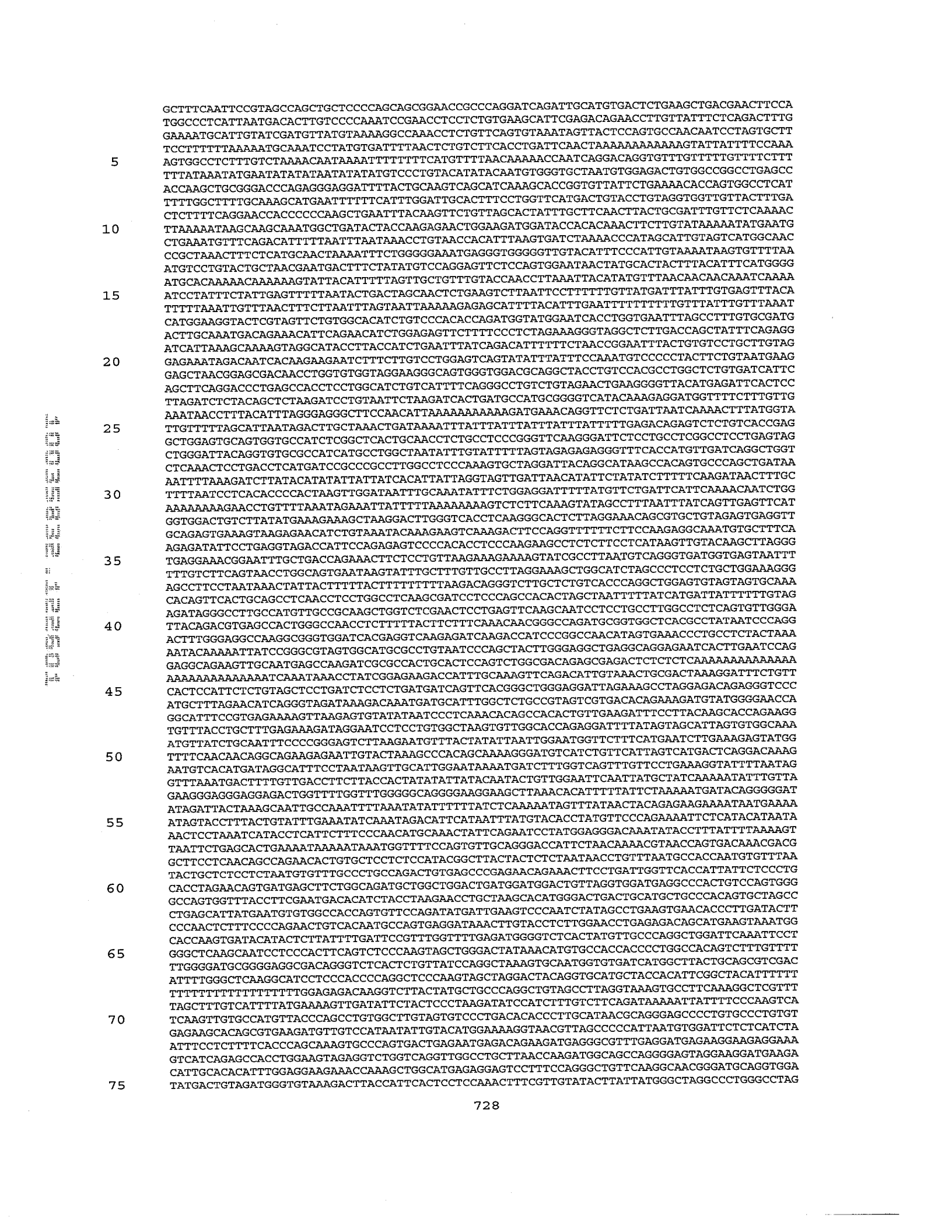
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 34

MOUSE NOMENCLATURE

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Celera	mCG15940

HUMAN NOMENCLATURE

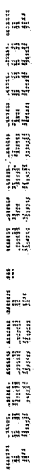
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MOUSE SEQUENCE - GENOMIC

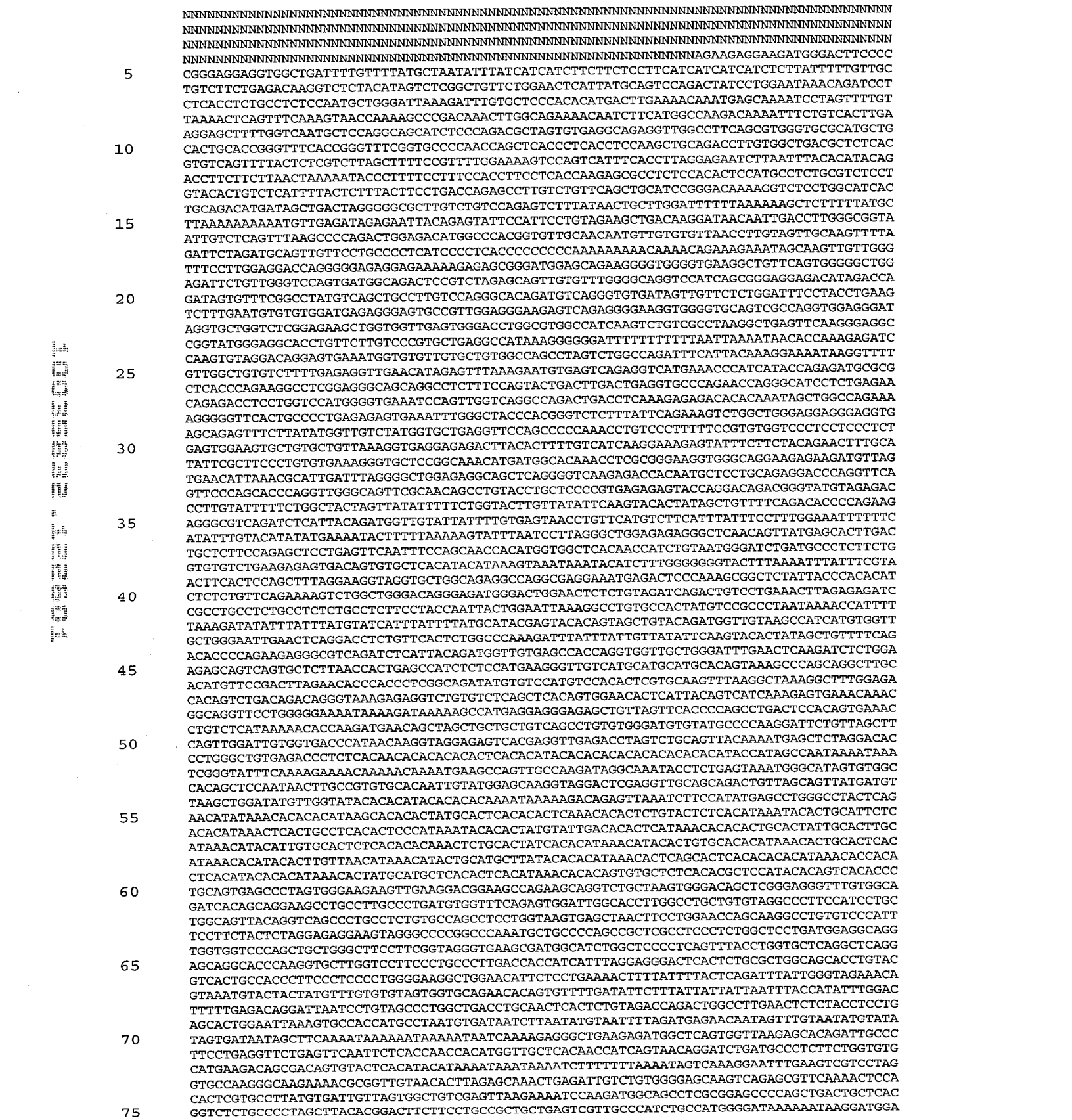
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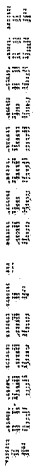
Replacement Sheet

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MOUSE SEQUENCE - mRNA

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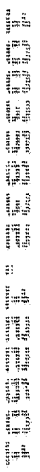
MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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HUMAN SEQUENCE - mRNA
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Table 35

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Celera	mCG12743

HUMAN NOMENCLATURE

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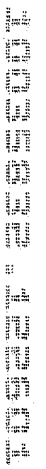
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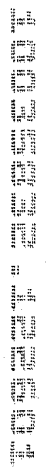
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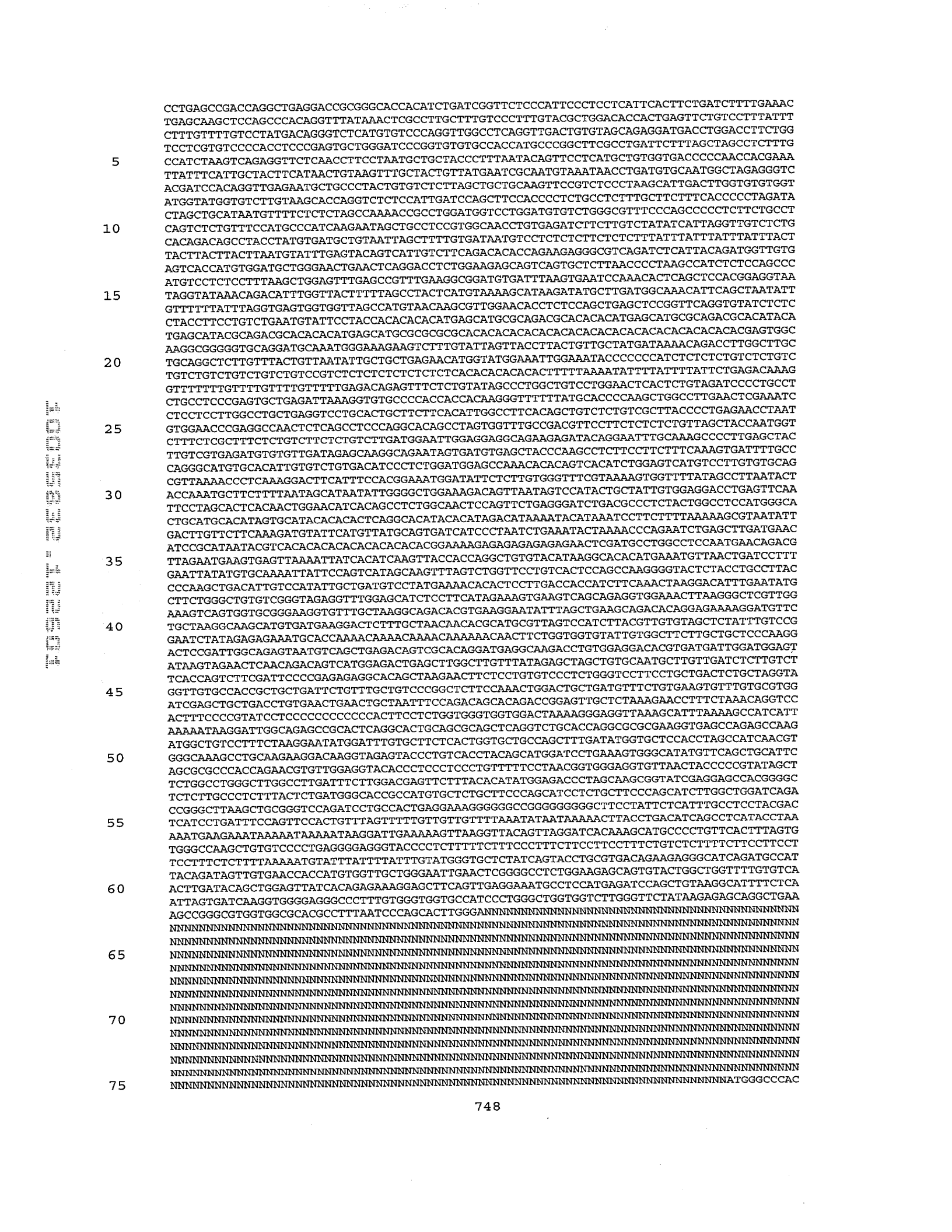


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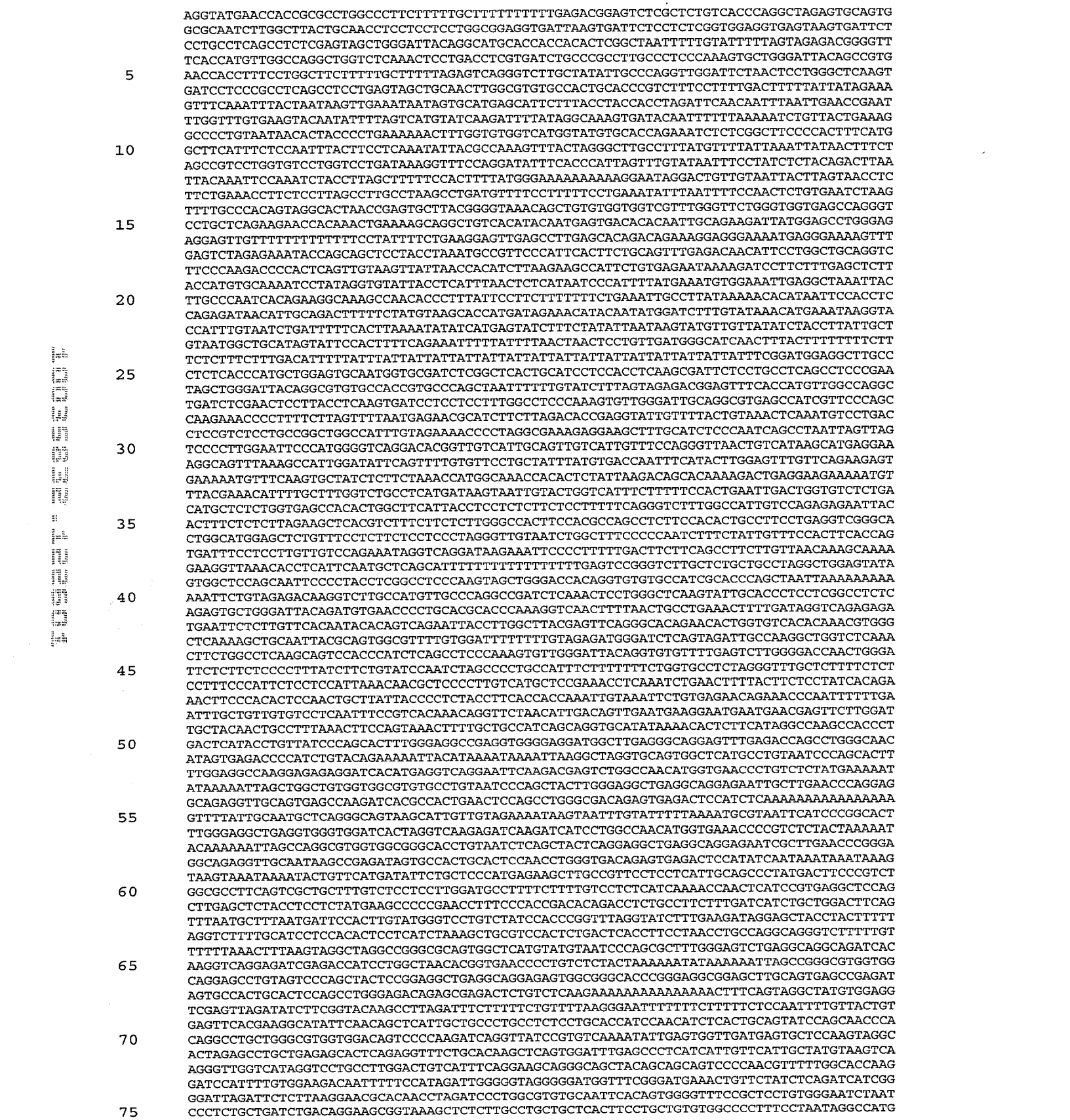
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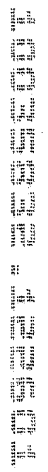
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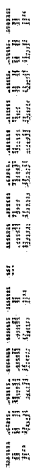
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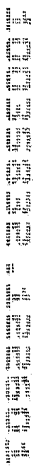




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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 36

MOUSE NOMENCLATURE

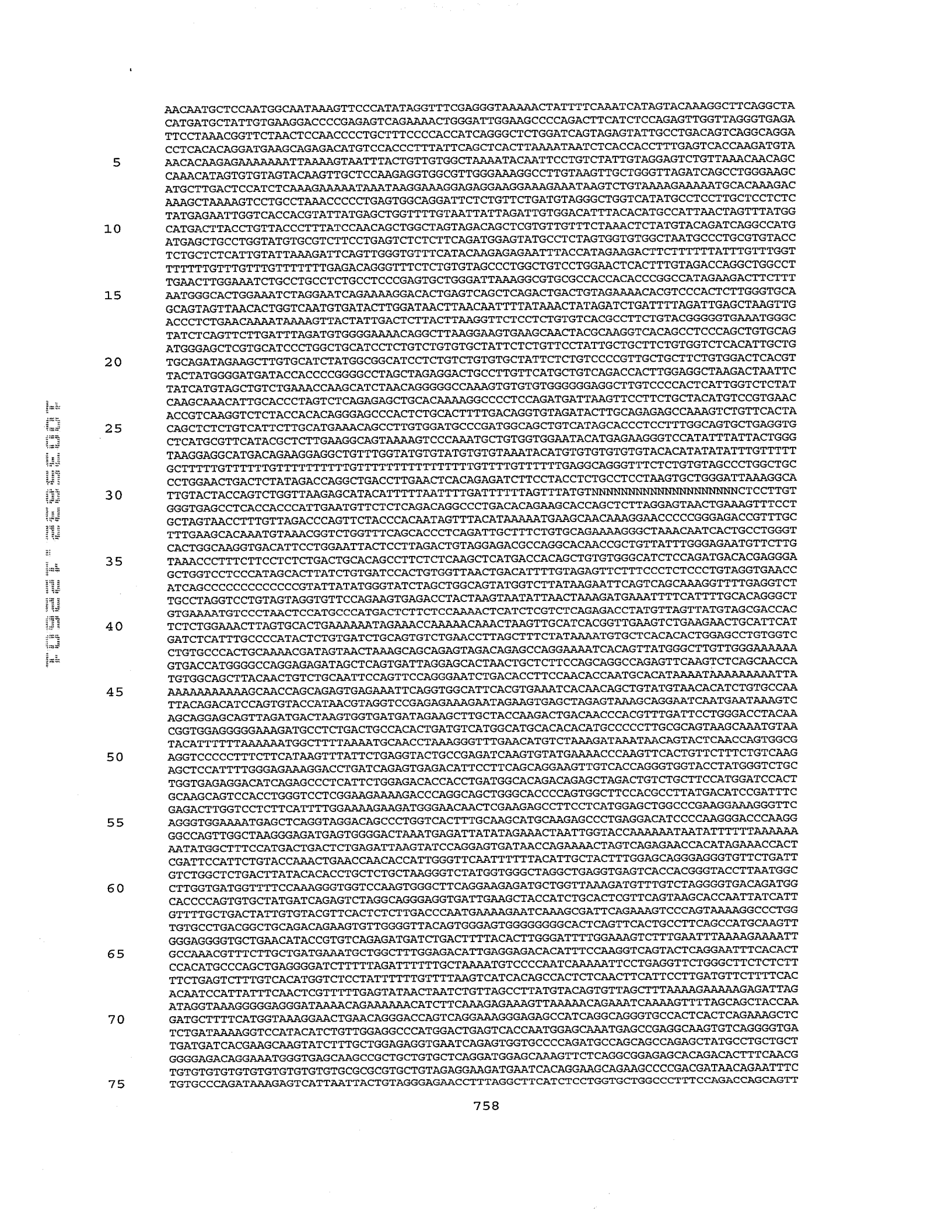
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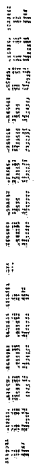
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MOUSE SEQUENCE - GENOMIC

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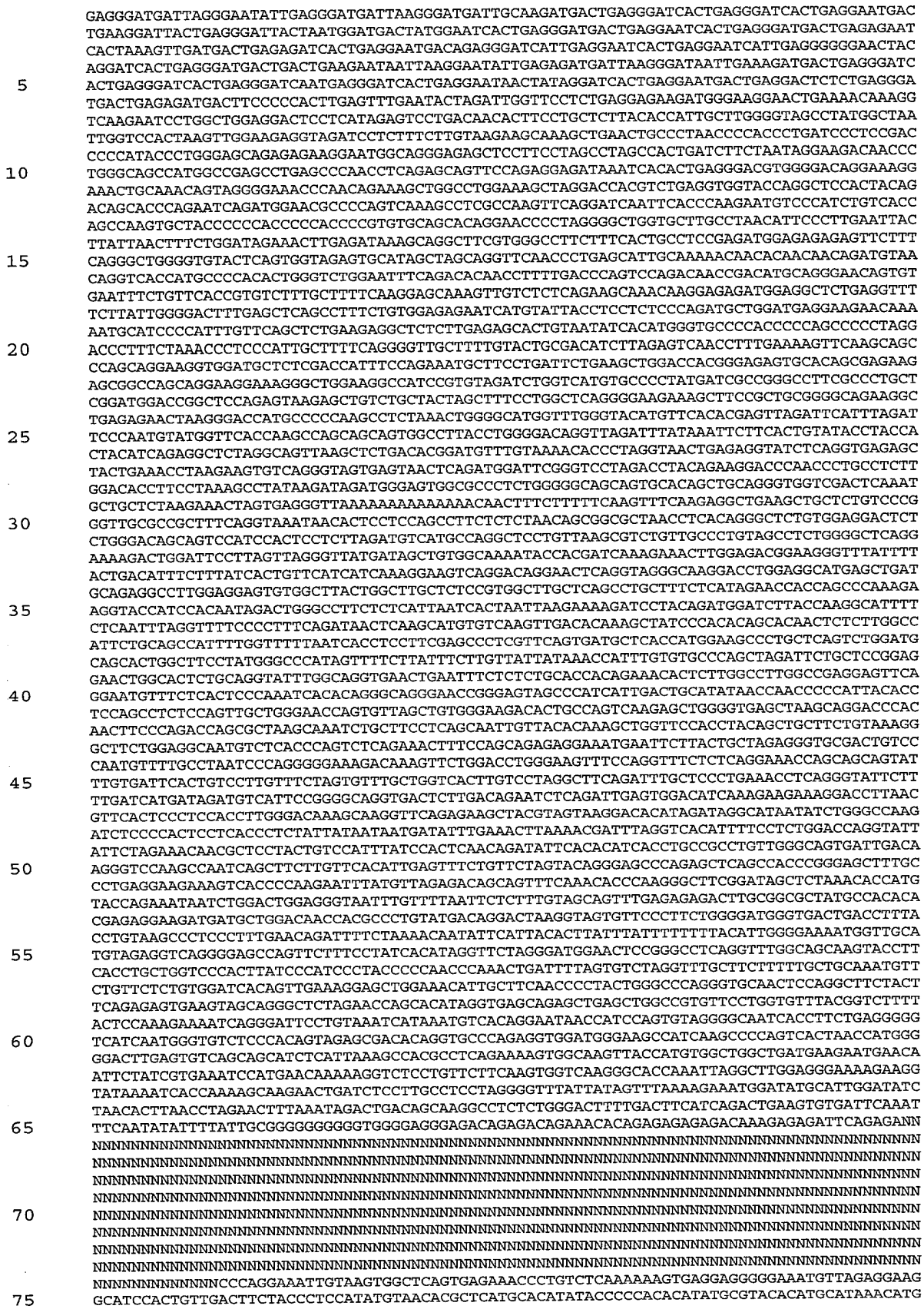
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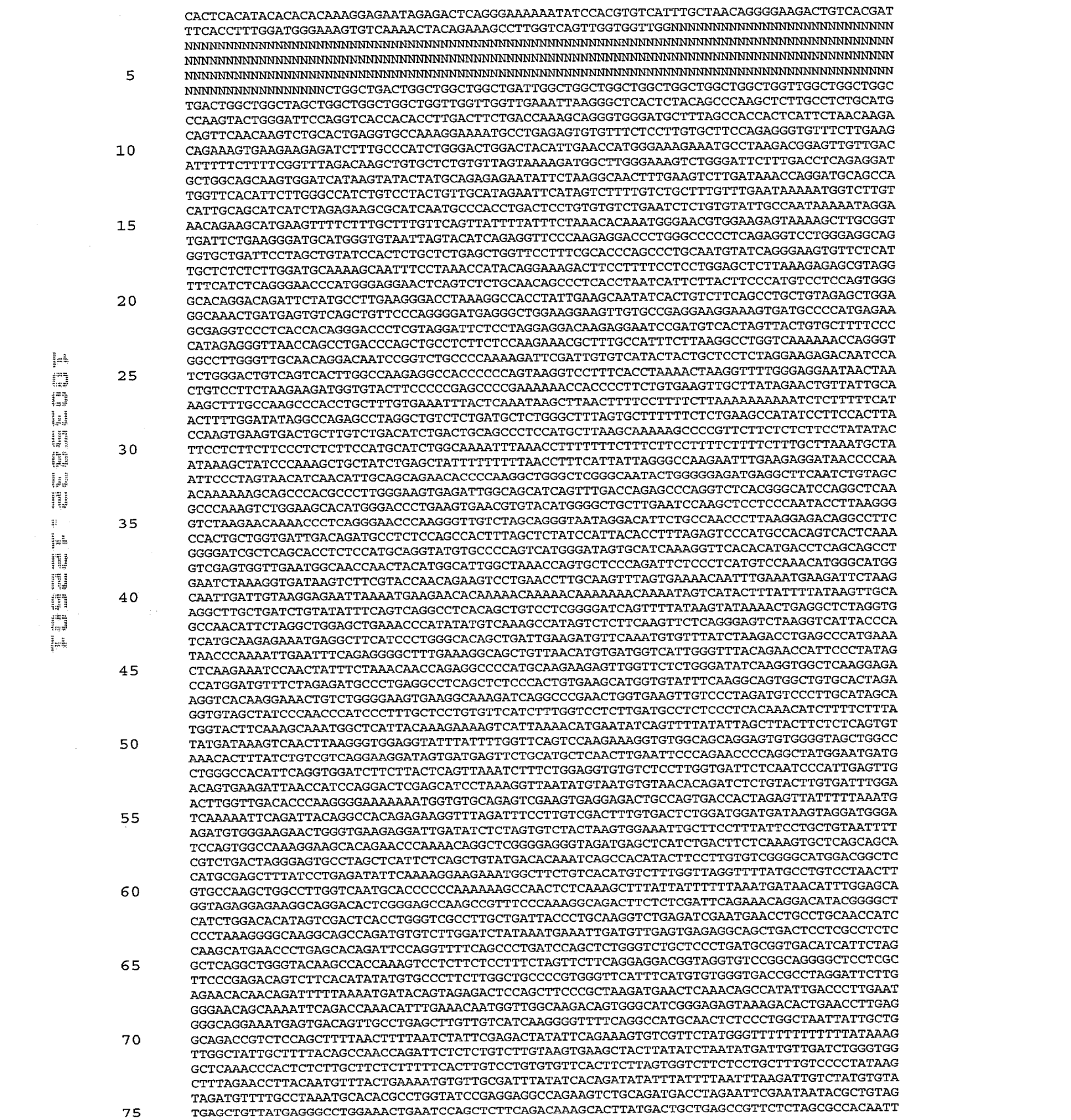


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MOUSE SEQUENCE - mRNA

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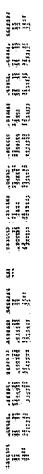
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MOUSE SEQUENCE - CODING

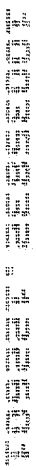
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HUMAN SEQUENCE - GENOMIC

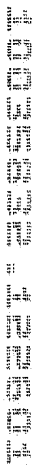
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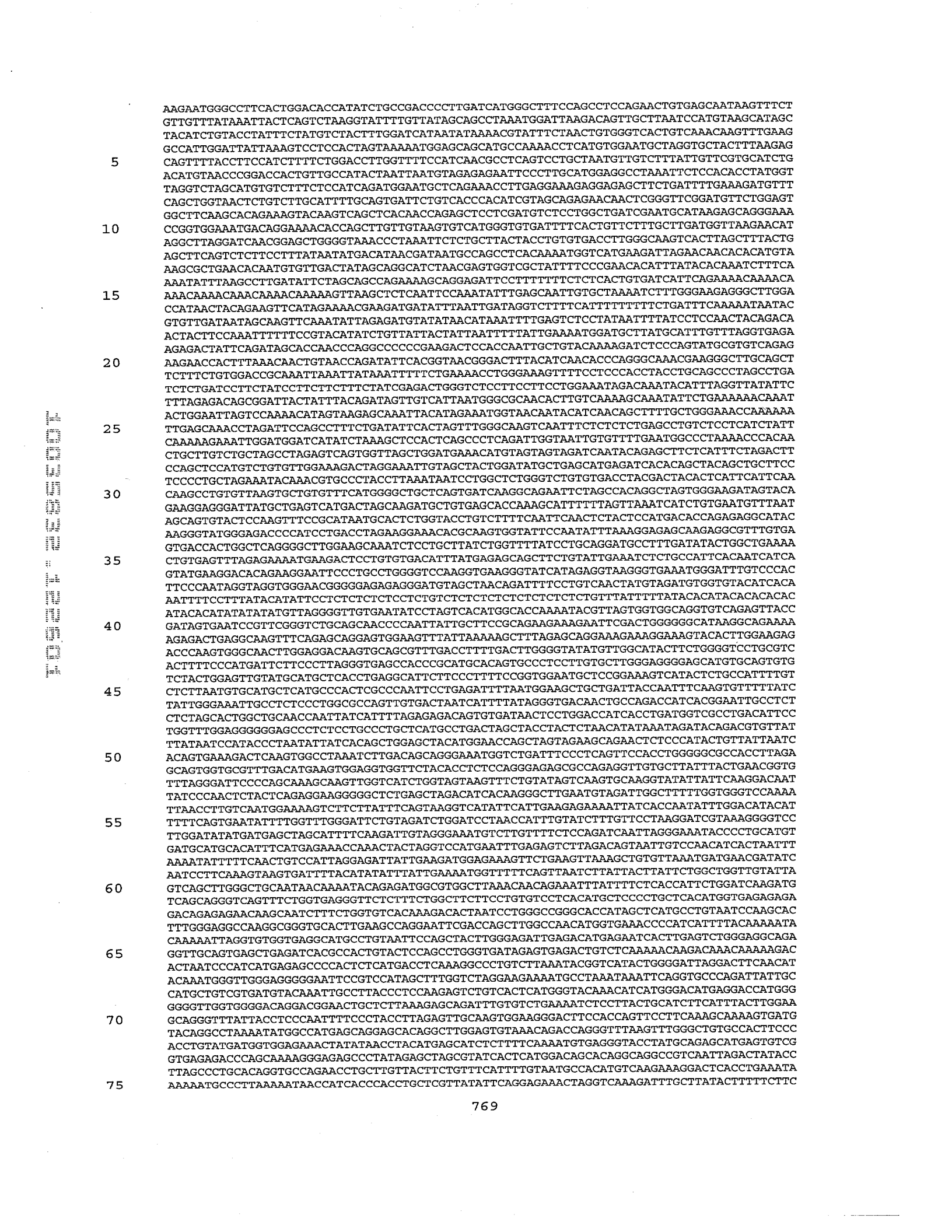
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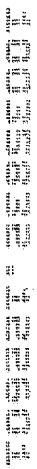
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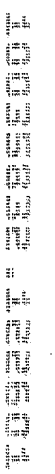
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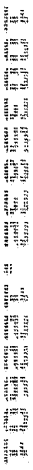
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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Table 37

MOUSE NOMENCLATURE

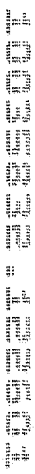
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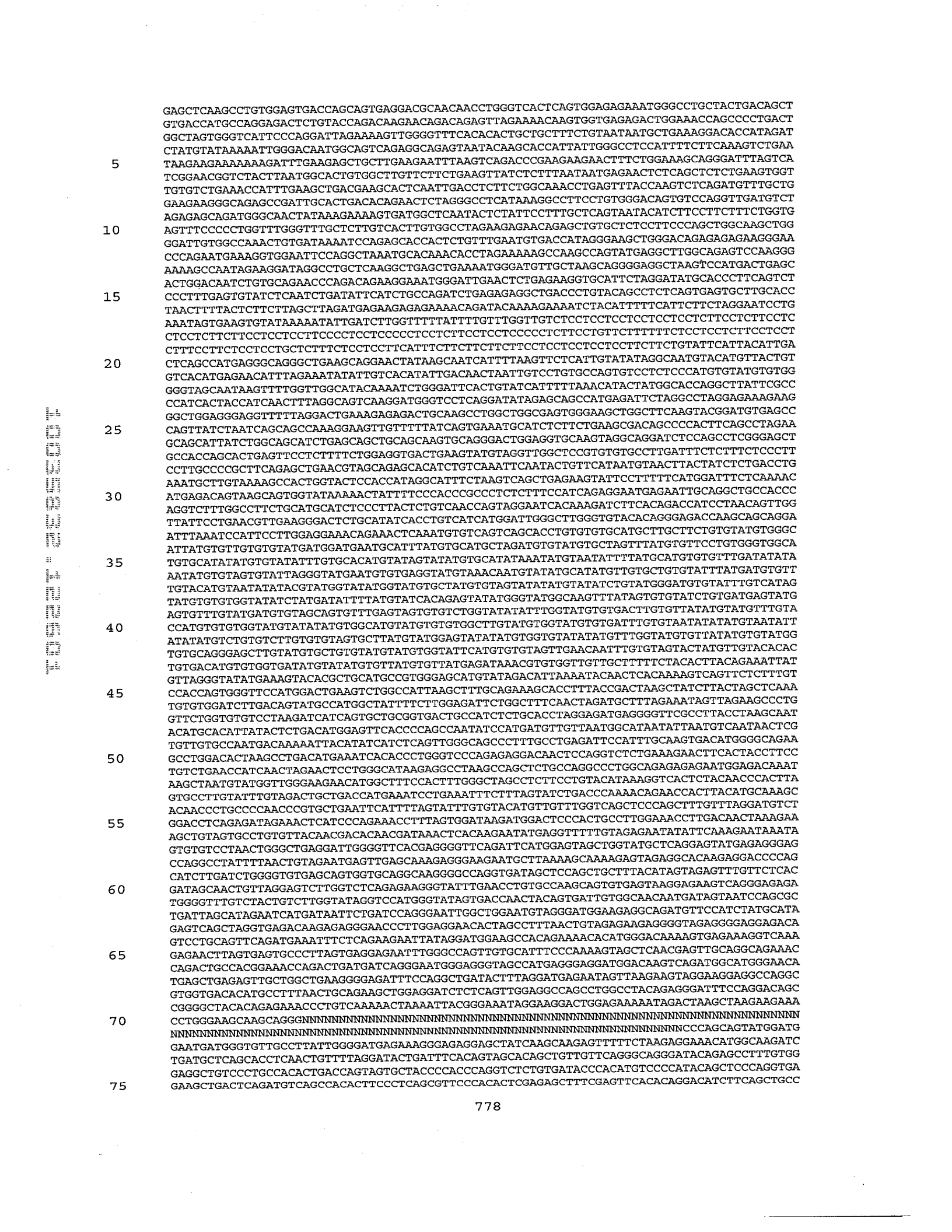
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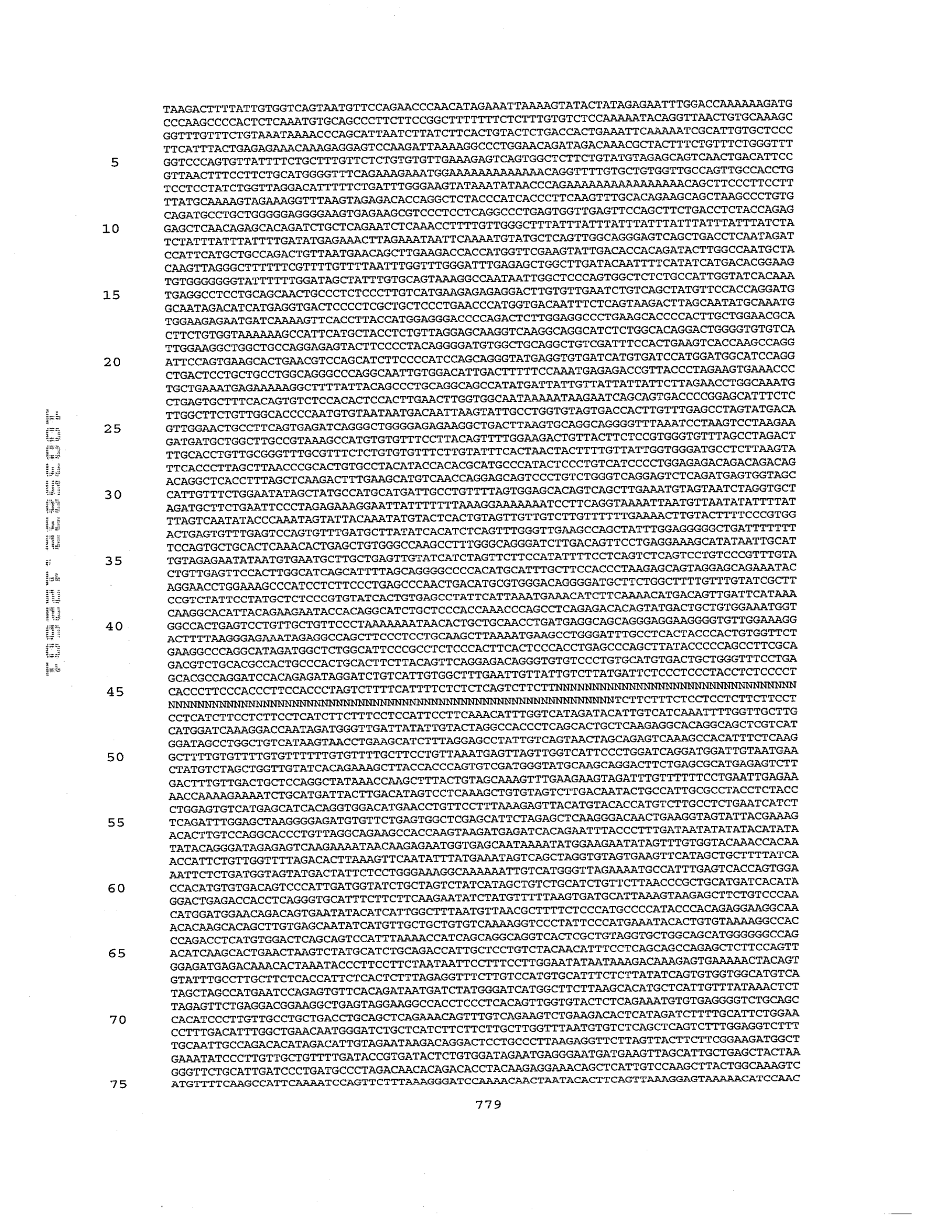
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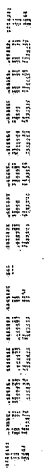


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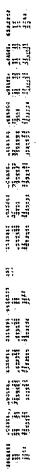
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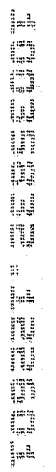
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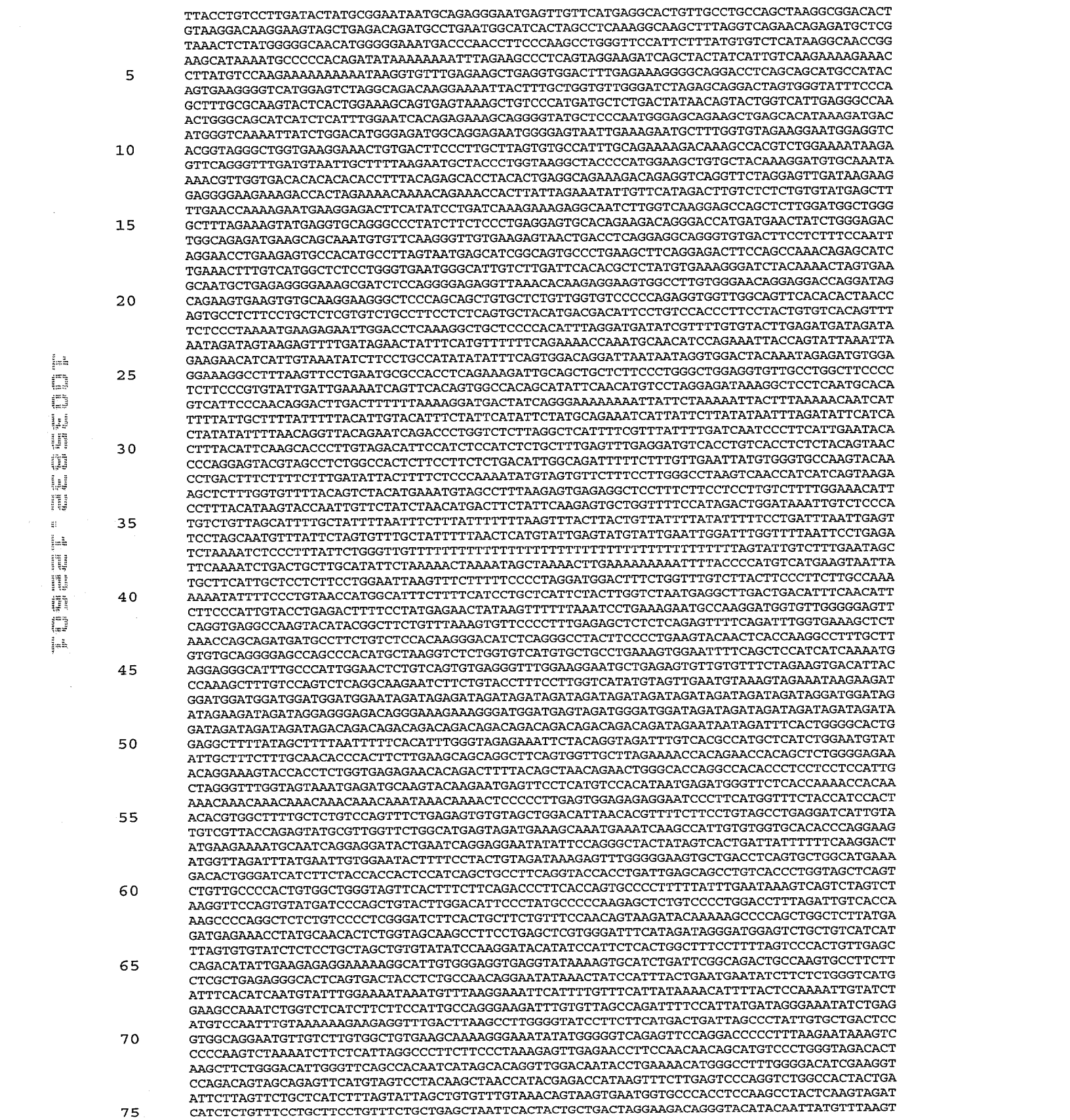
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MOUSE SEQUENCE - mRNA

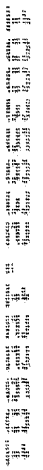
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MOUSE SEQUENCE - CODING
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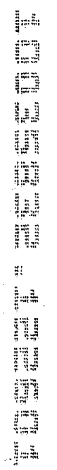
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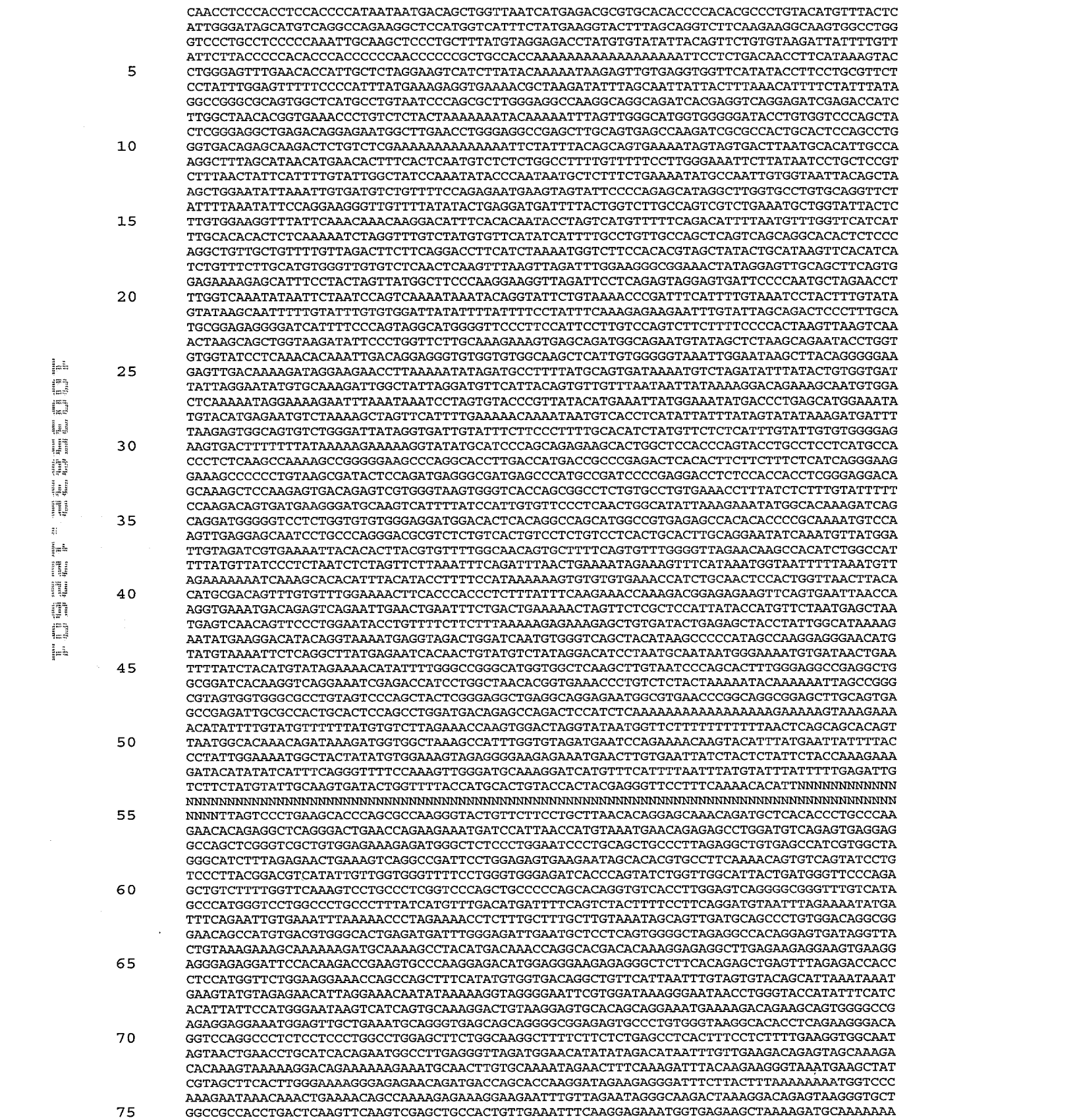


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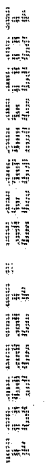


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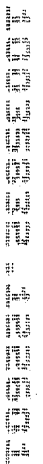
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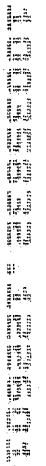


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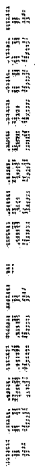
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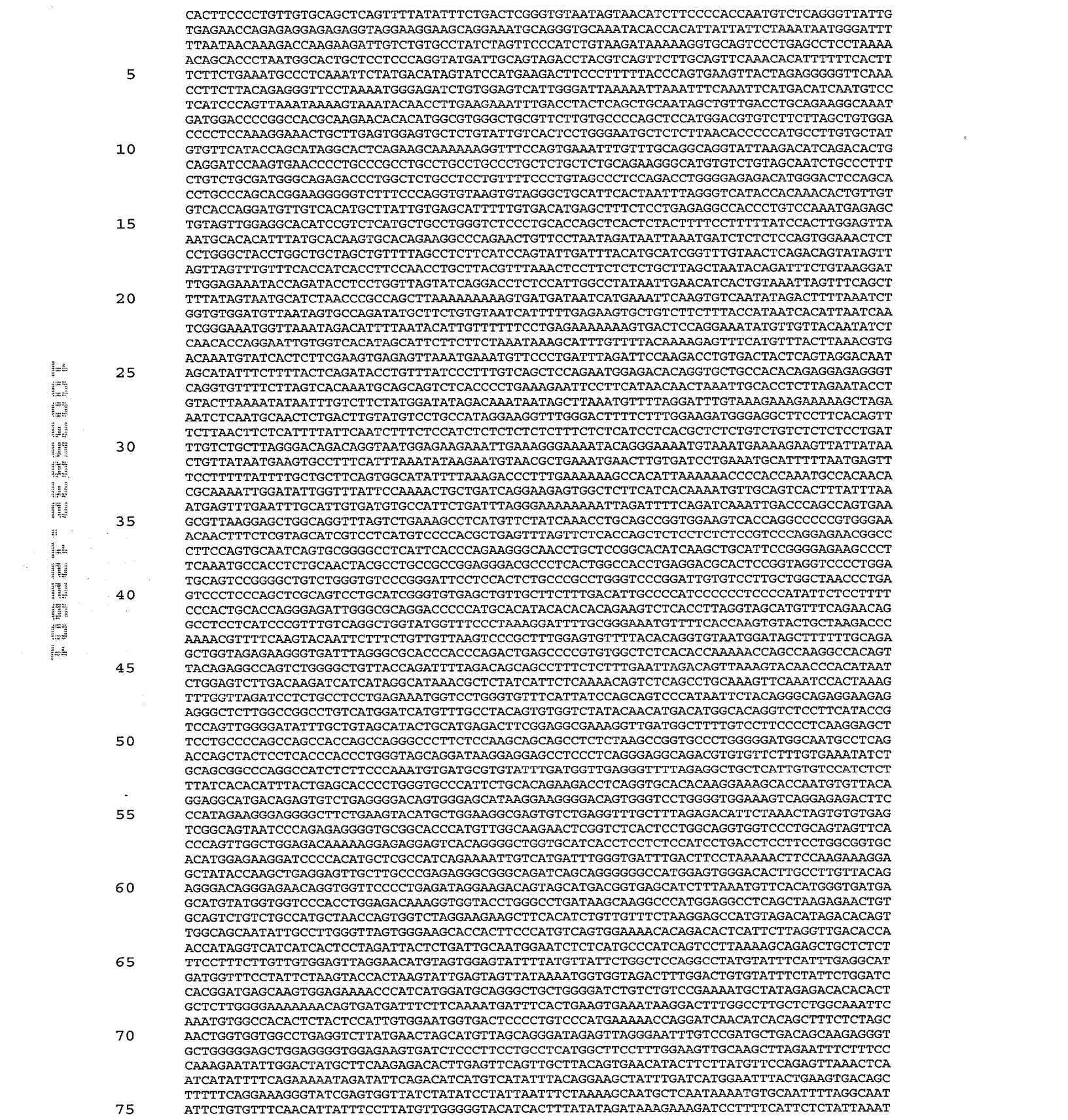
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HUMAN SEQUENCE - mRNA
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Attorney Docket No. 2008P

Table 38

MOUSE NOMENCLATURE

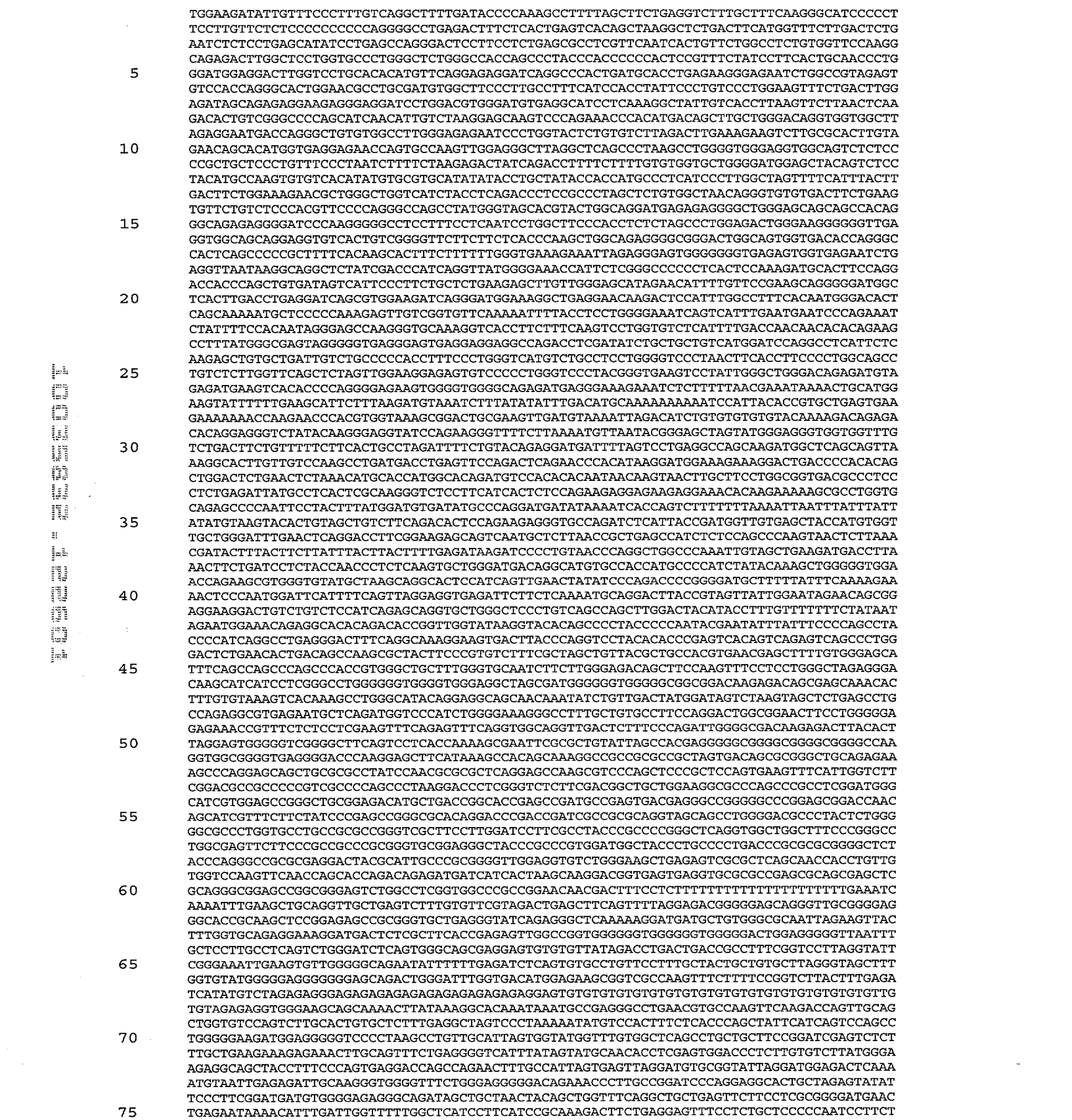
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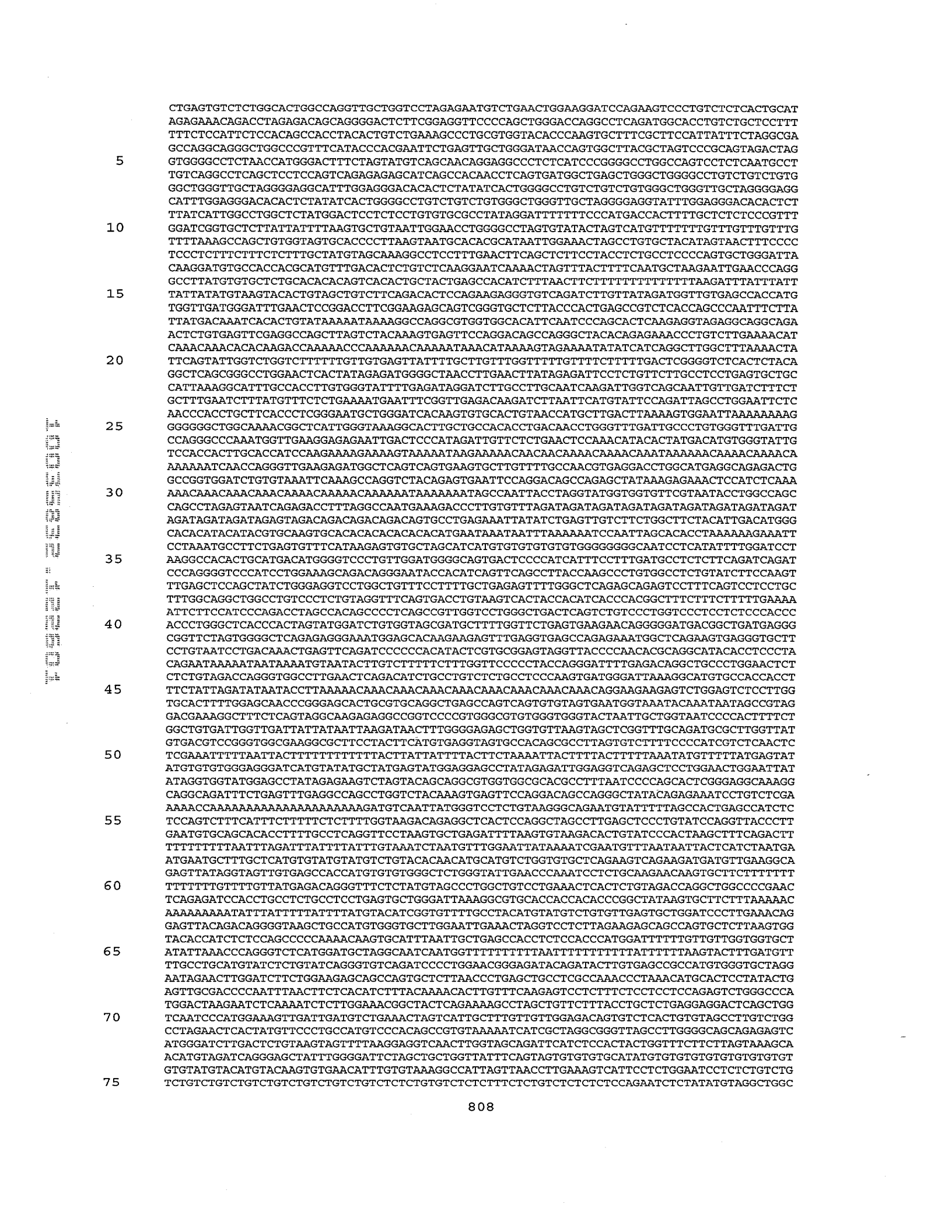
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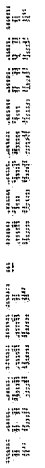
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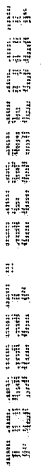




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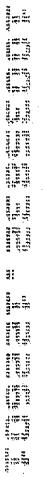
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MOUSE SEQUENCE - mRNA
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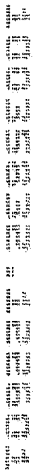
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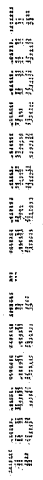
HUMAN SEQUENCE - GENOMIC
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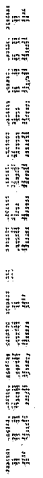
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TTTTTTCATTCATGTTTTTCTCCTCTCAACTTACTCATTTCAGTTCTTTCTTTTTTTAACCCCTAAAAATTAGACTCCTTTATTAT
TTTATTGAGACTATGCTTTGTCTGGACTTACCTTTATGTTACCATTCTTTTTGTTCATTTTCCCTTTTTTGCATTTCTCTTTTTTG

GGGGATCATTTACCTATATCTTTAAATCCTTTATAAGTTCTTTTAGAGAAGTTCTCTTTGTAAACTTCCCCTGGGCTTGTTTCTTA
TAAATGTTATCATTTTCCCTATTGGTATTGAGTGATTGTTTTGCTGAATACACAATTTTGGGTGAATAGTATTTTATTTATTTATT
TTTTTTTTTTTTTGAGGTGAAGTCGTACTCATTGTGTCACCCAGGTTGAAGTGCAGTGGCACGATCTCGGCTCACTGCAACCTCTG
CCTCCCAGGTTCAAGTGATTCTCCTGACTCAGCCTCCTGAGTAGCTGGGATTACAGGCATCCACCACCATGTCTGGCTAATTTTTT
TTATTTTTTTTTTTTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCCGACCTCAAGTGATCTGCT
CGCCTTGGCCTCCTGAAGTGCTGGGATTACAGGCATGAGCCACTGCACCCAGCCTTTTCTTATCATTTTATATGAGTAATTCCACT
GTCTTCTGGCTTCATTGTTGTGAGATCTGCTGCTATTCTAATTATCATTCTTTGTTAGGTCTTCTGTGTTTTTTCTCTGCTTTCCA
GATCTTCTATTTATATTCATGCCCTAAAGATTCACTACGATGTGAGAAGGCATGATTTTATTTTTCCTTATCCTATTTGGGATACA
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ATGGCAAGAGTTATAAACAGCT

HUMAN SEQUENCE - mRNA

CGGCCCGCTGGAGAGGAAGCCCGAGAGCTGCCGCGCGCCTGCCGGACGAGGGCGTAGAAGCCAGGCGTCAGAGCCCGGGCTCCGGT
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CGTGGTCTTGGTGGACCAGCACCACTGGCGGTACCAGAGCGGCAAGTGGGTGCAGTGTGGAAAGGCCGAGGGCAGCATGCCAGGAA
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AAAAAAAAA

HUMAN SEQUENCE - CODING
ATGGGCATCGTGGAGCCGGGTTGCGGAGACATGCTGACGGGCACCGAGCCGATGCCGGGGAGCGACGAGGGCCGGGCGCCTGGCGC
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Table 39

MOUSE NOMENCLATURE

ICSGNM	Stat5b
Celera	mCG20224

HUMAN NOMENCLATURE

HGNC	STAT5B
Celera	hCG16577

MOUSE SEQUENCE - GENOMIC

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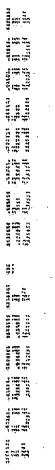
MOUSE SEQUENCE - mRNA

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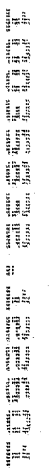
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MOUSE SEQUENCE - CODING
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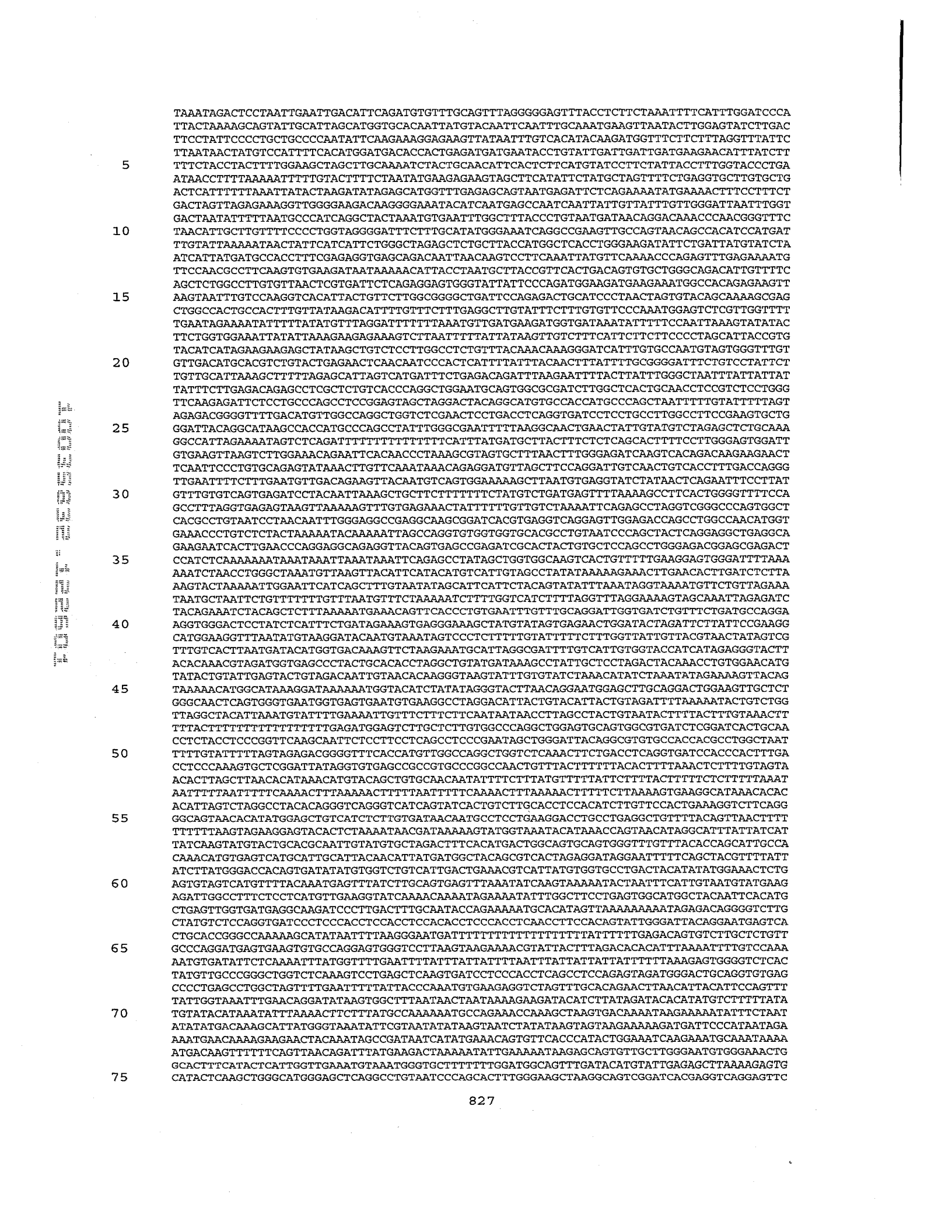
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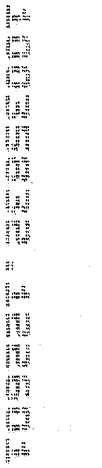
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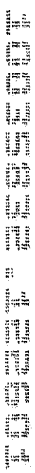


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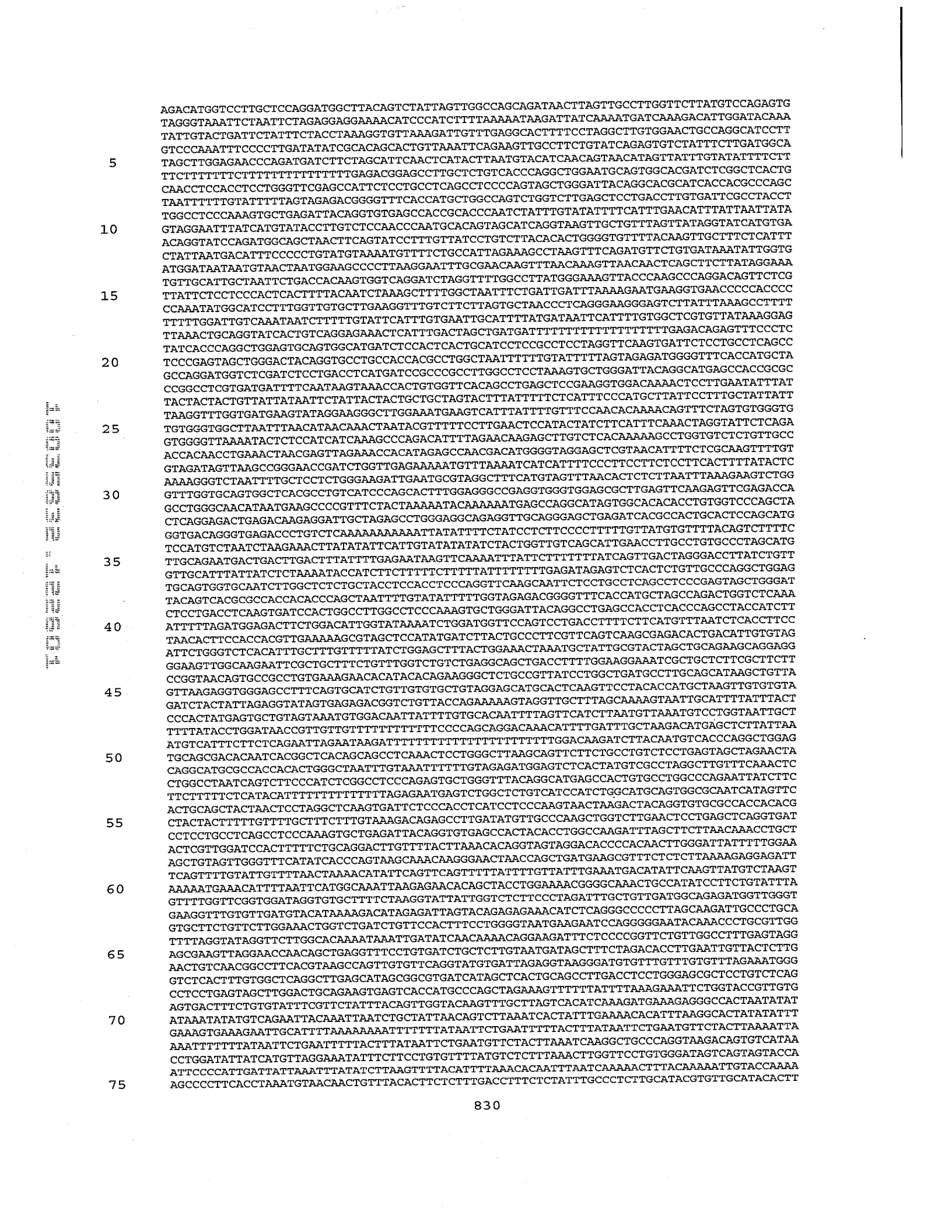


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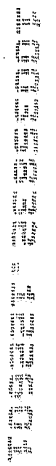
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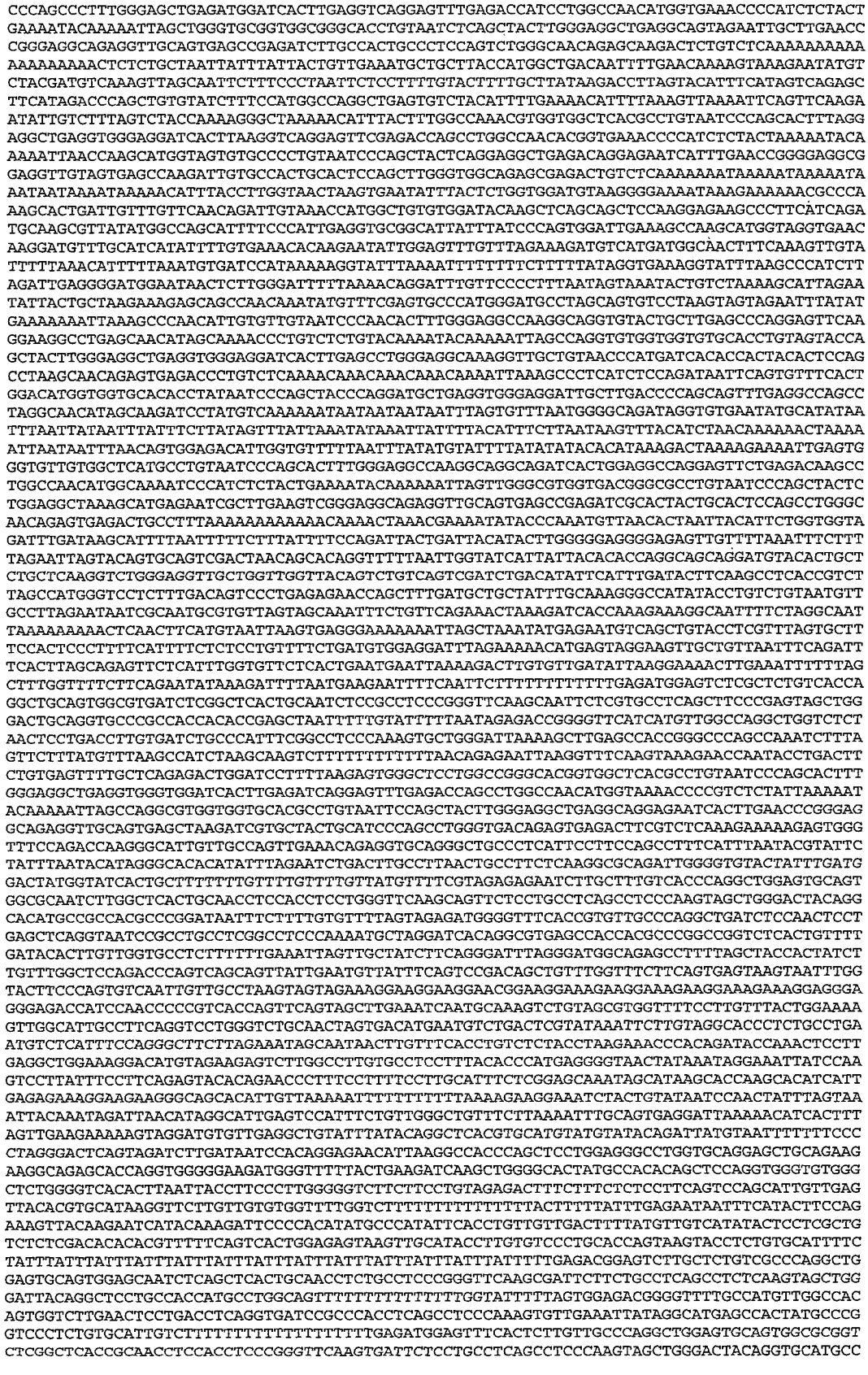
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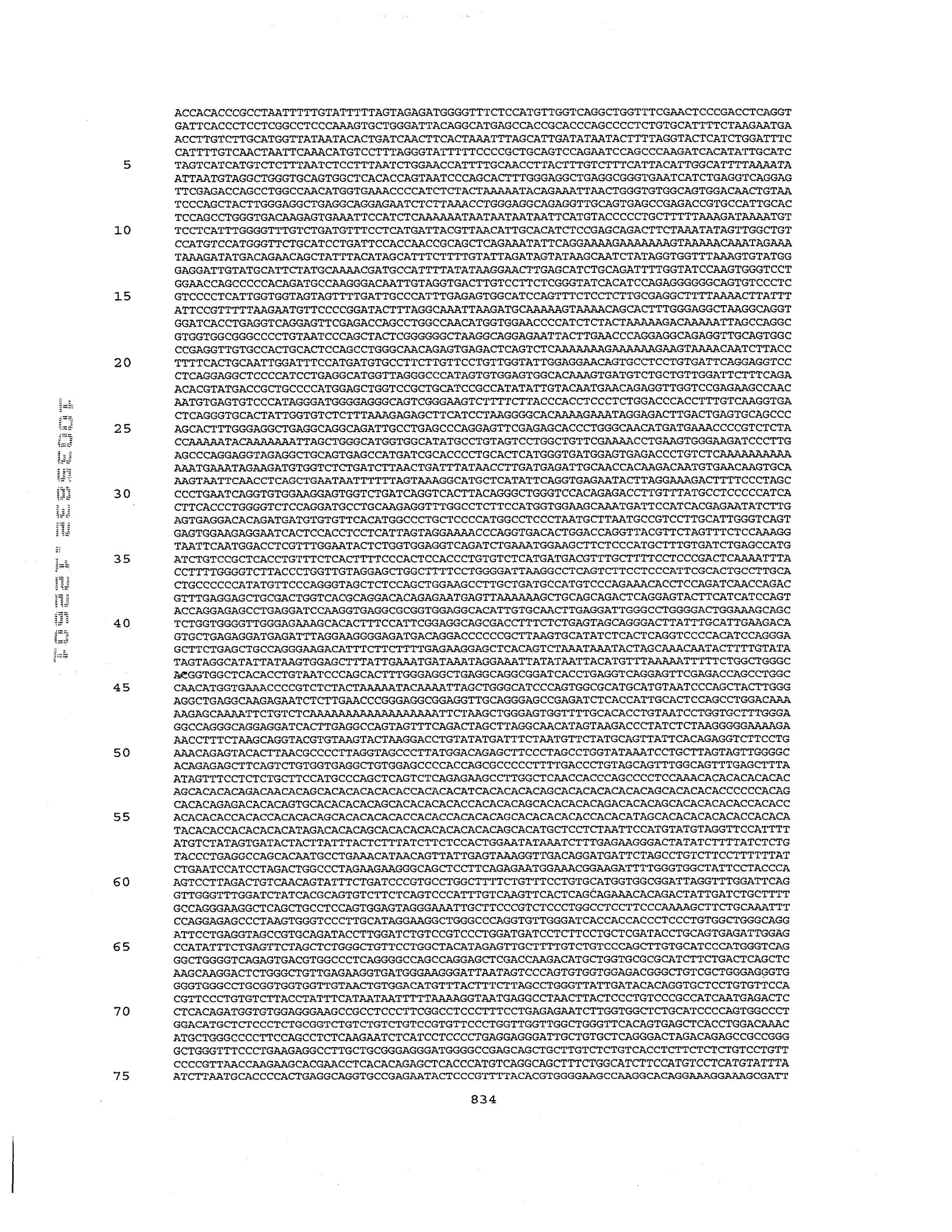
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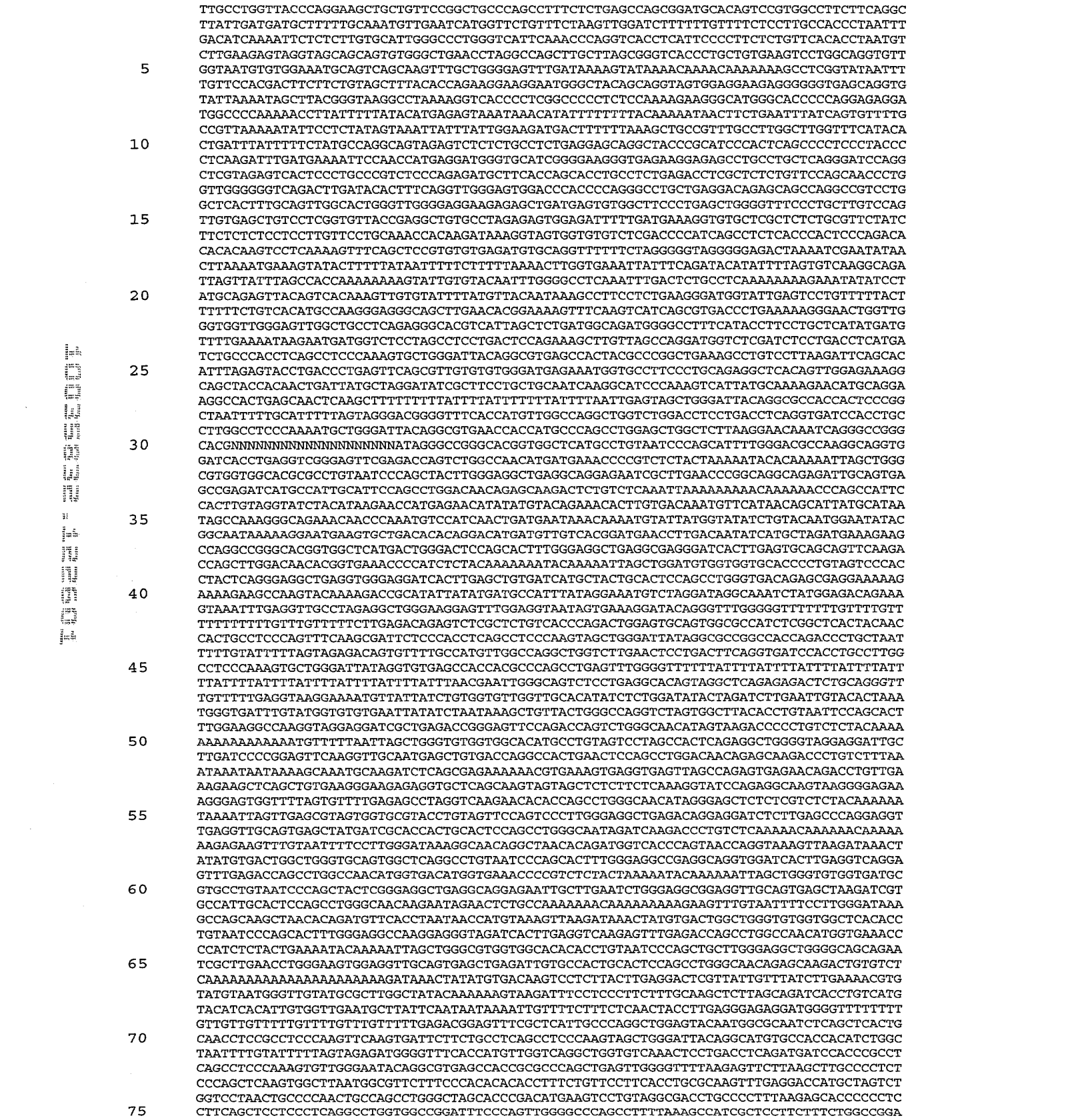




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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 40

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ICSGNM Sema4d

Celera mCG1273

HUMAN NOMENCLATURE

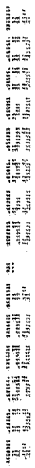
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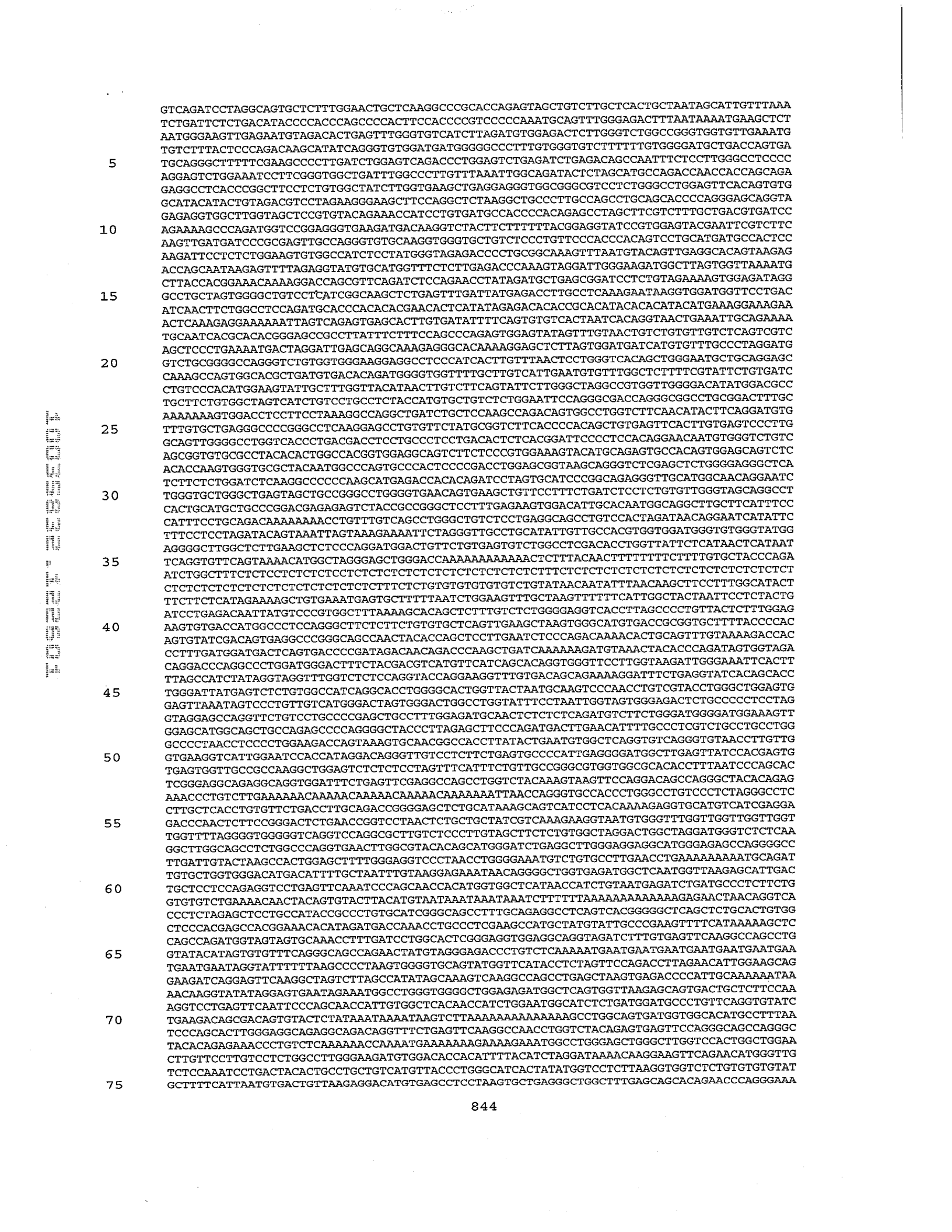
MOUSE SEQUENCE - GENOMIC

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Electronic Acknowledgement Receipt
EFS-Web 2.2.5

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MOUSE SEQUENCE - mRNA

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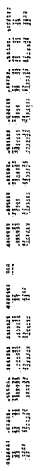
MOUSE SEQUENCE - CODING

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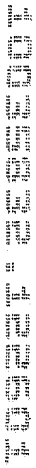
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HUMAN SEQUENCE - GENOMIC
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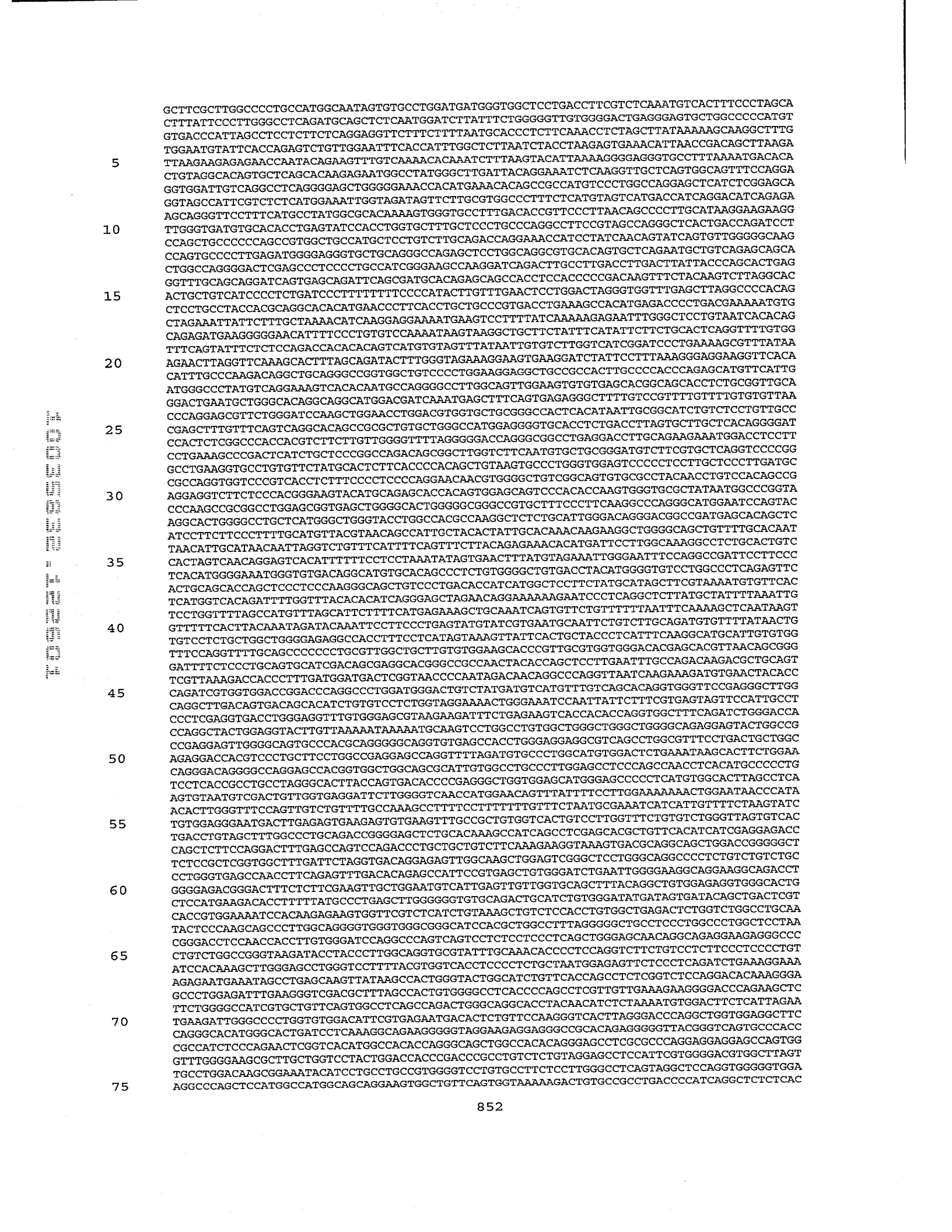
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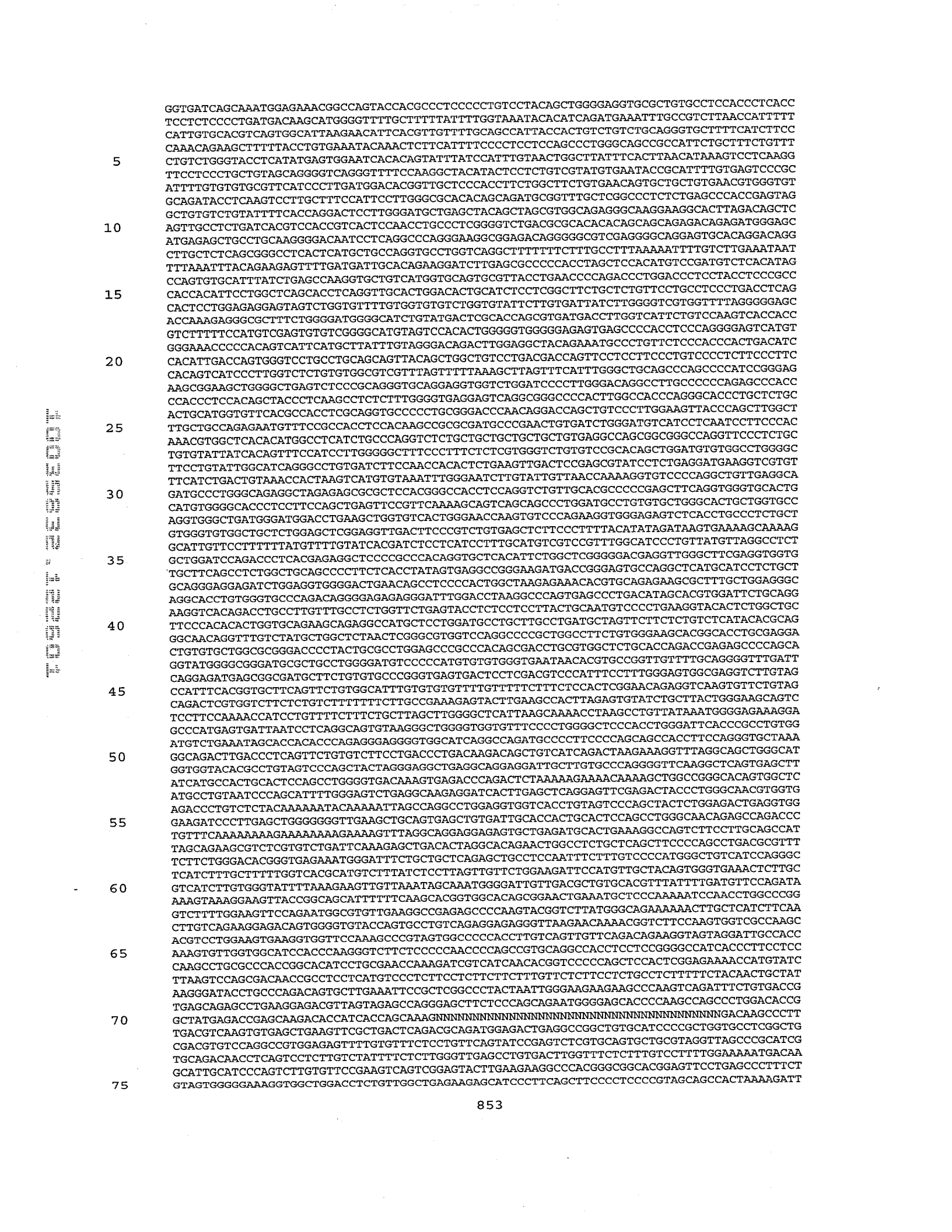
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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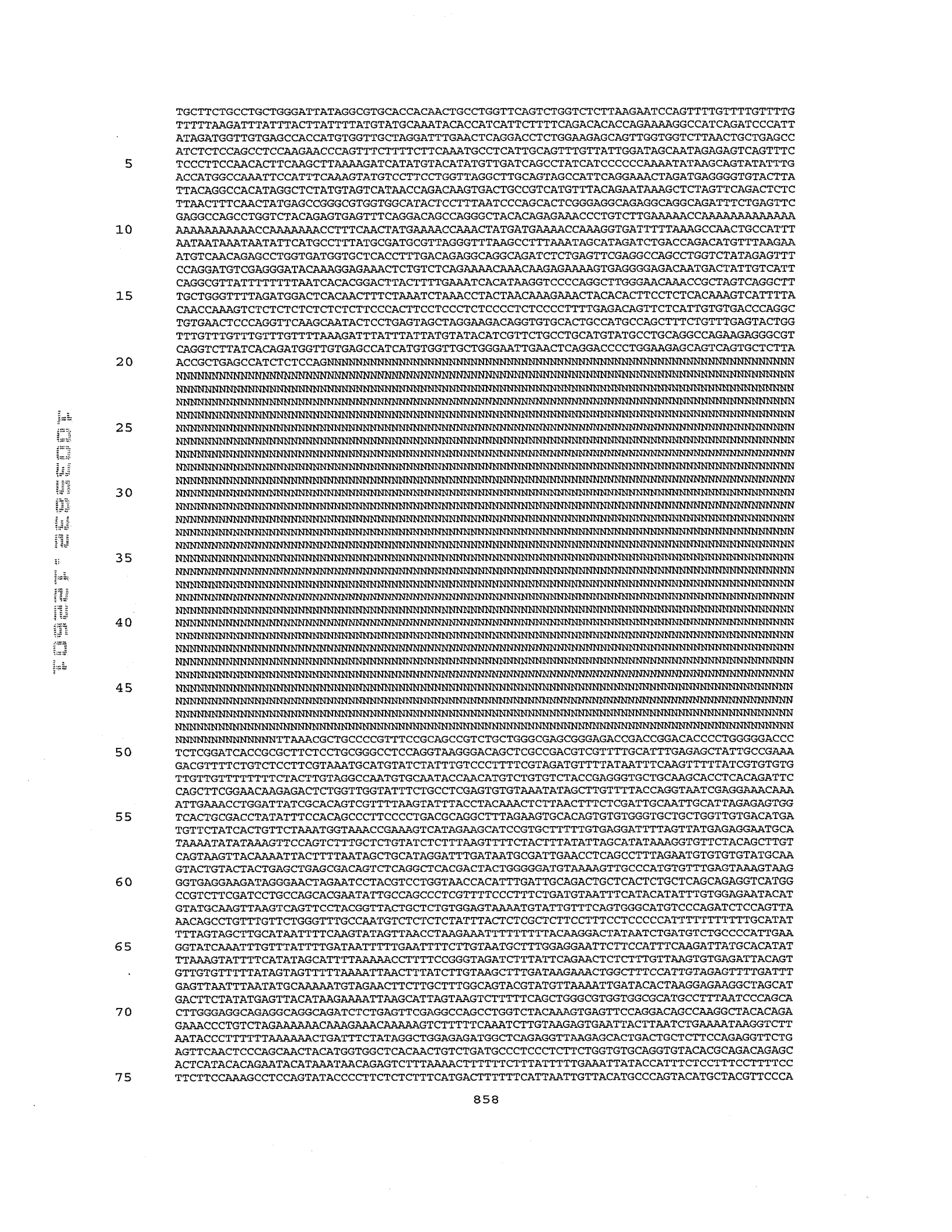
Table 41

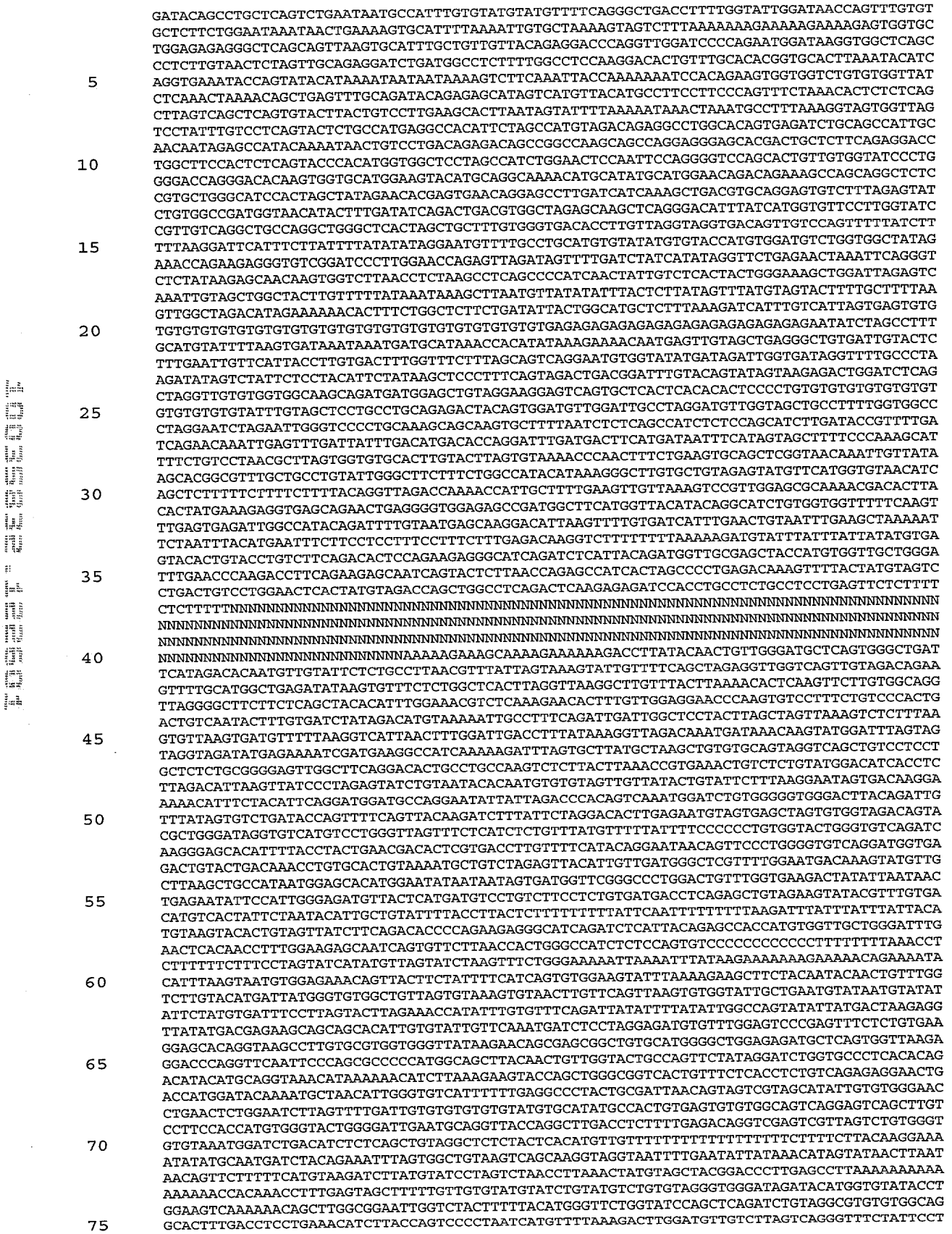
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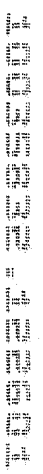
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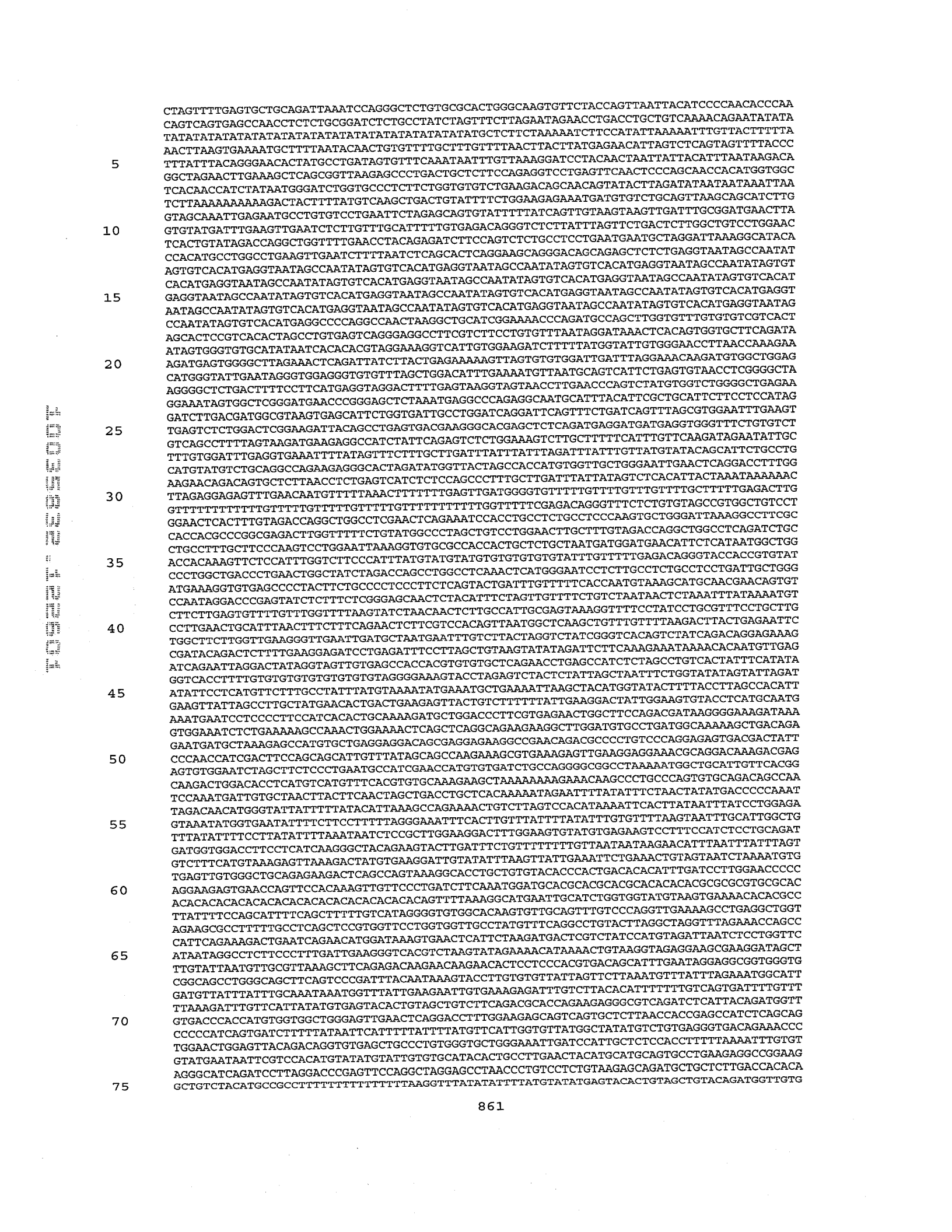
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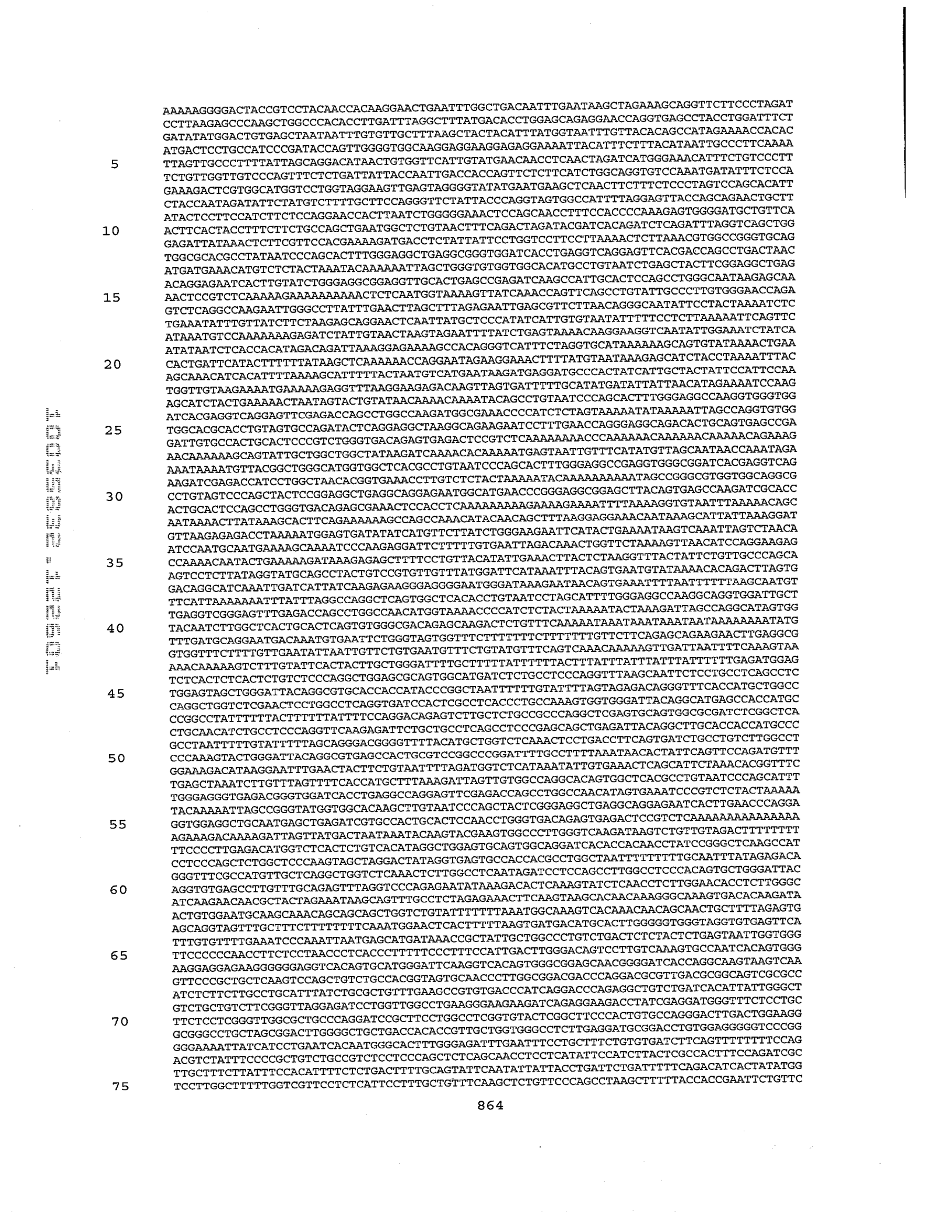
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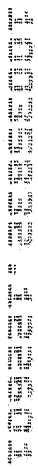
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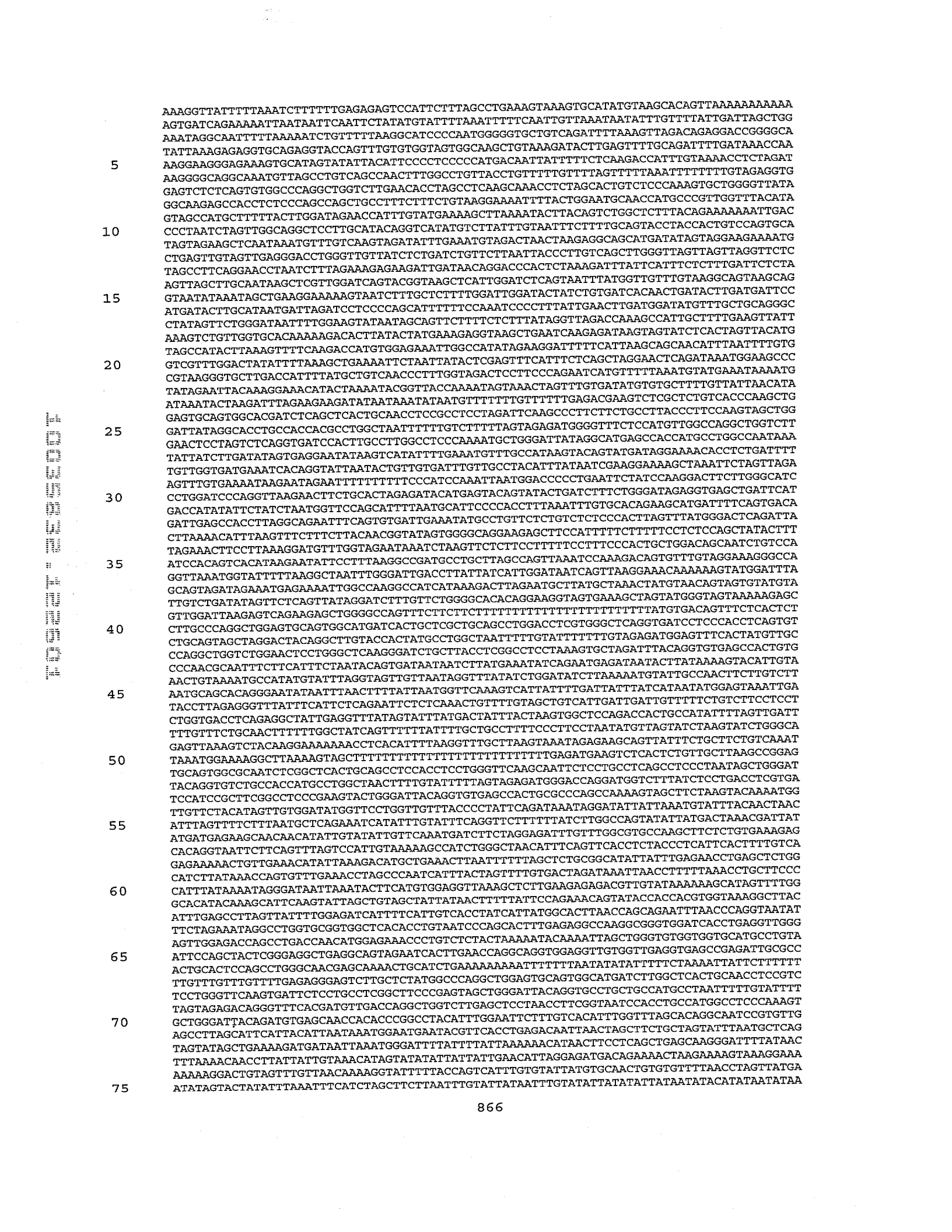
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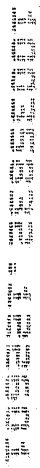
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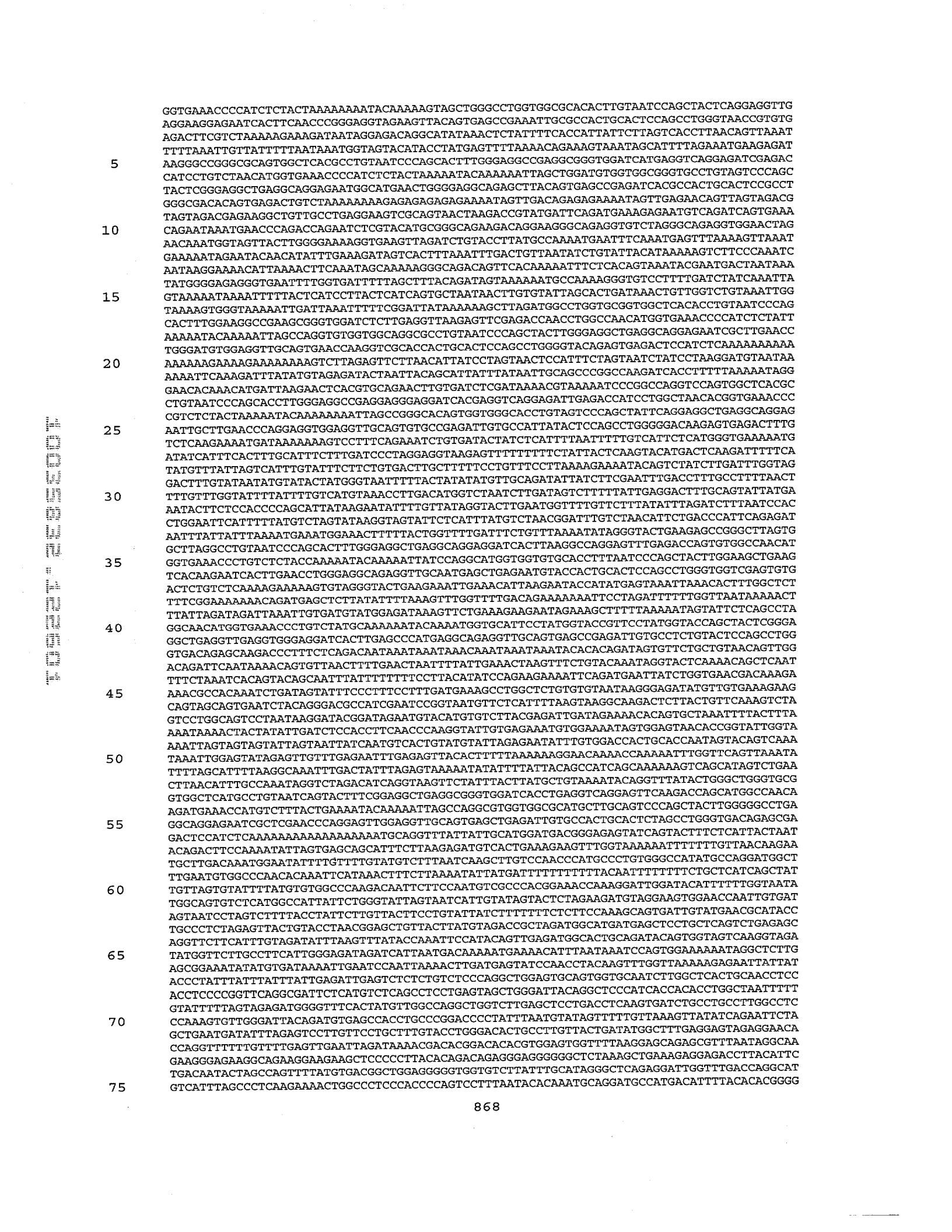
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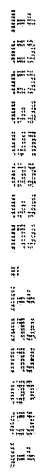
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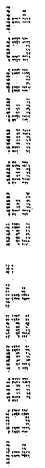
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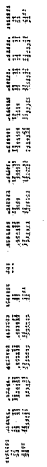
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 42

MOUSE NOMENCLATURE

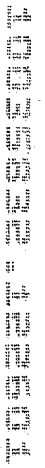
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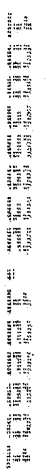
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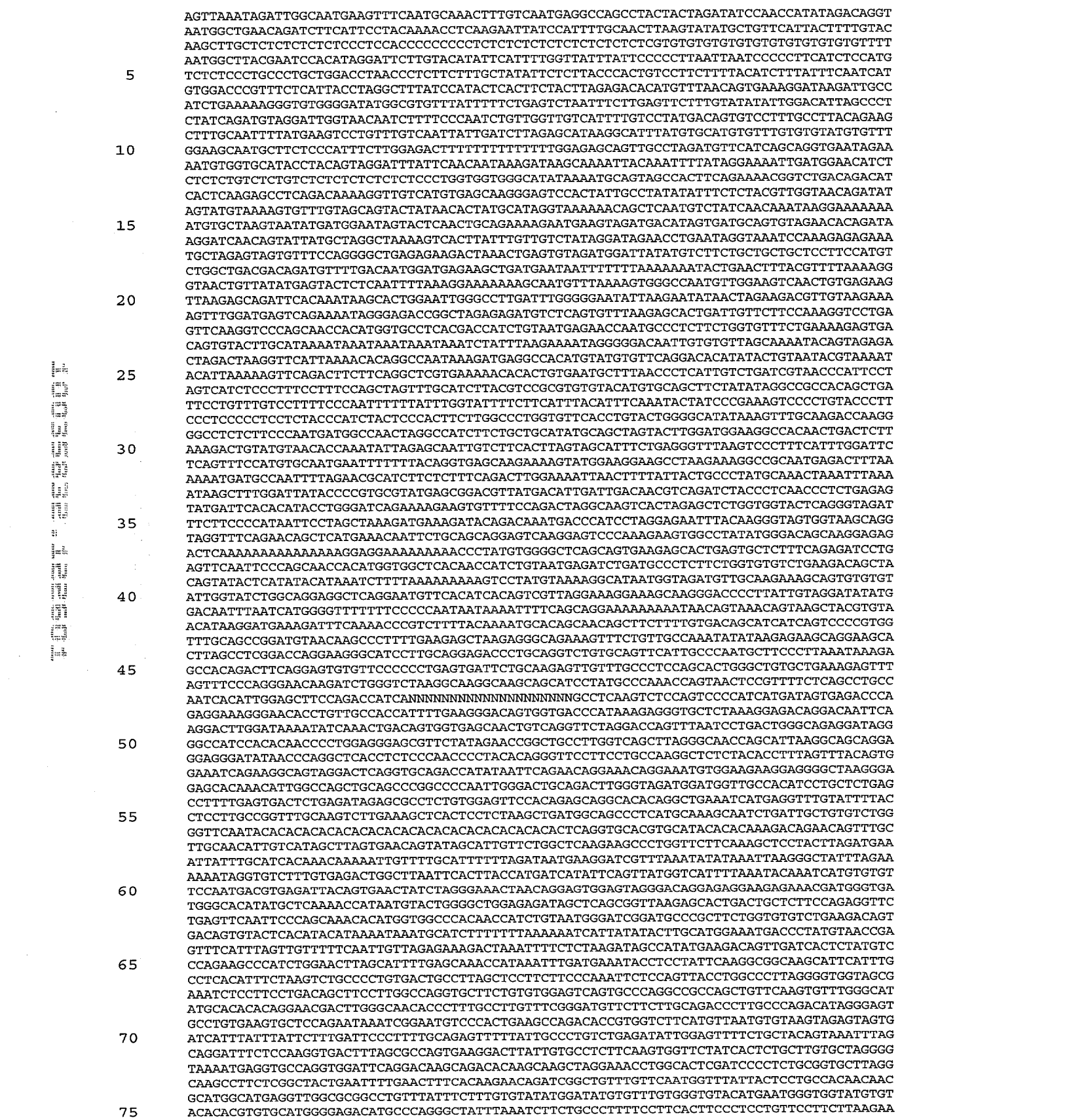
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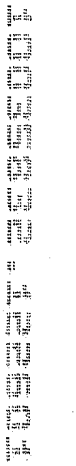


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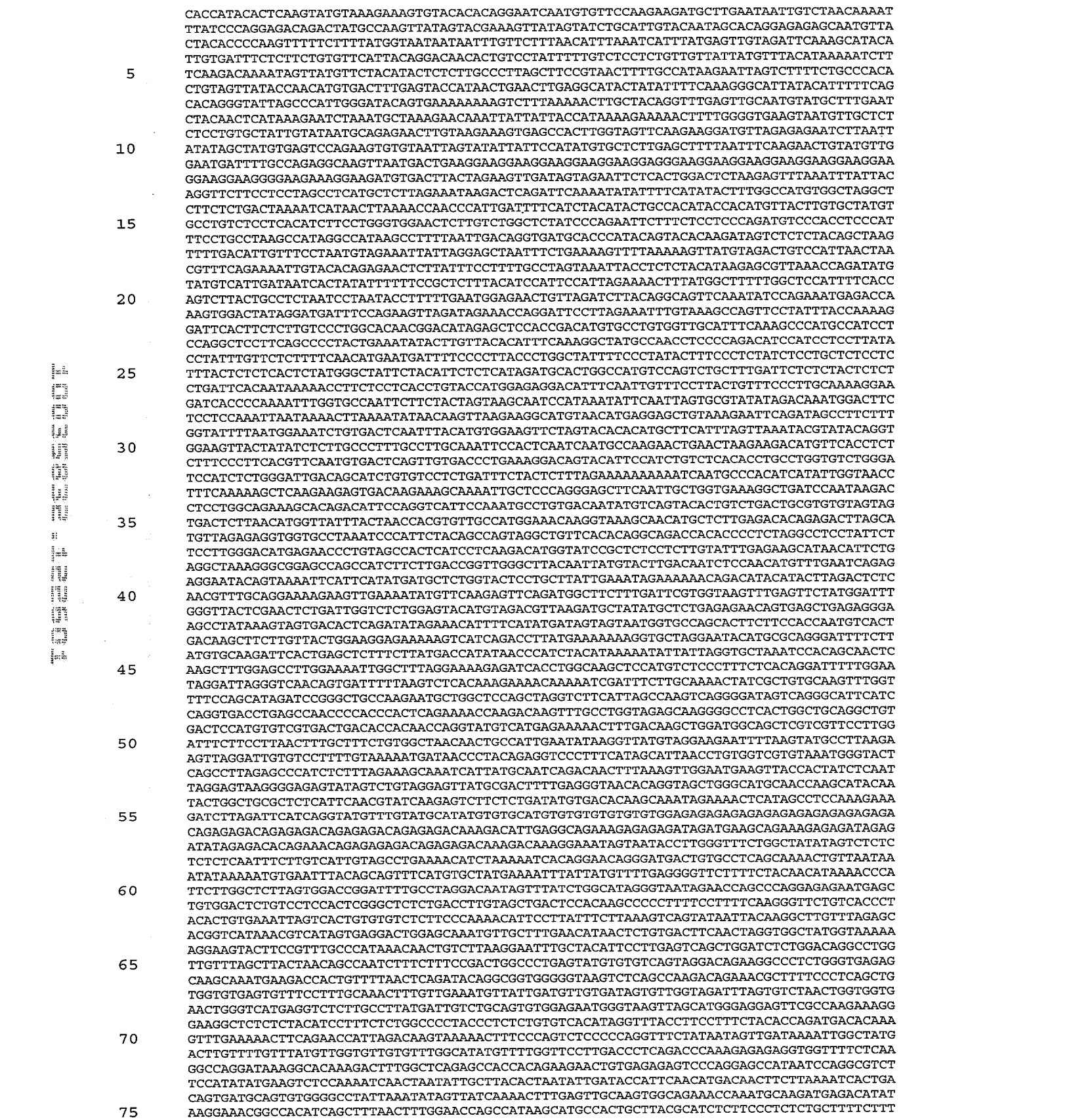


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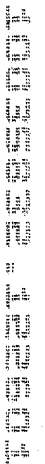


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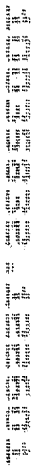
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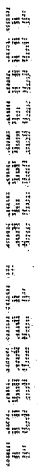
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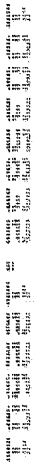


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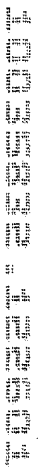
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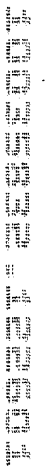
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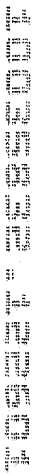


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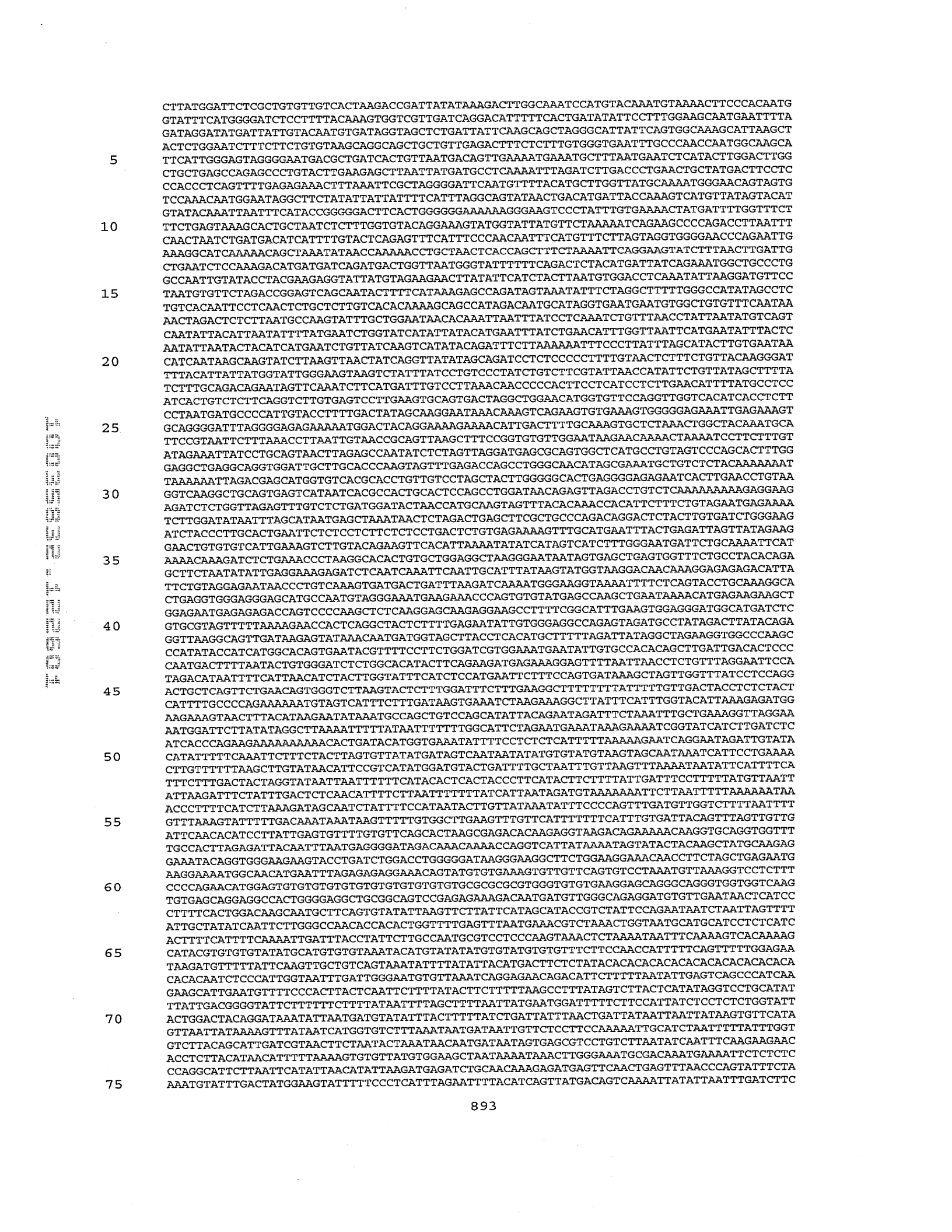
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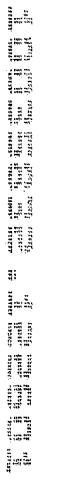
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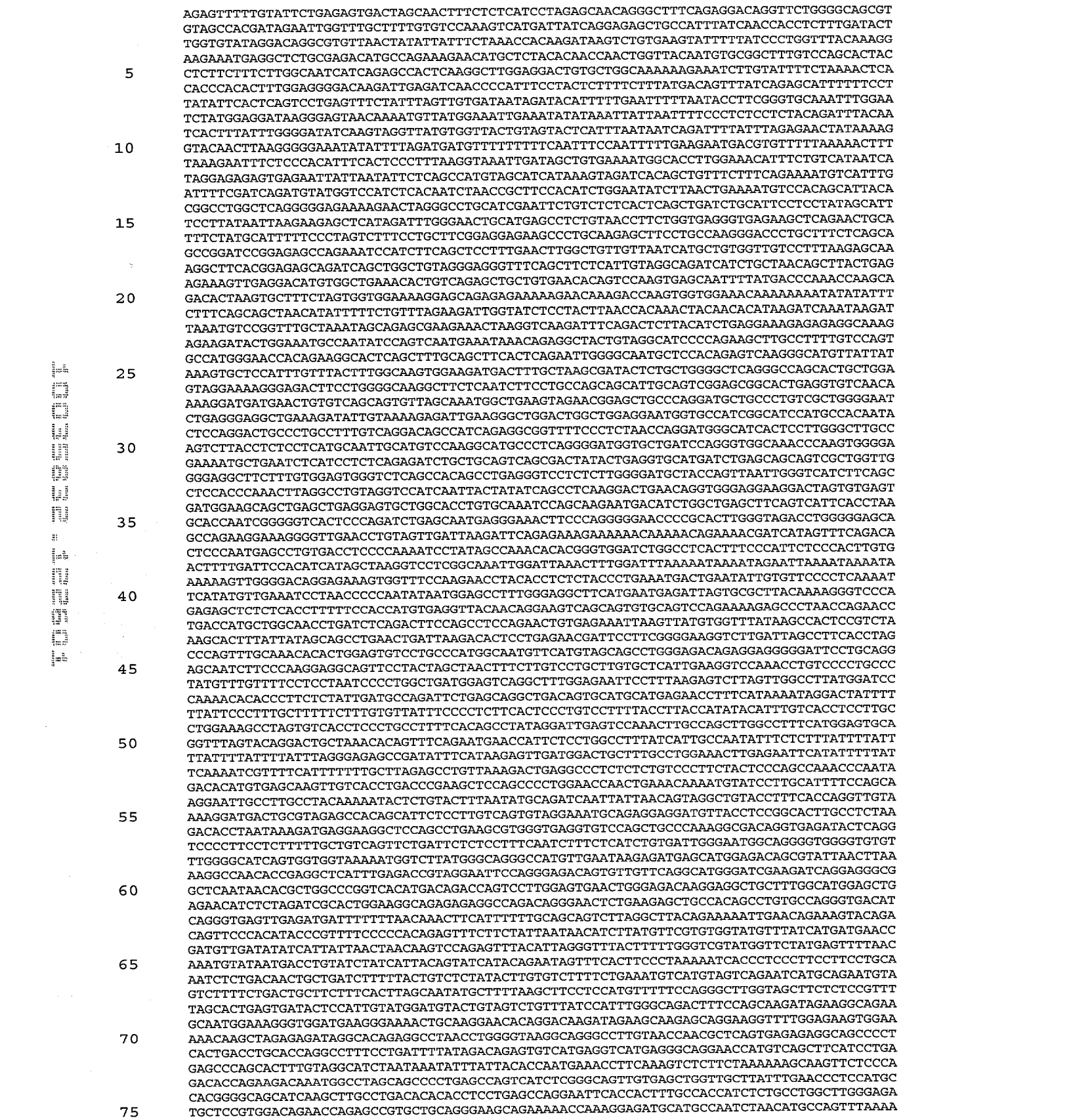
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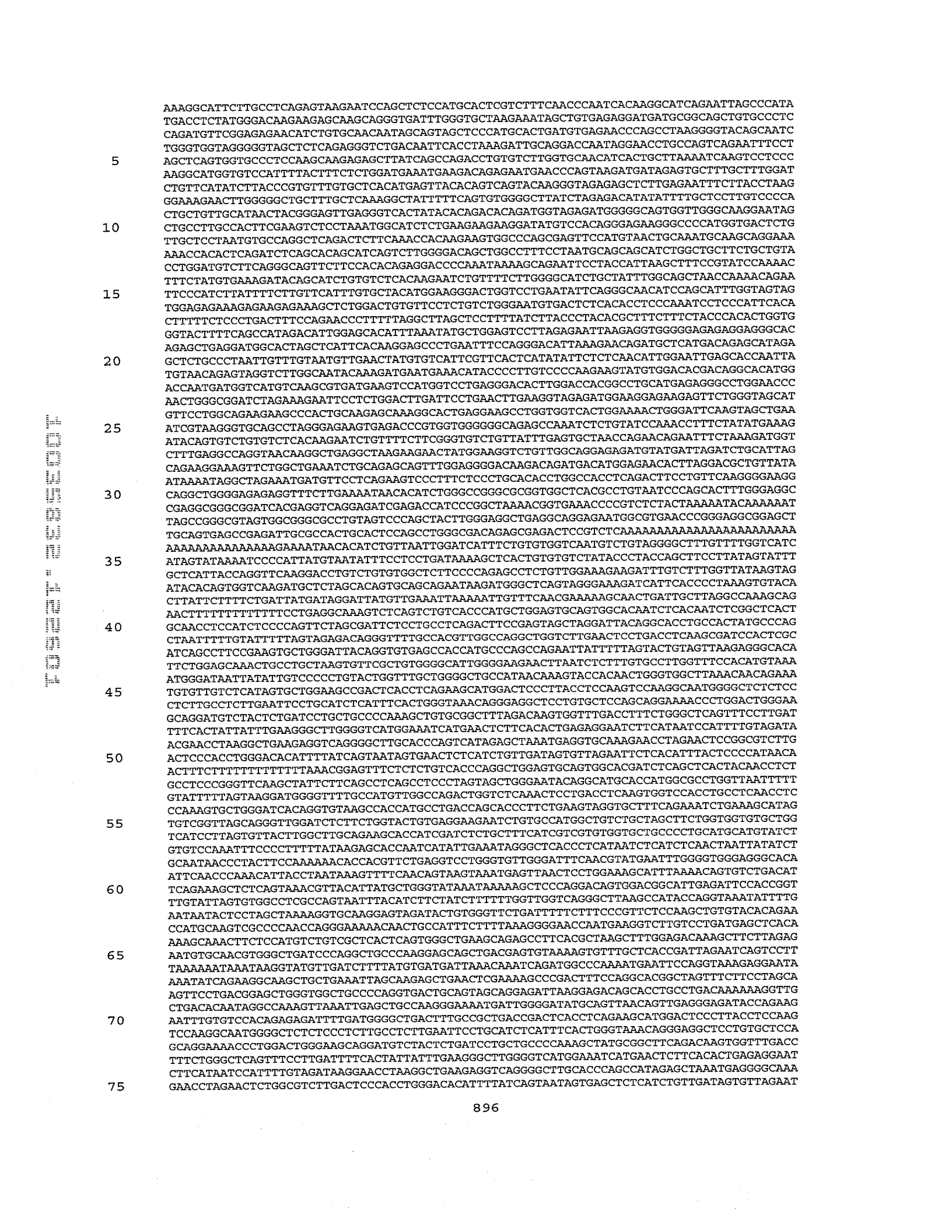
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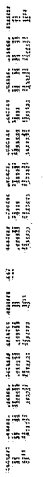


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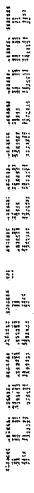


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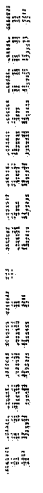
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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PCT/US95/15657

Table 43

MOUSE NOMENCLATURE

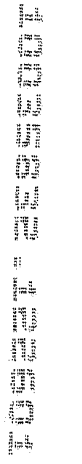
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HUMAN NOMENCLATURE

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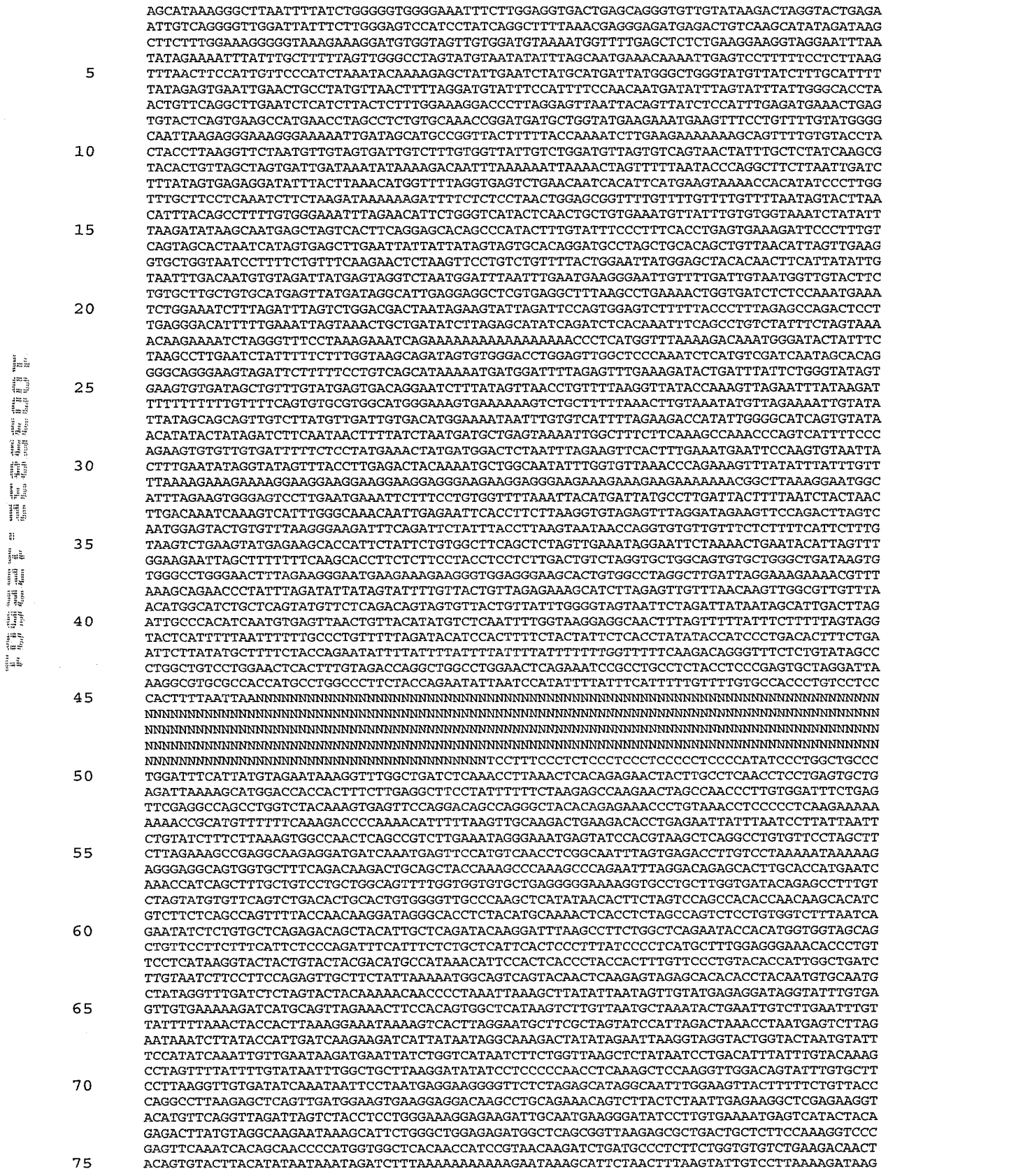
MOUSE SEQUENCE - GENOMIC

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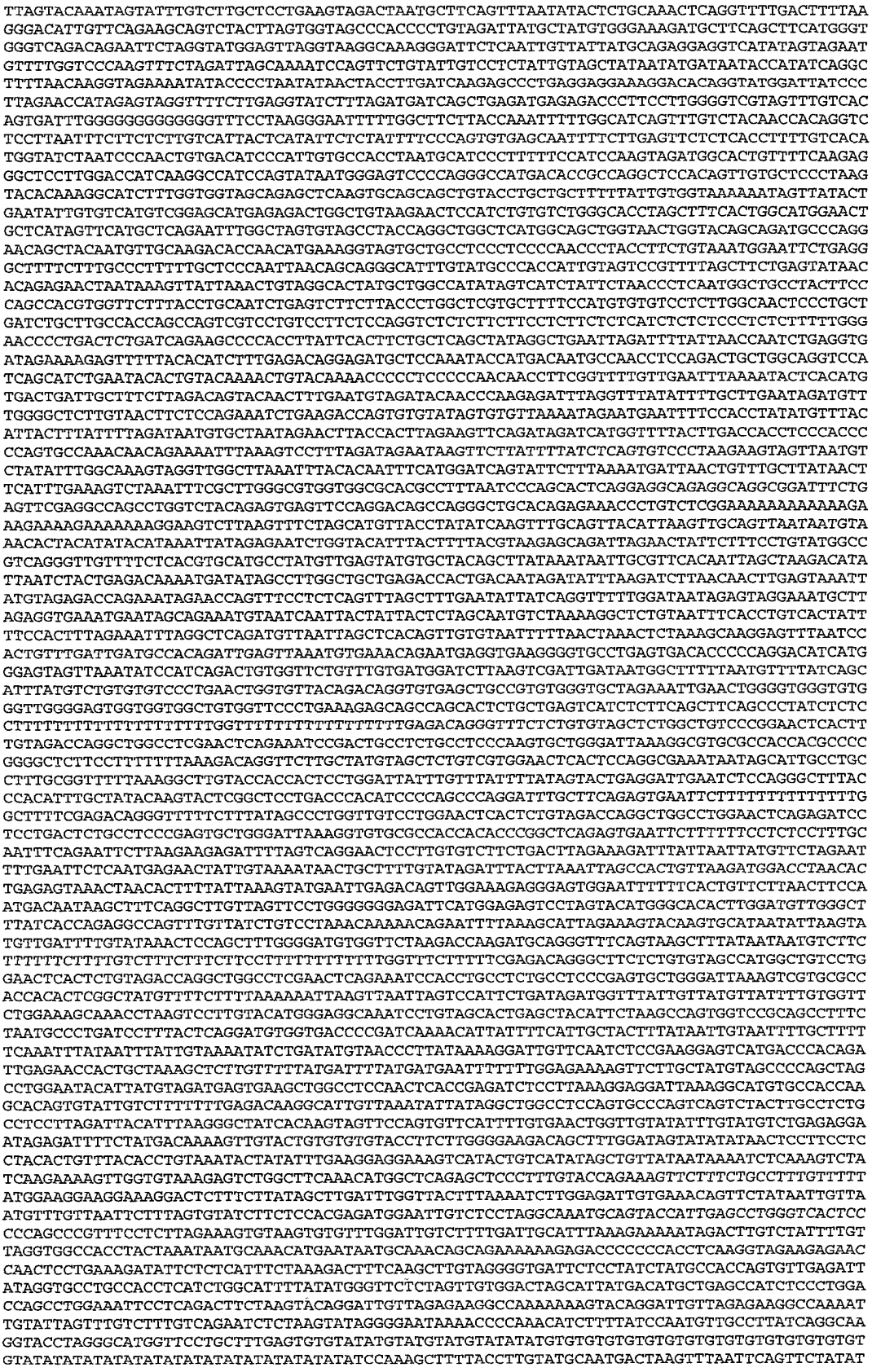


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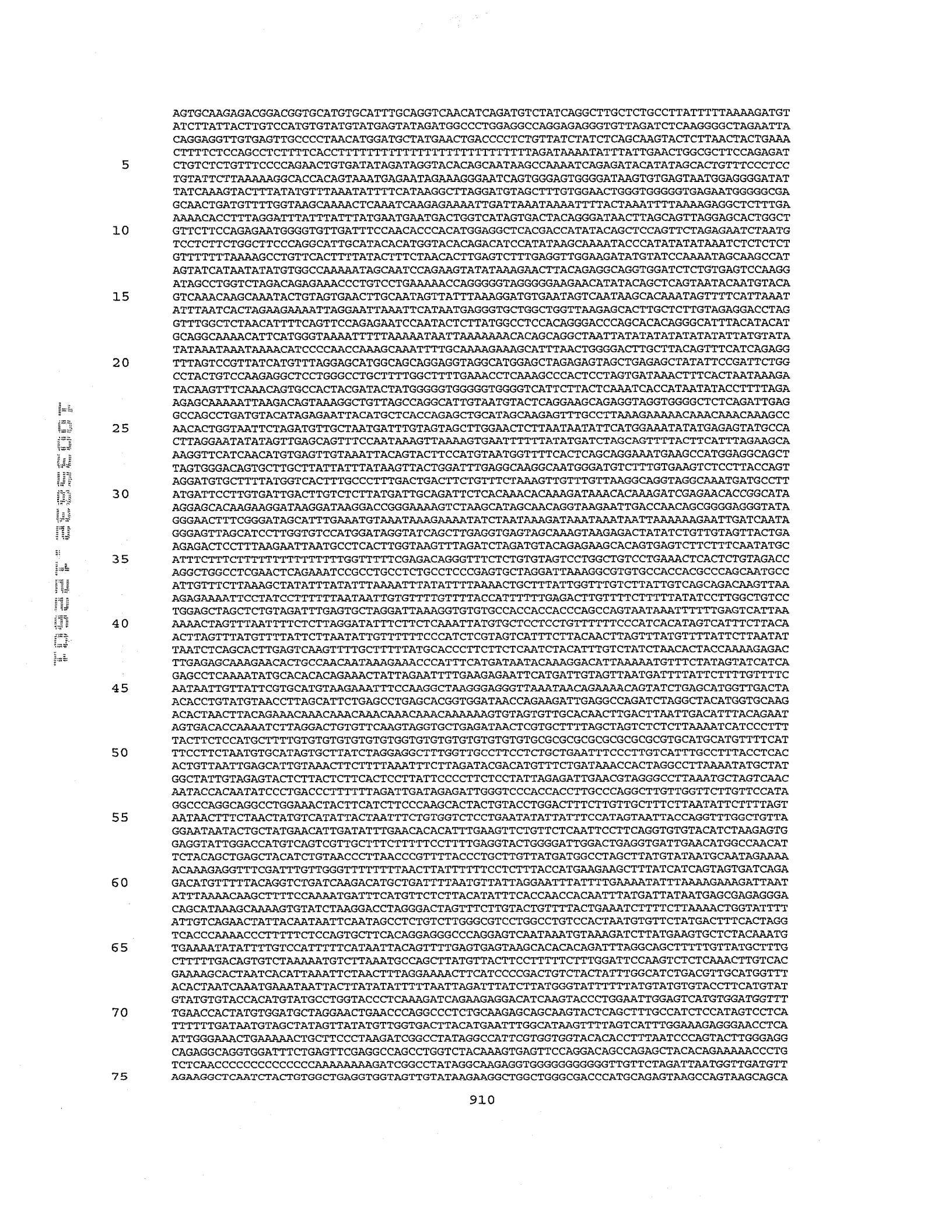
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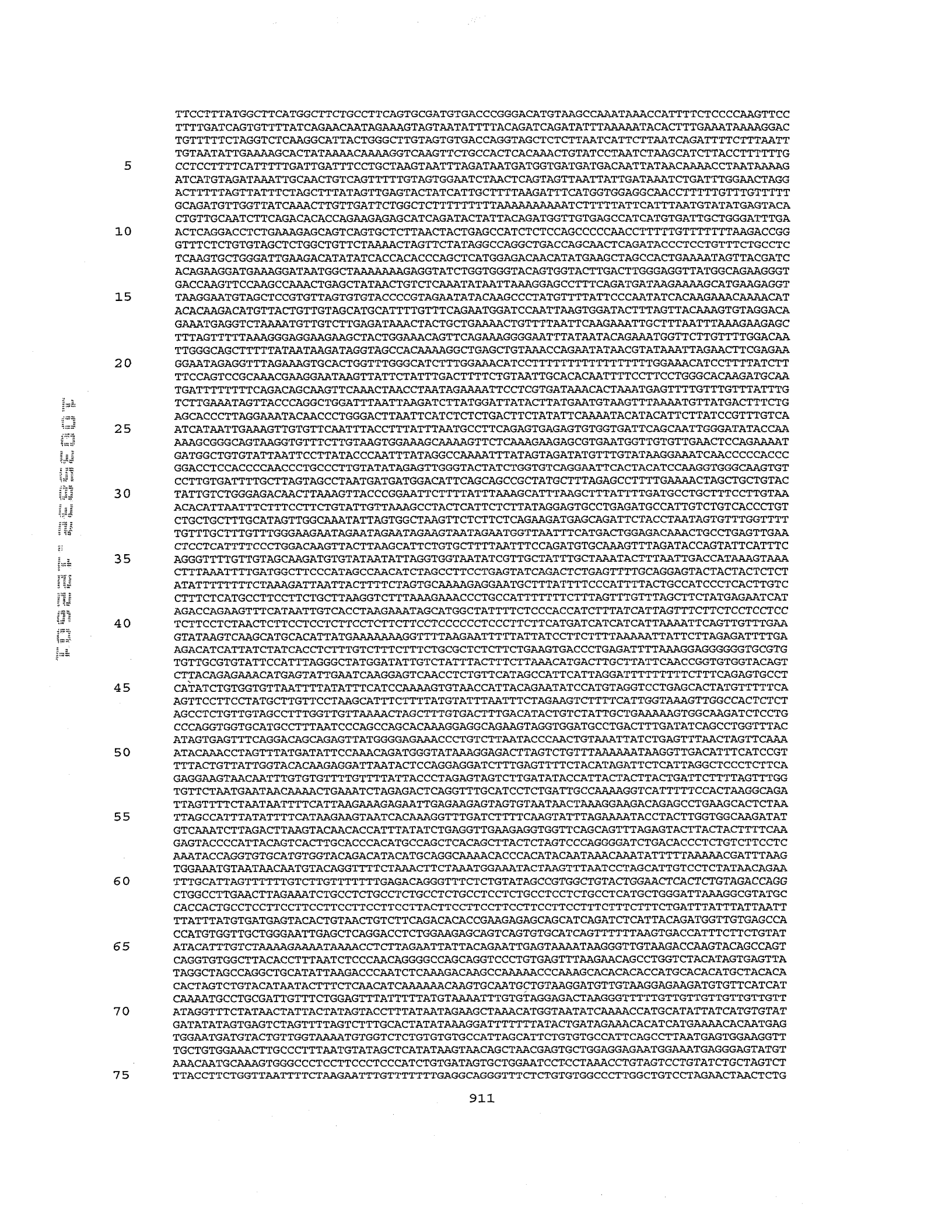
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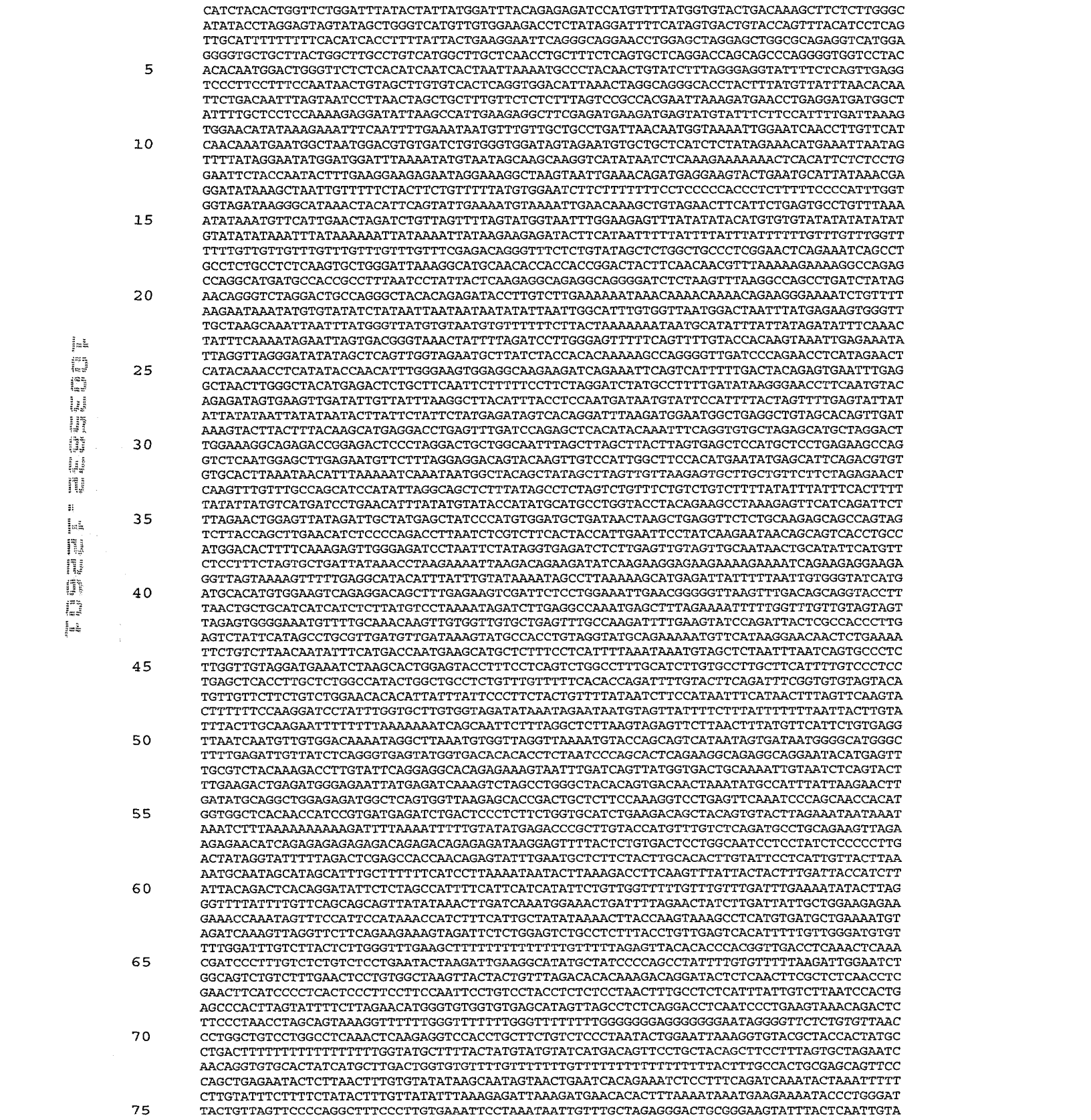
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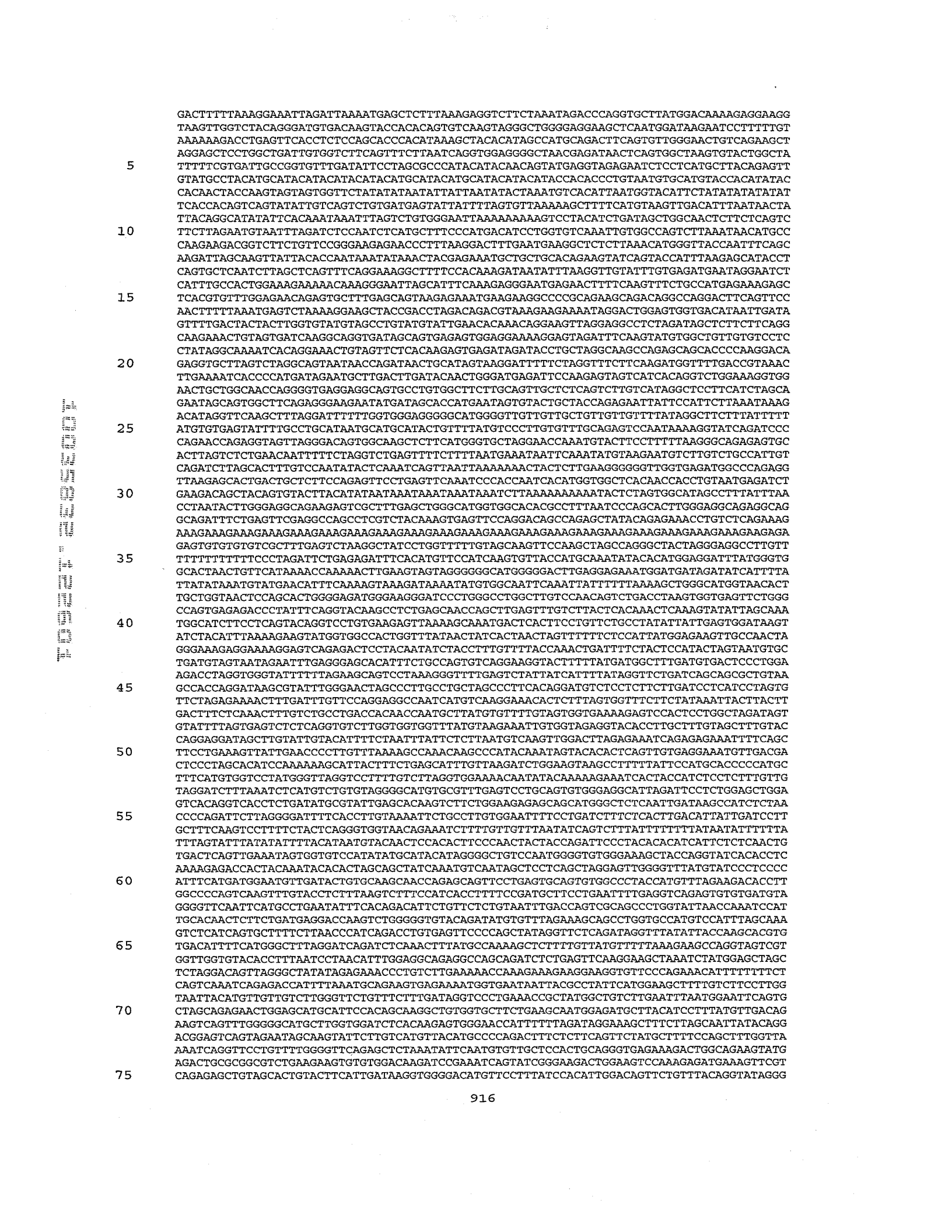


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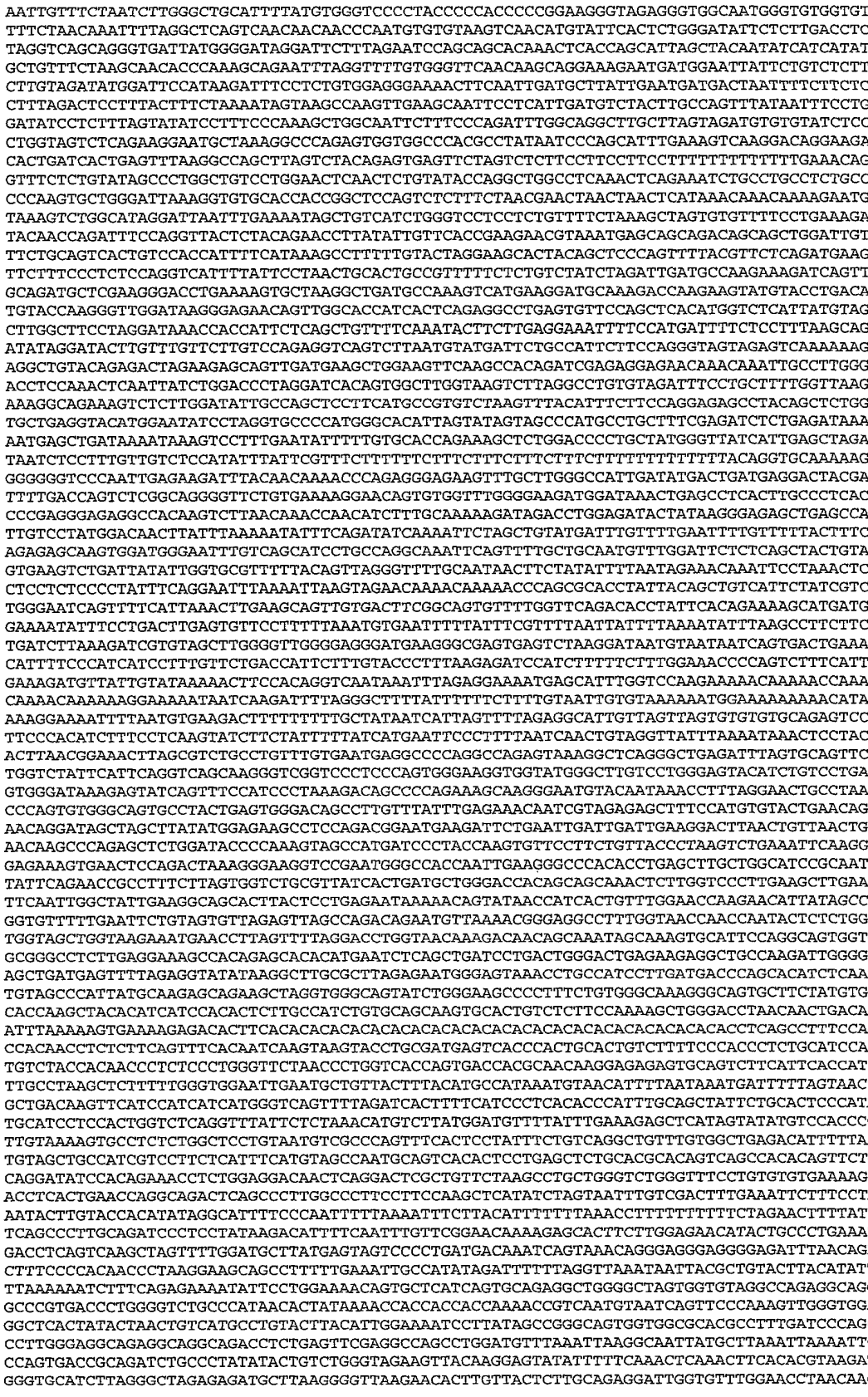


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Tuesday, June 26, 2007 3:35:06 PM



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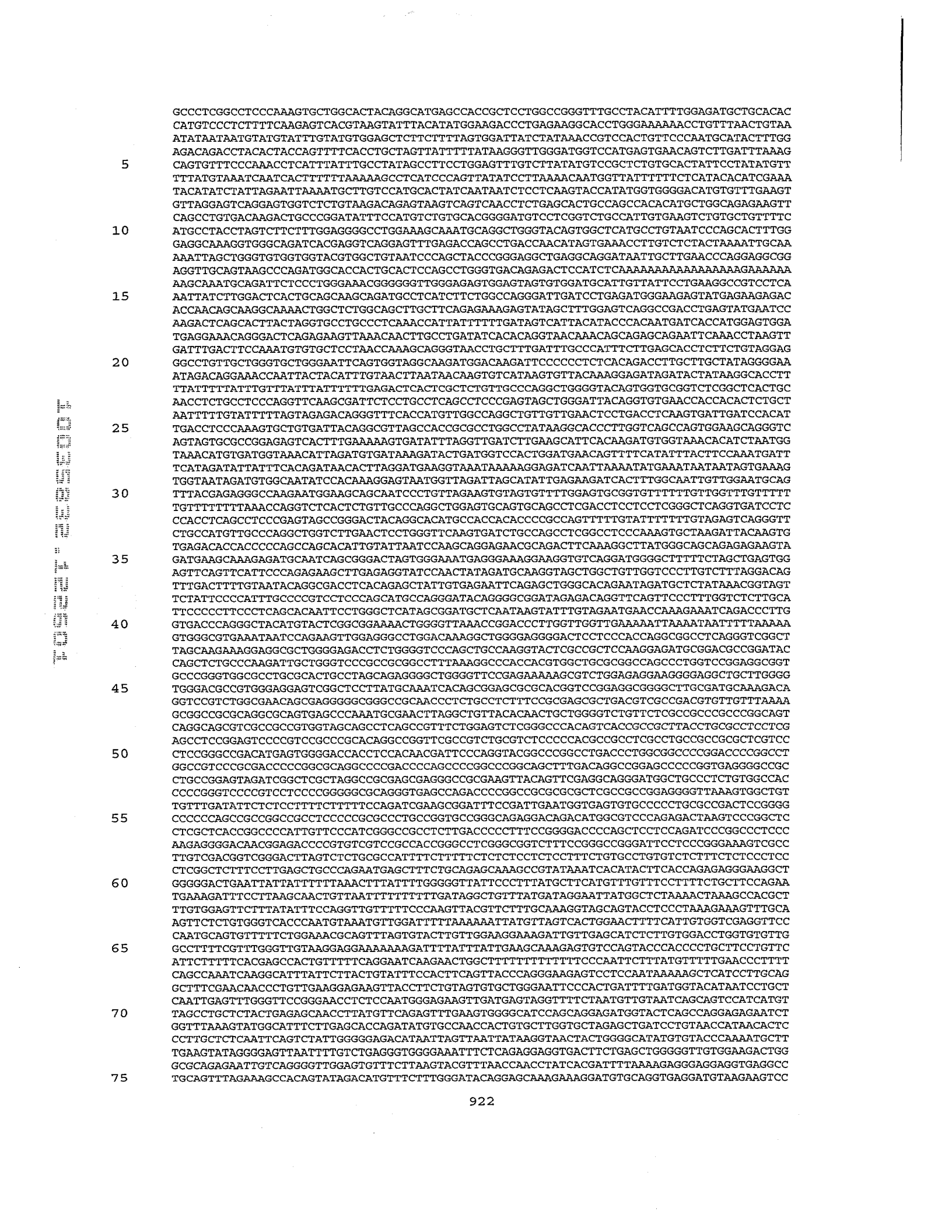
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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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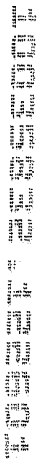
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HUMAN SEQUENCE - GENOMIC
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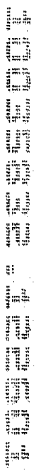
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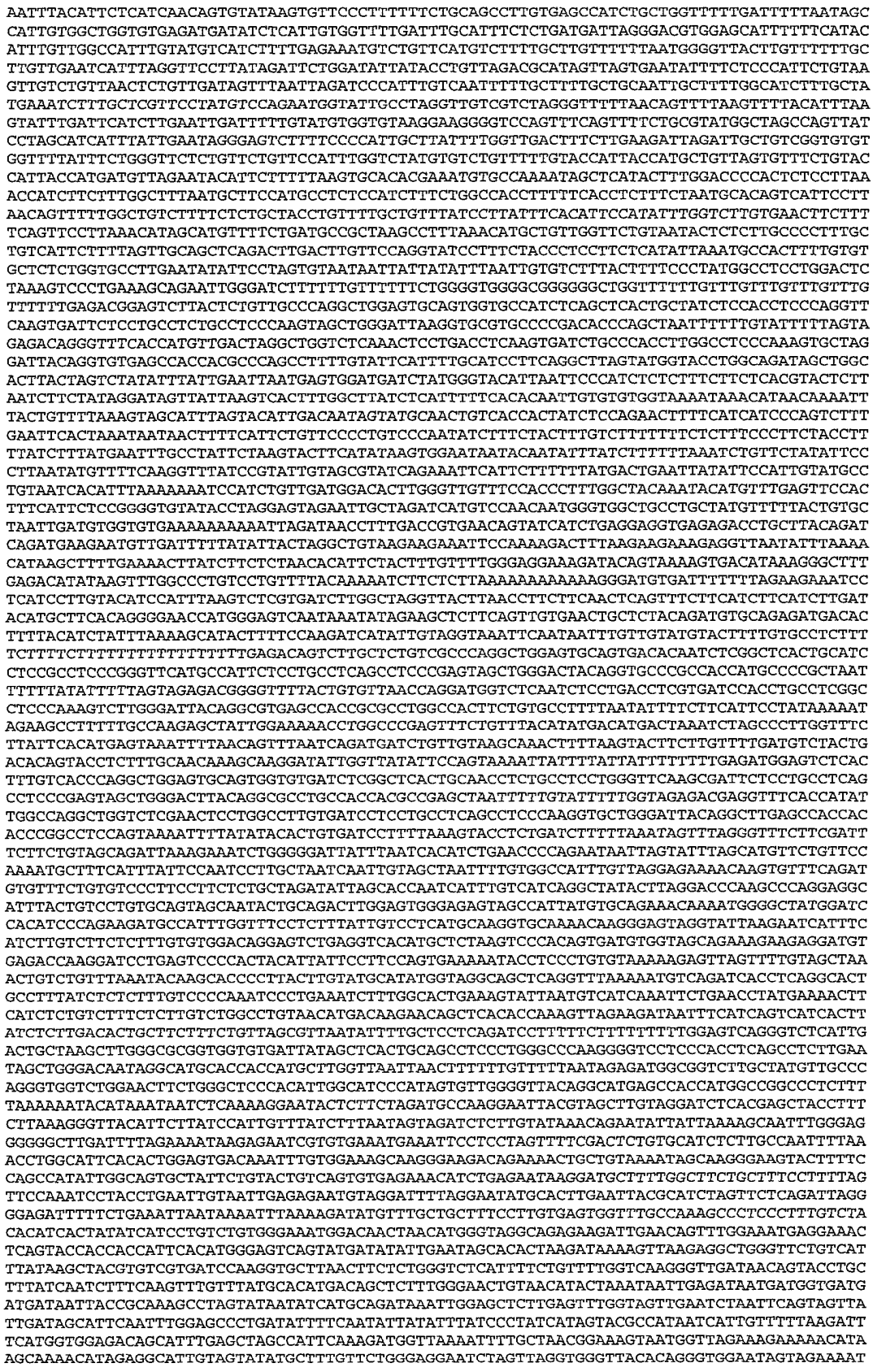
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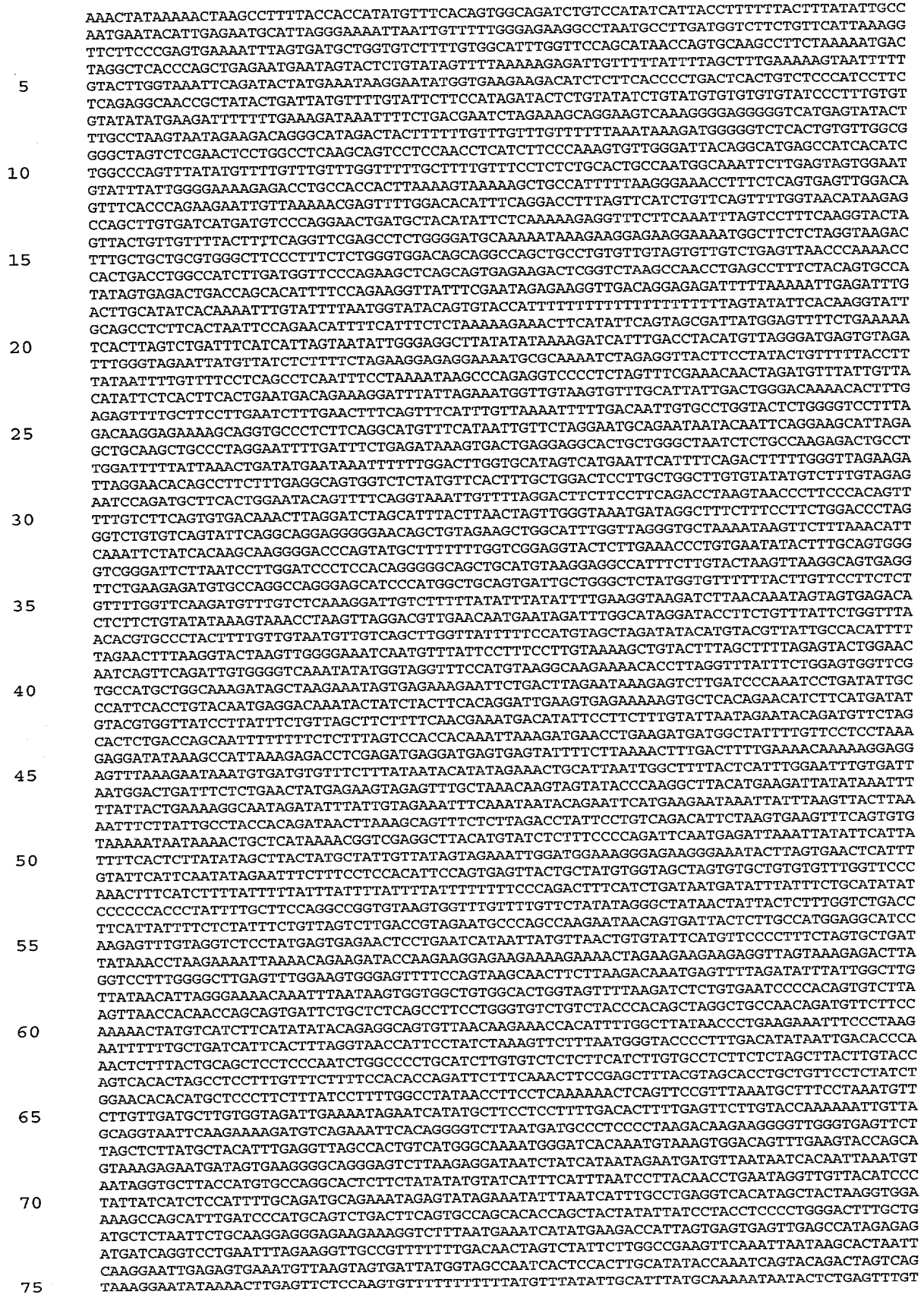
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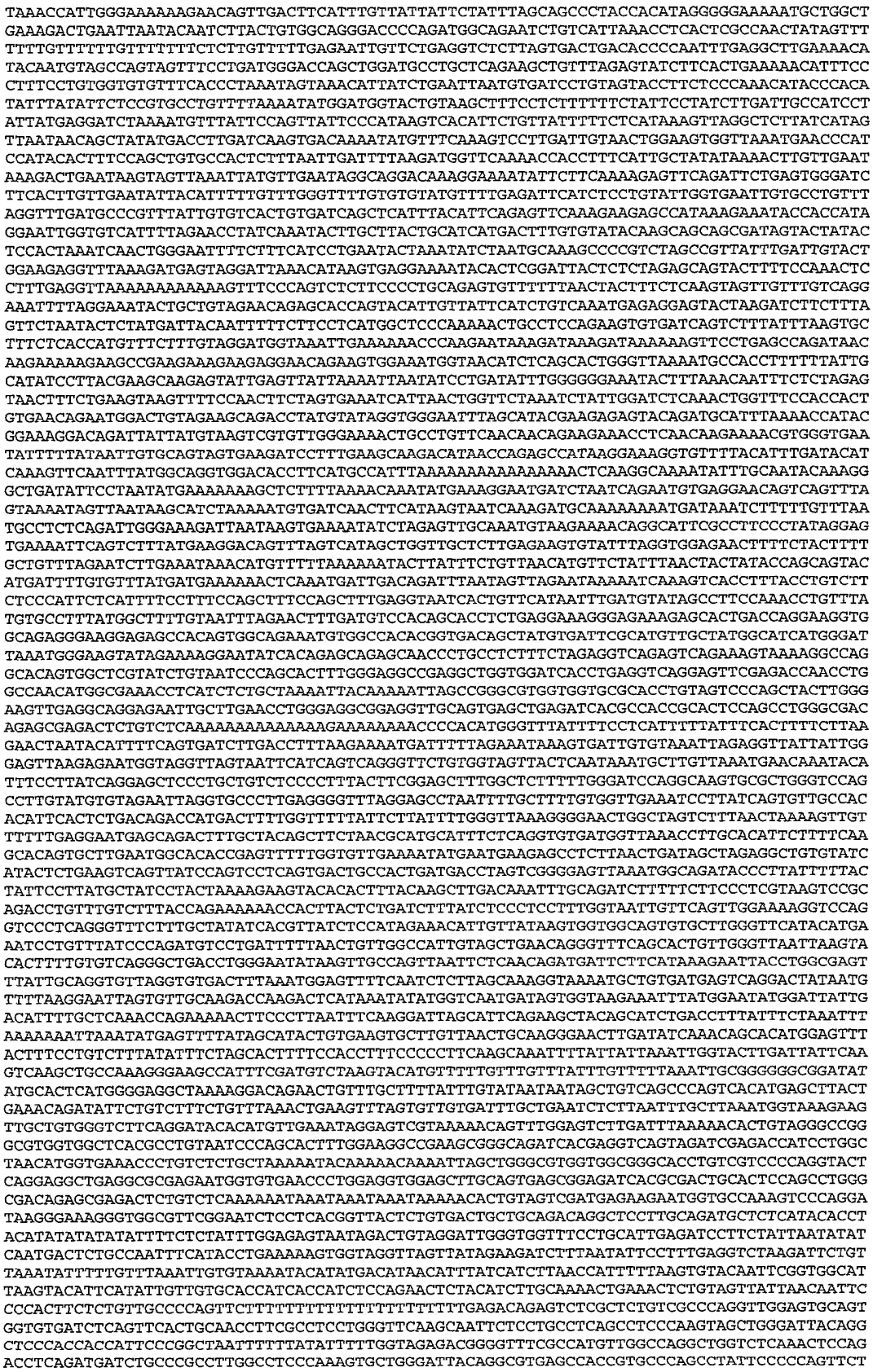


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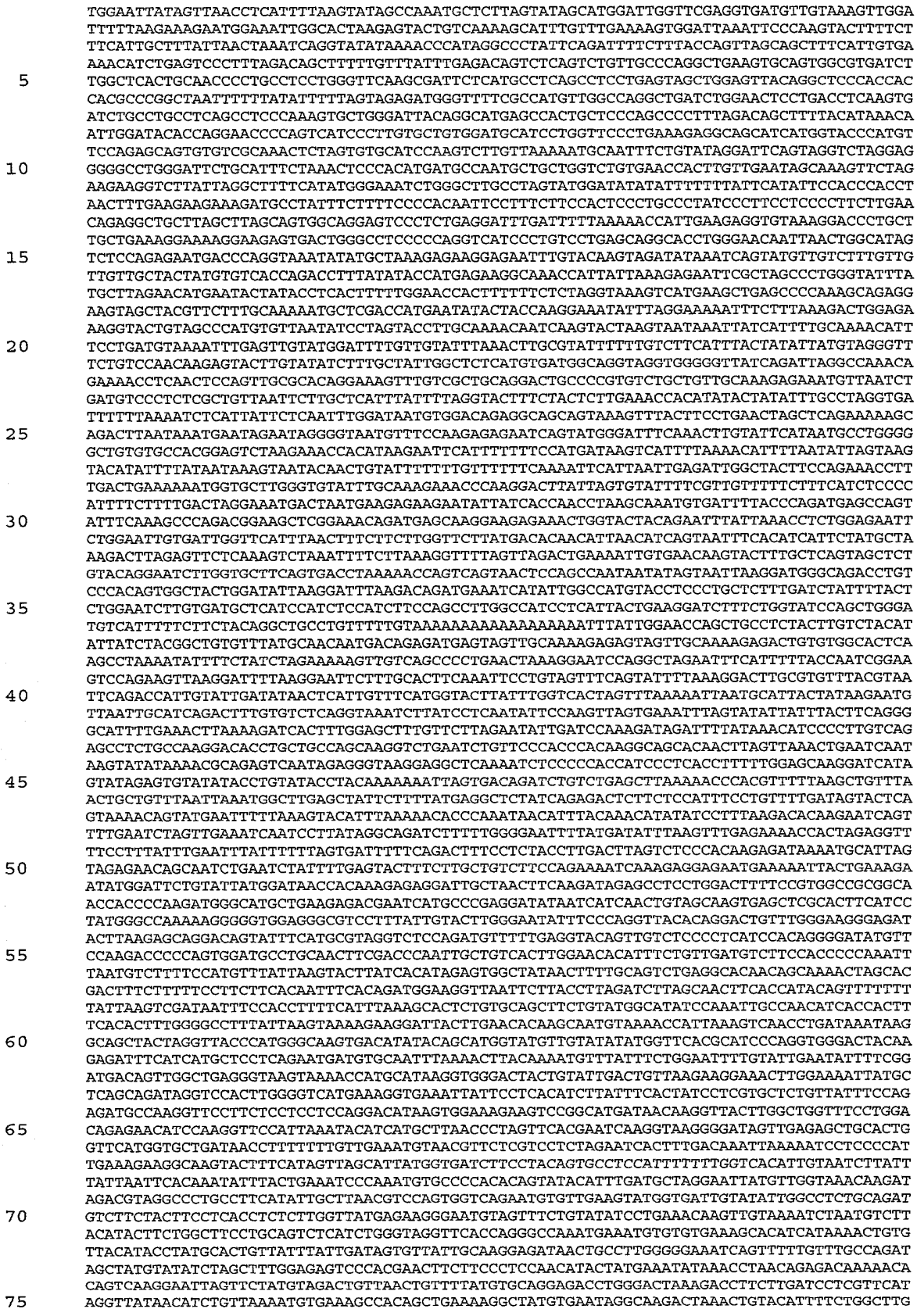


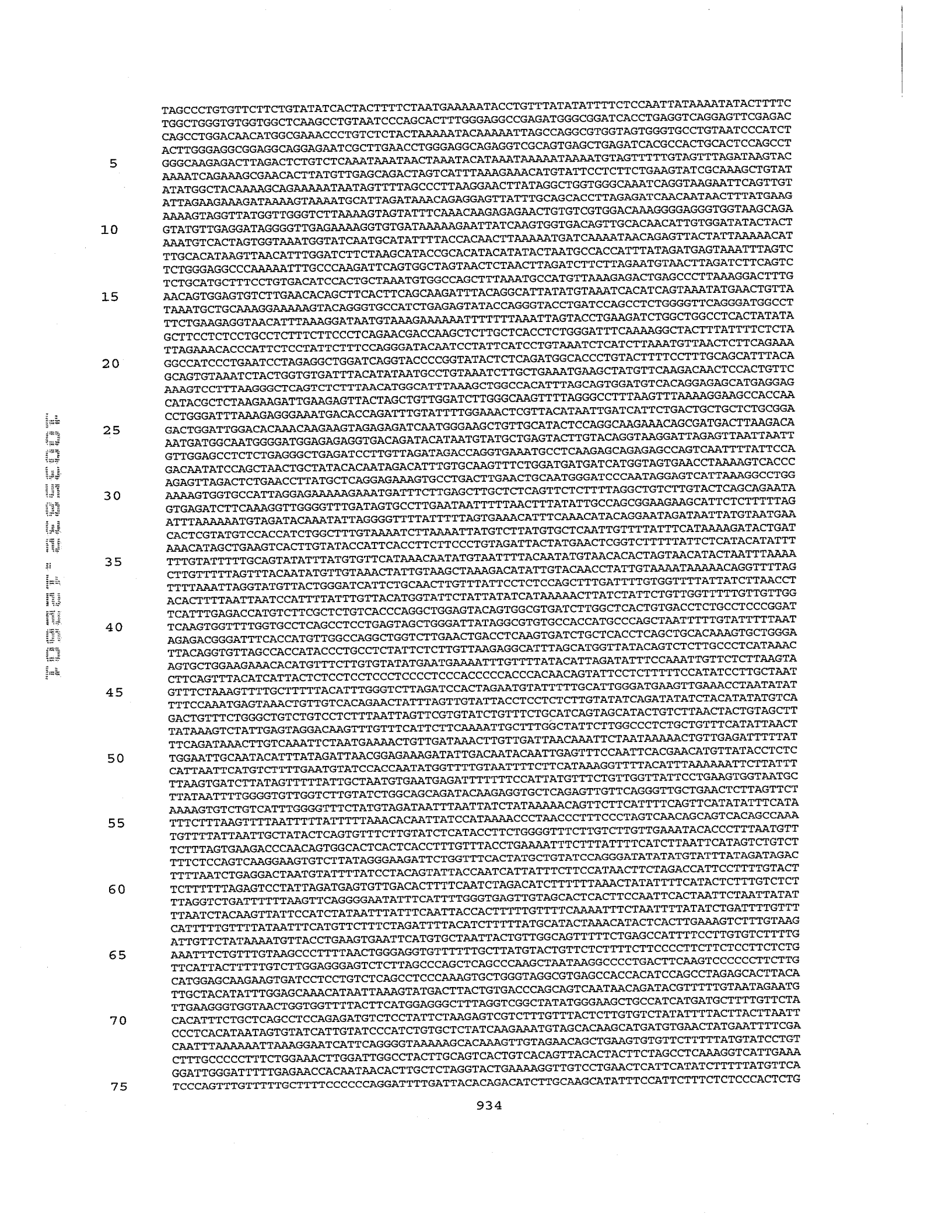
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 44

MOUSE NOMENCLATURE

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Celera	mCG15978

HUMAN NOMENCLATURE

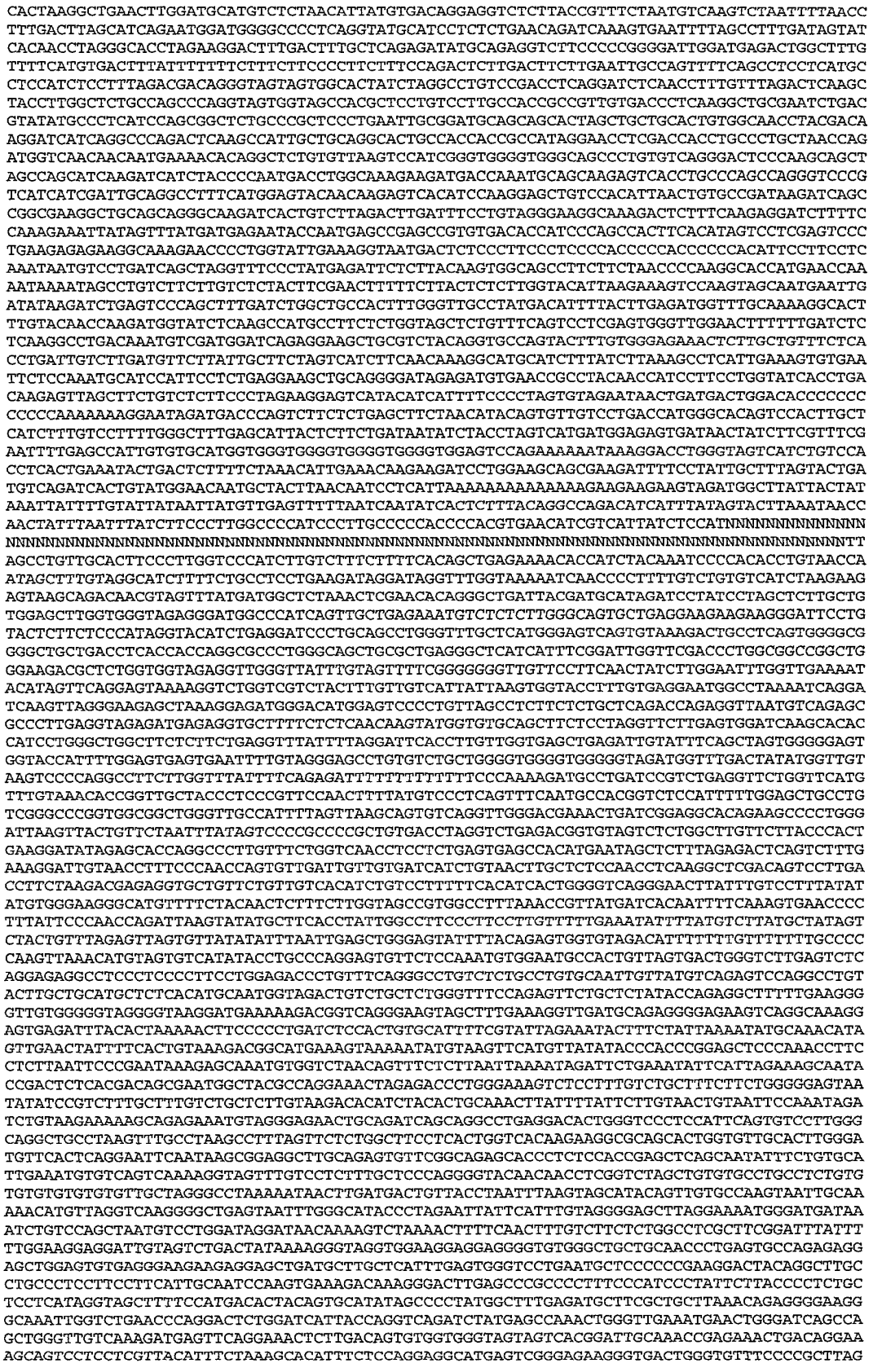
HGNC	DUSP10
Celera	hCG25031

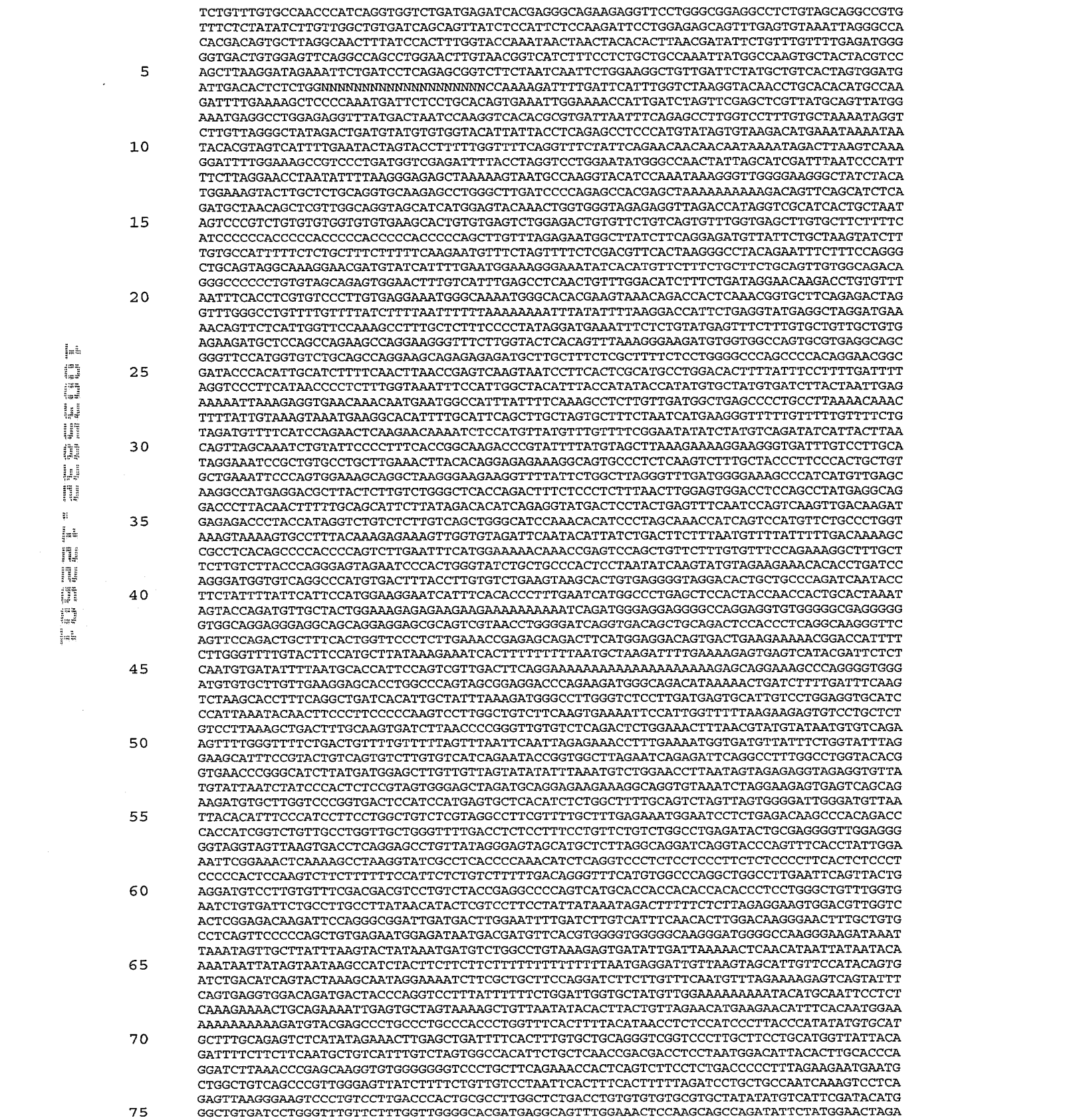
MOUSE SEQUENCE - GENOMIC

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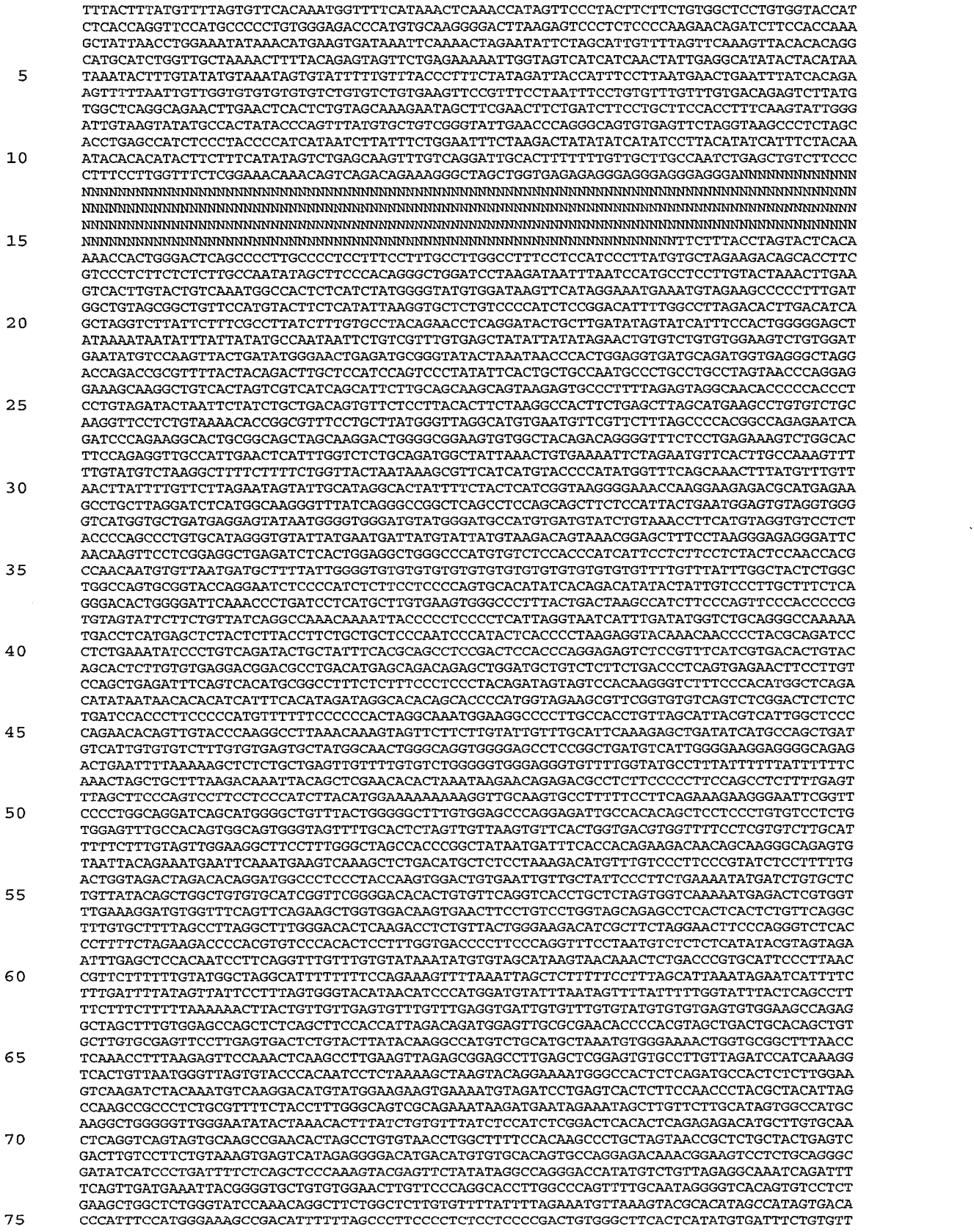
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Replacement Sheet



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Sequence Listing

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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC
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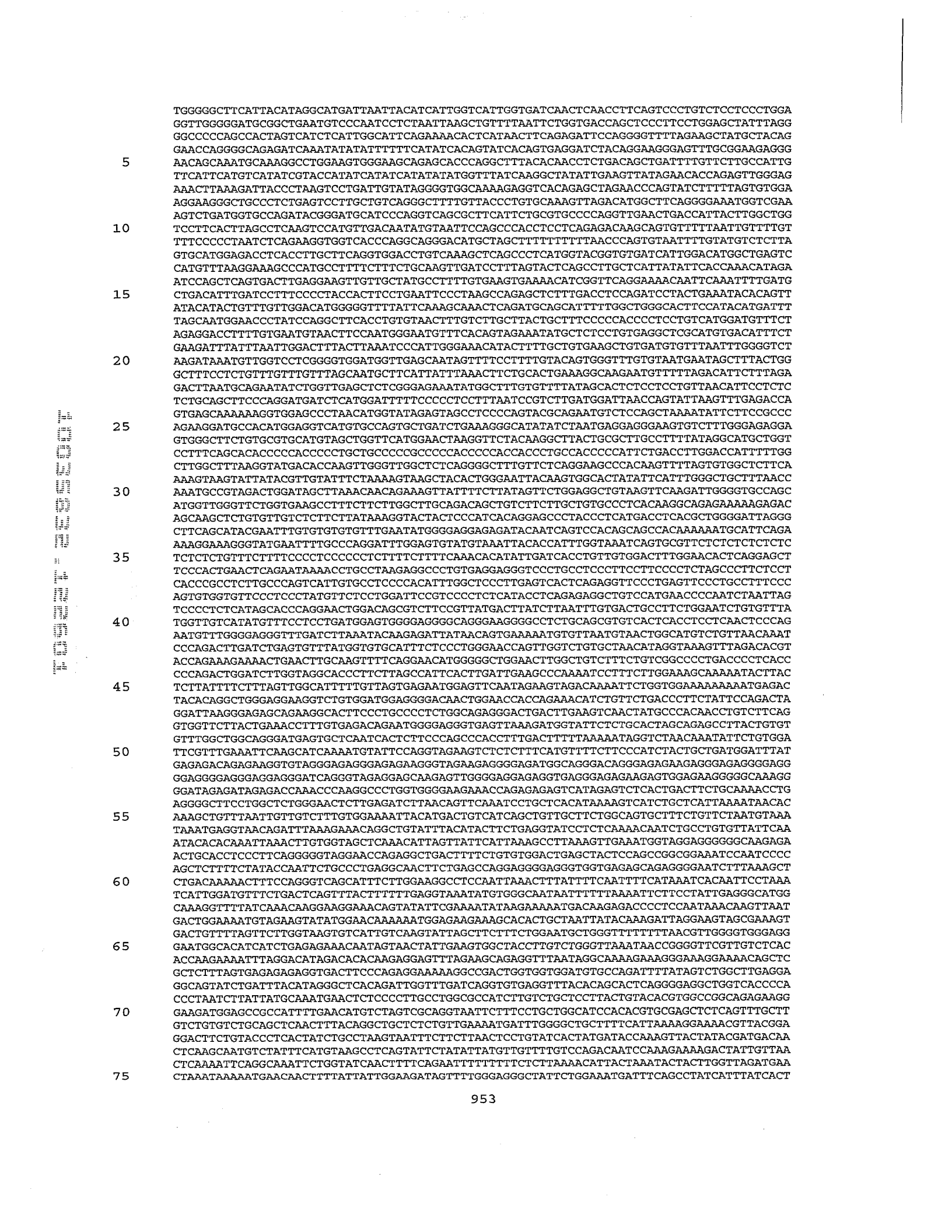
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Filed: June 22, 2001

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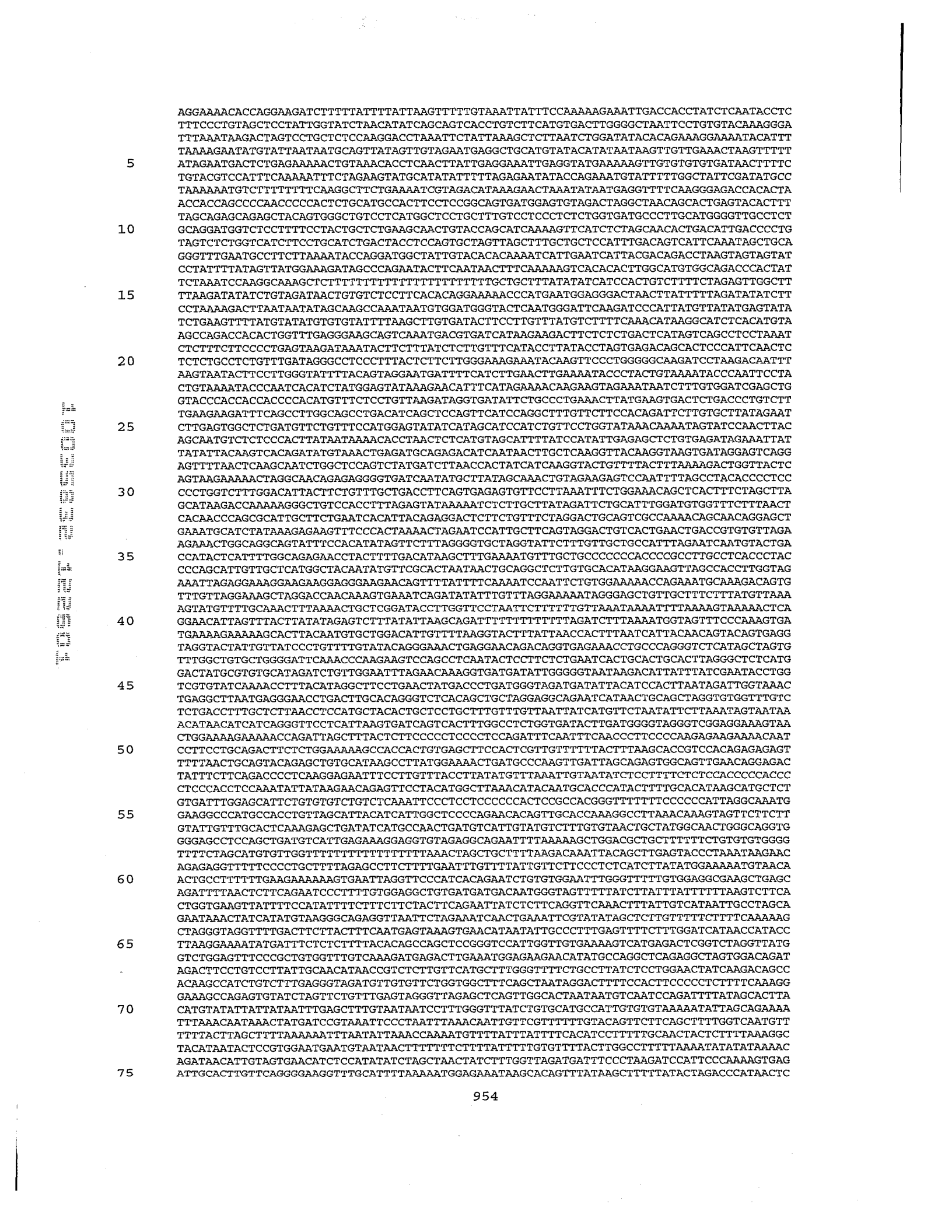
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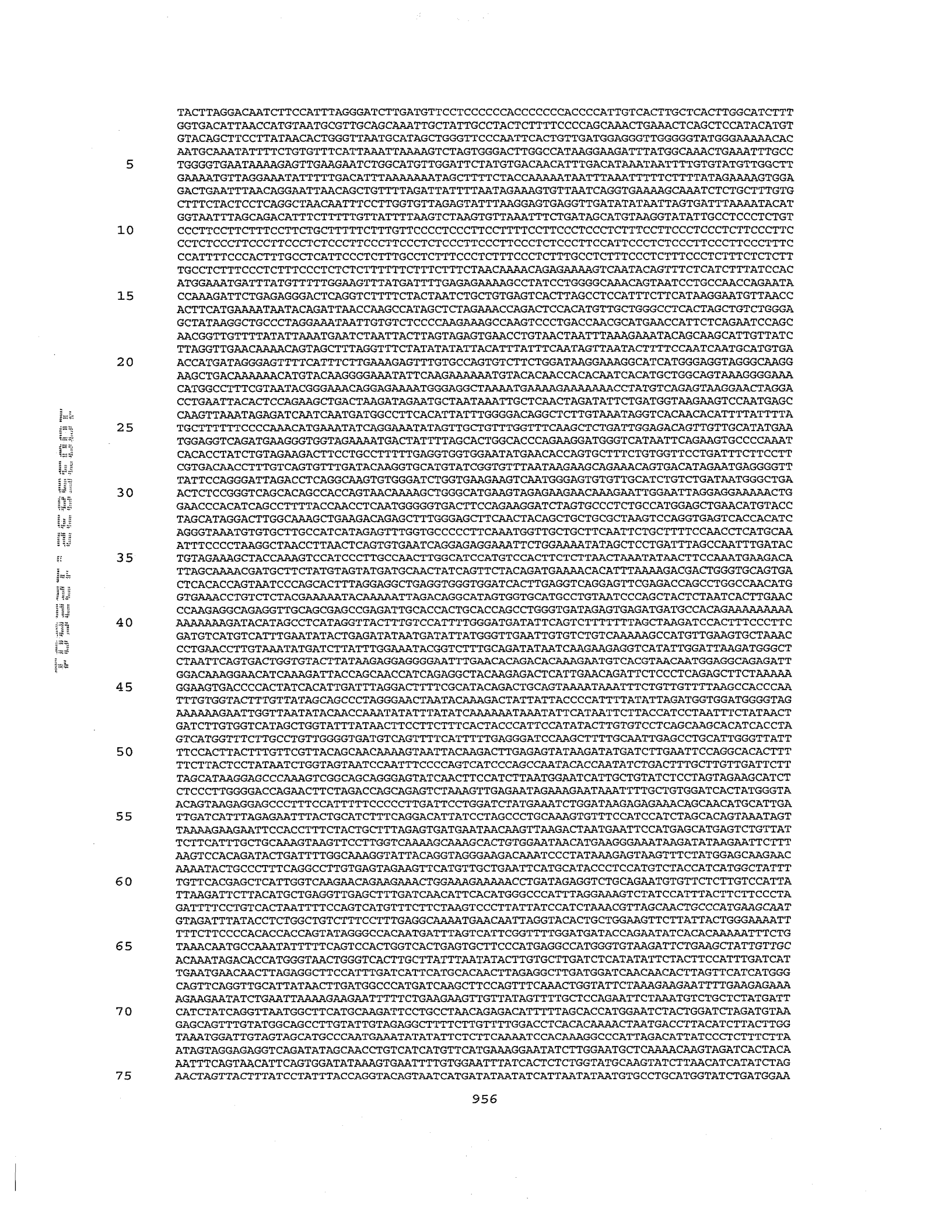


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HUMAN SEQUENCE - mRNA

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Table 45

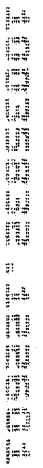
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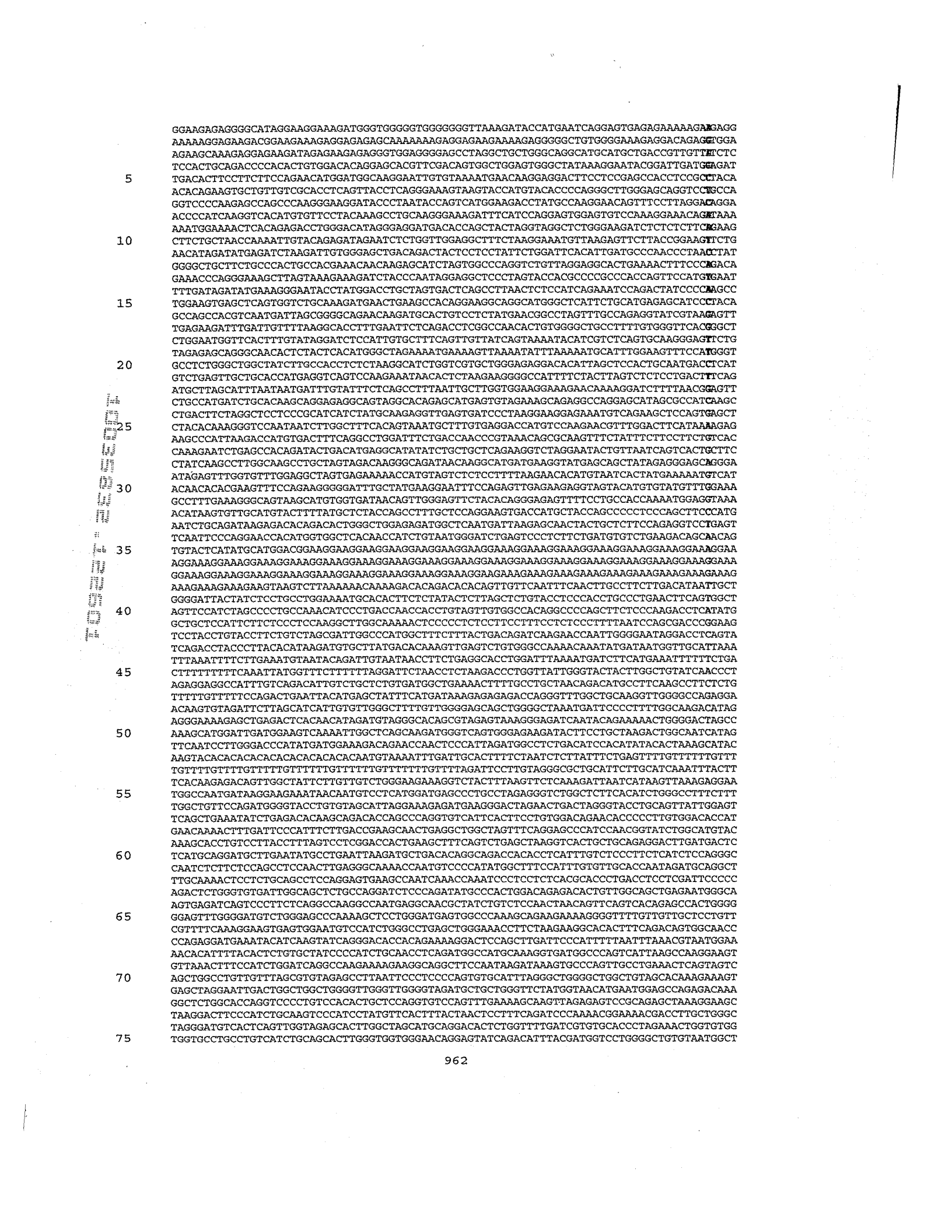
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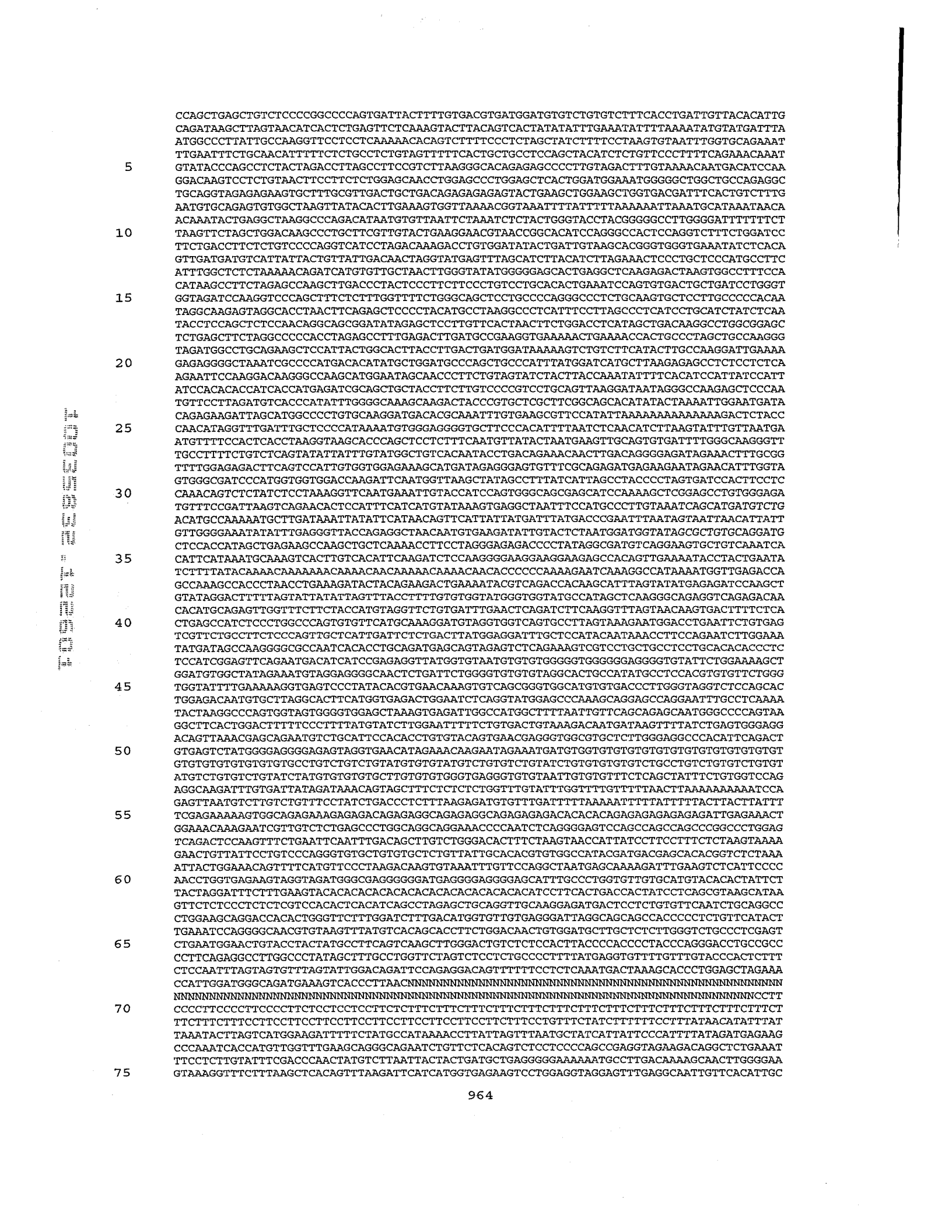
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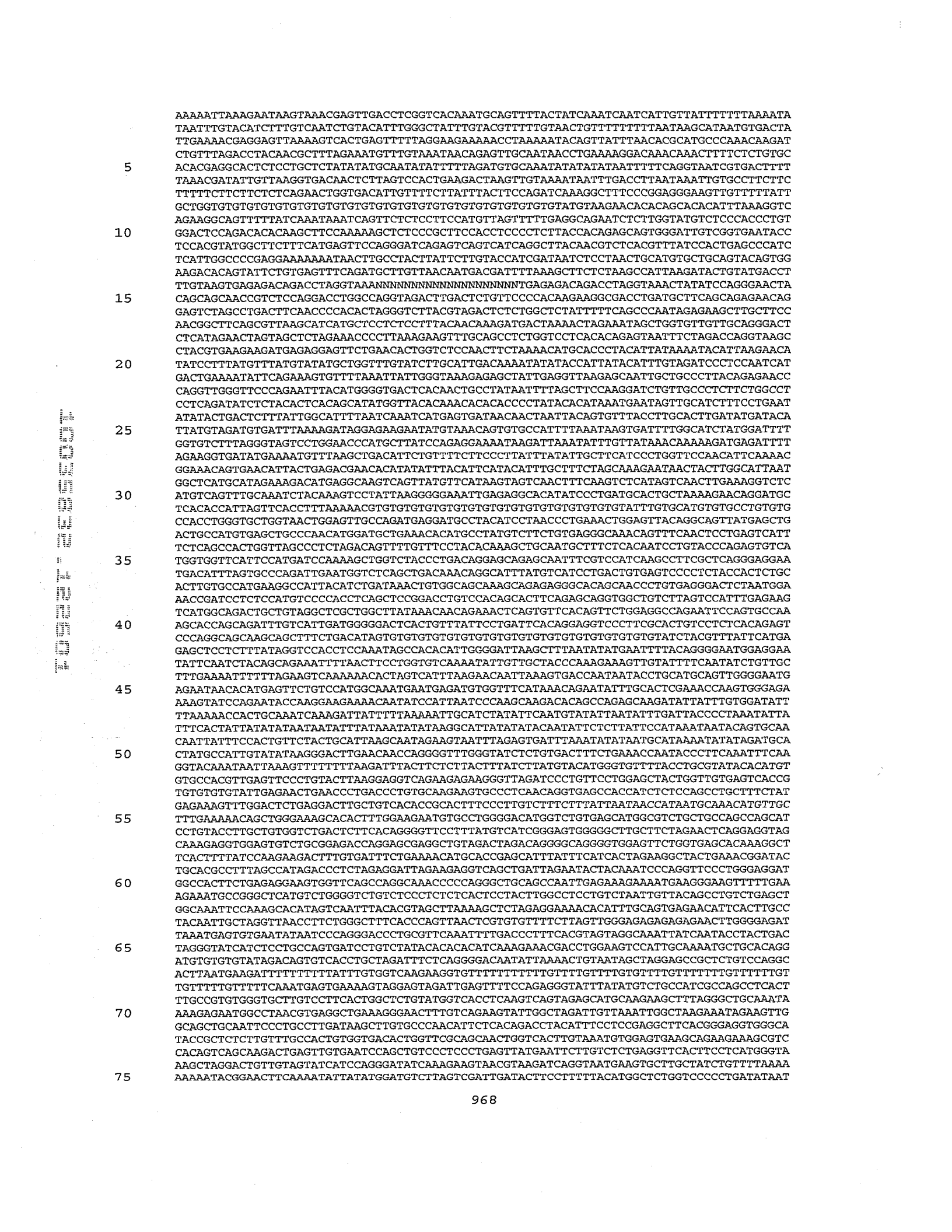
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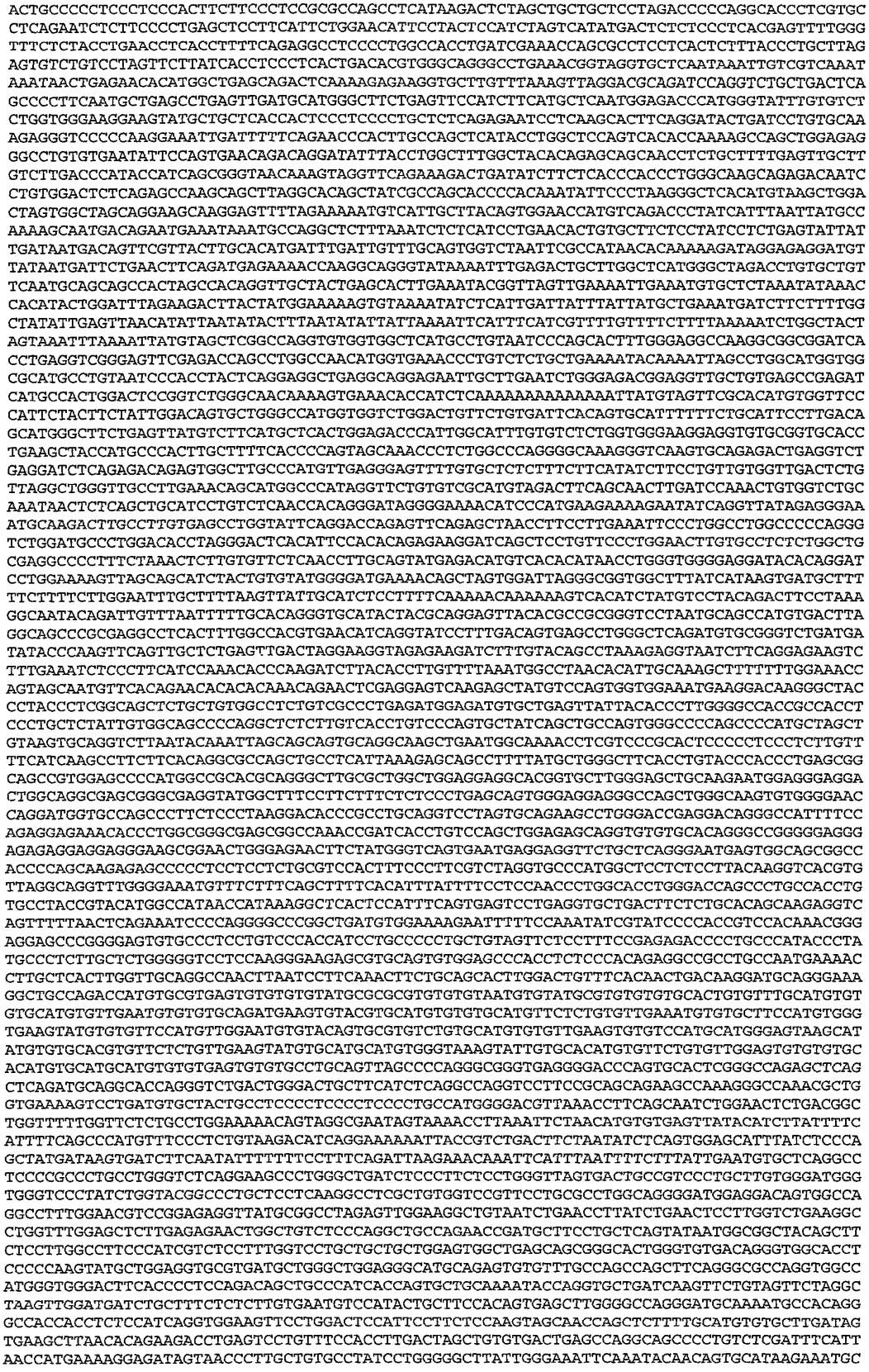
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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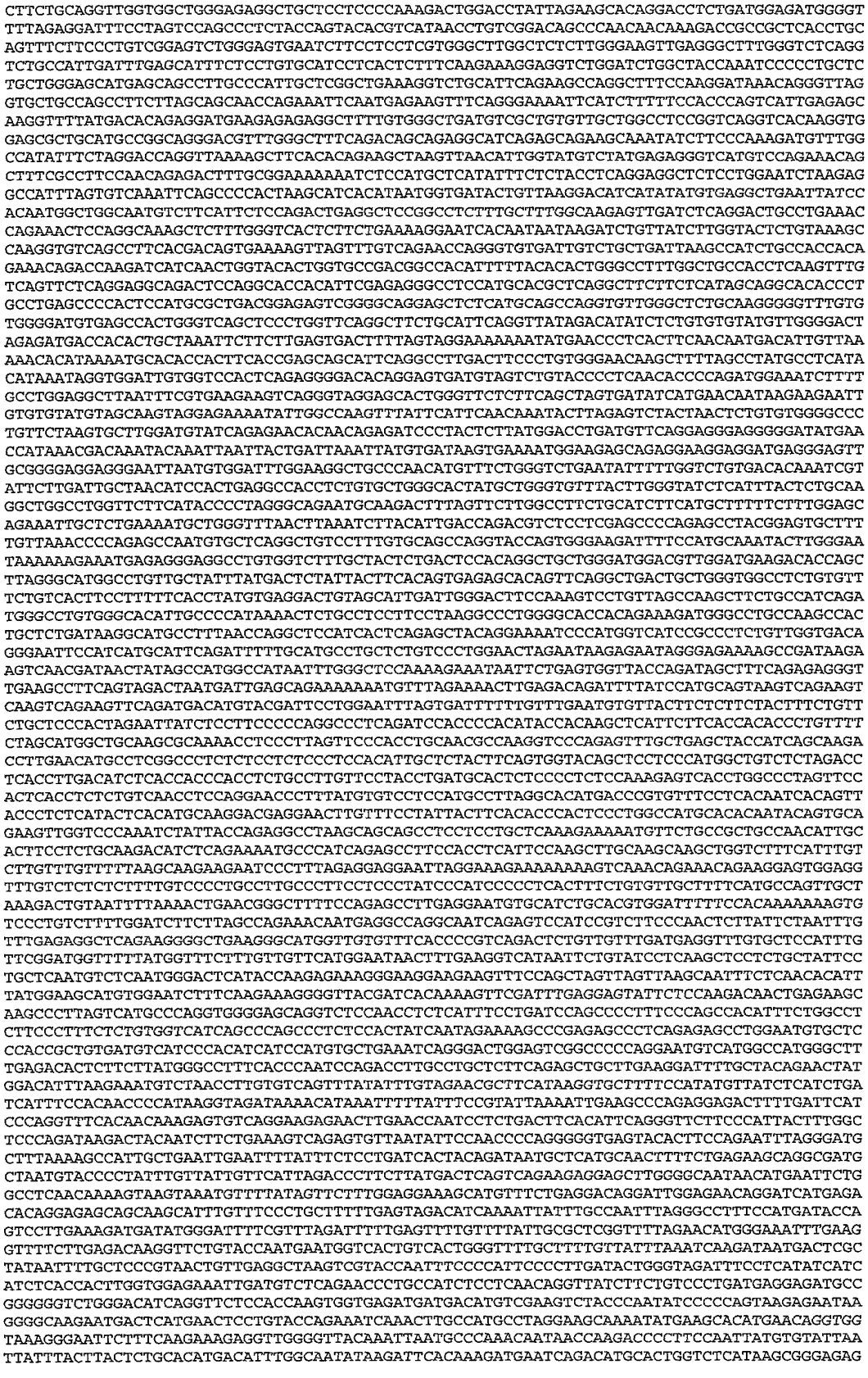
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Replacement Sheet



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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 46

MOUSE NOMENCLATURE

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Celera	mCG21547

HUMAN NOMENCLATURE

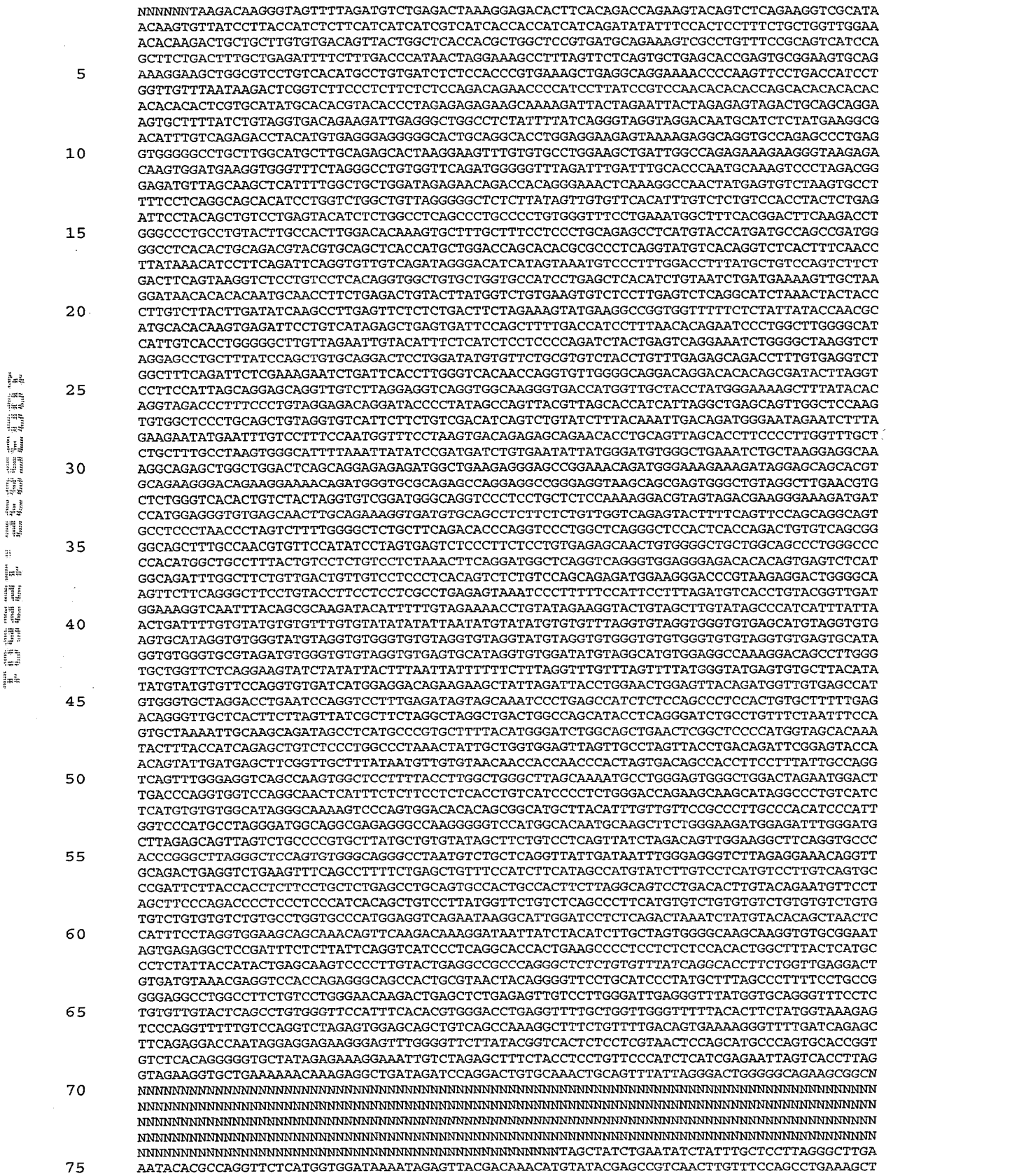
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Celera	hCG1640726

MOUSE SEQUENCE - GENOMIC

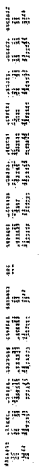
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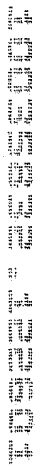
MOUSE SEQUENCE - mRNA

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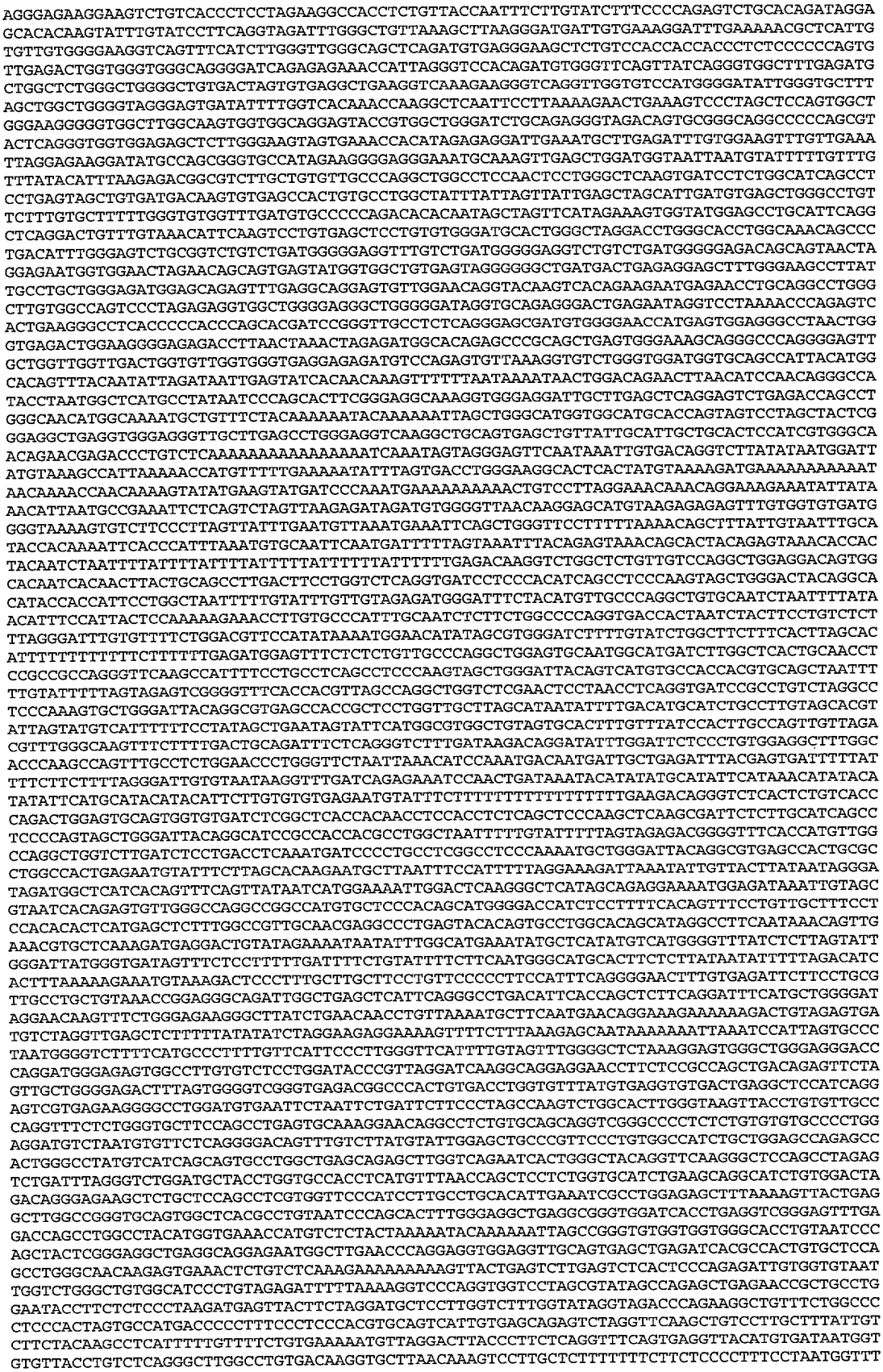
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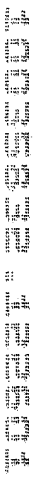
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 47

MOUSE NOMENCLATURE

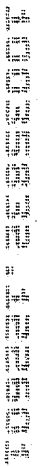
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HUMAN NOMENCLATURE

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MOUSE SEQUENCE - GENOMIC

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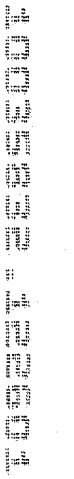
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MOUSE SEQUENCE - mRNA
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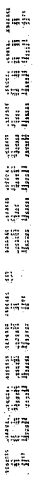
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HUMAN SEQUENCE - mRNA

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Table 48

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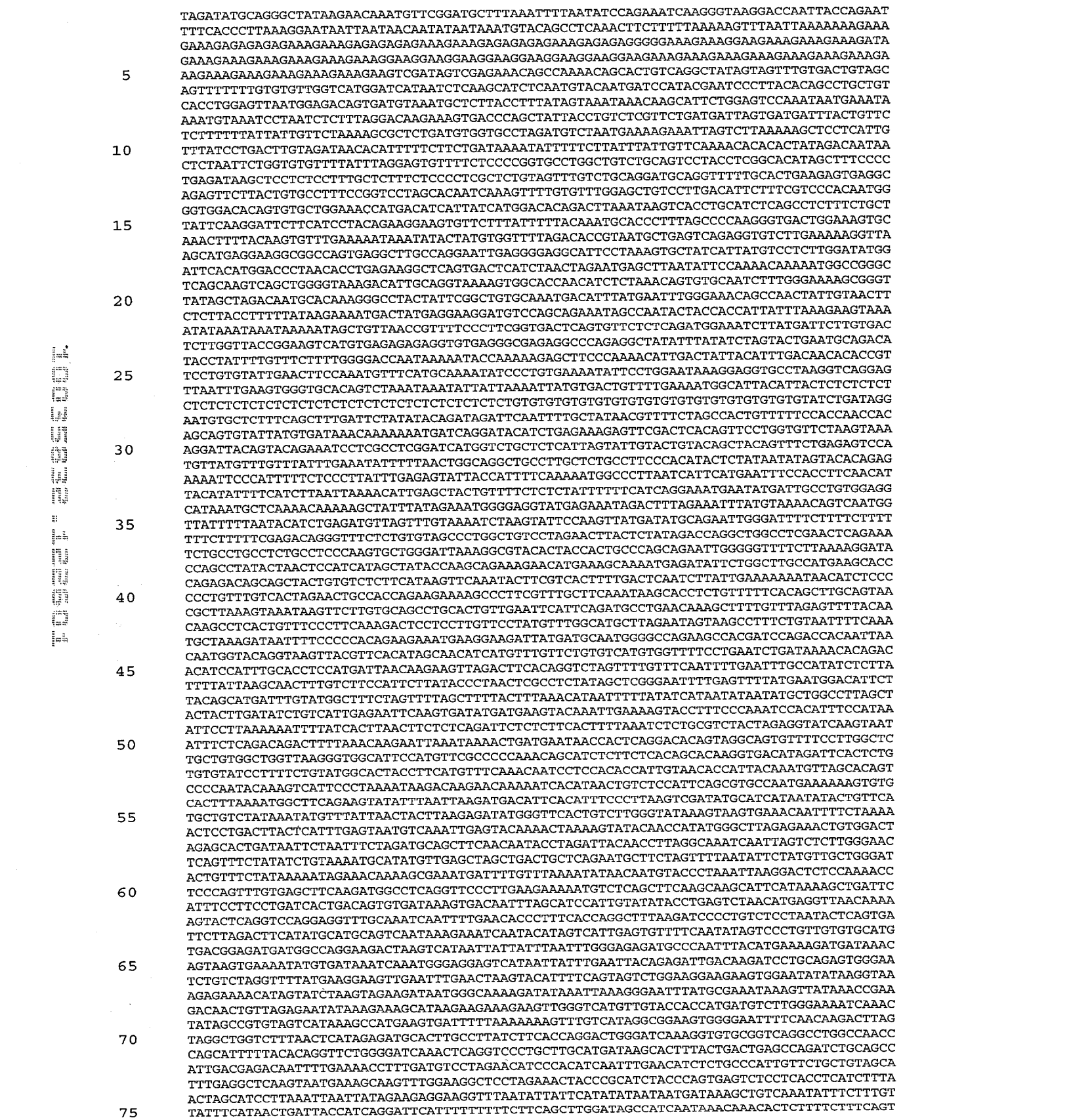
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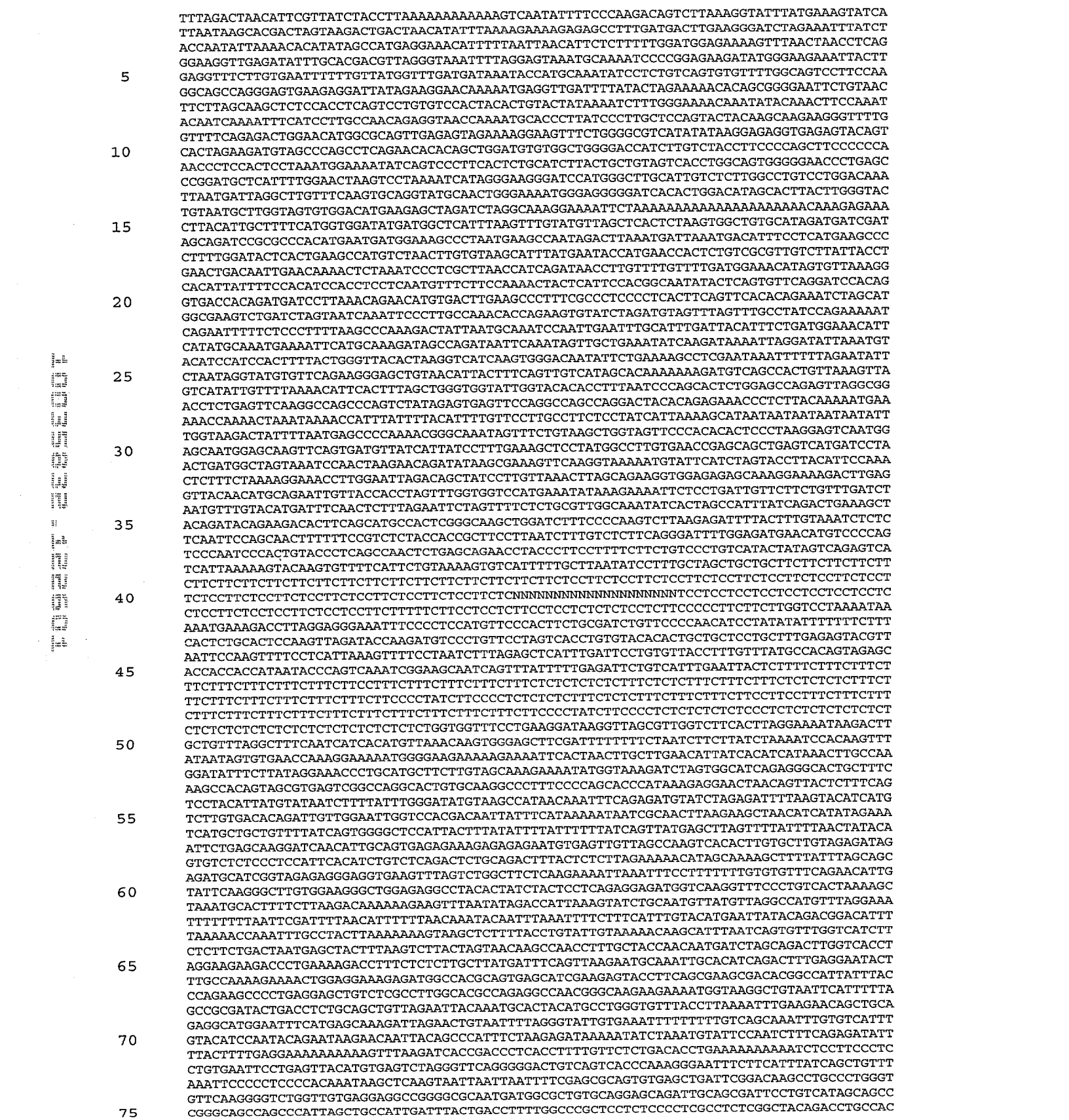
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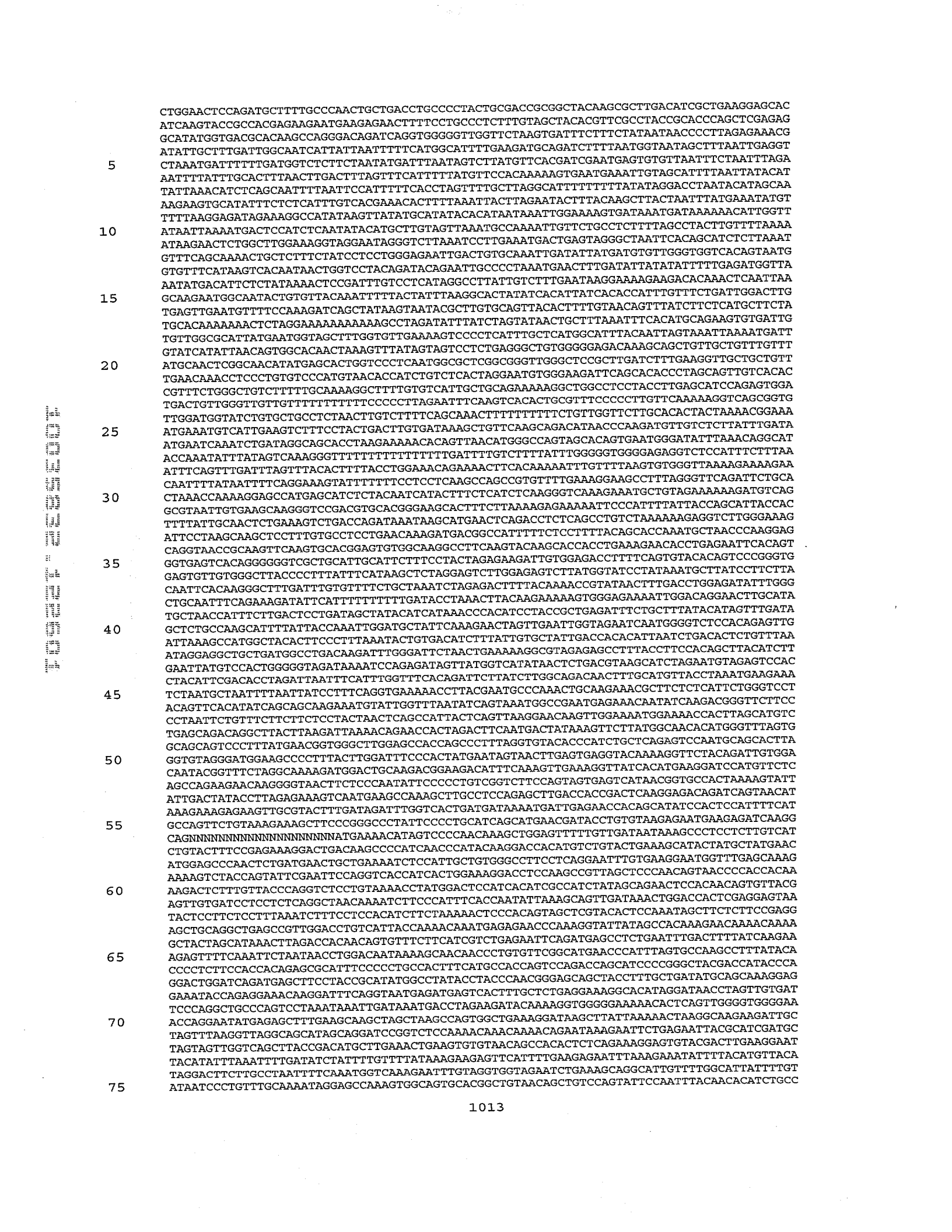


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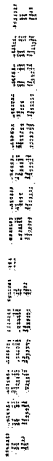
MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING
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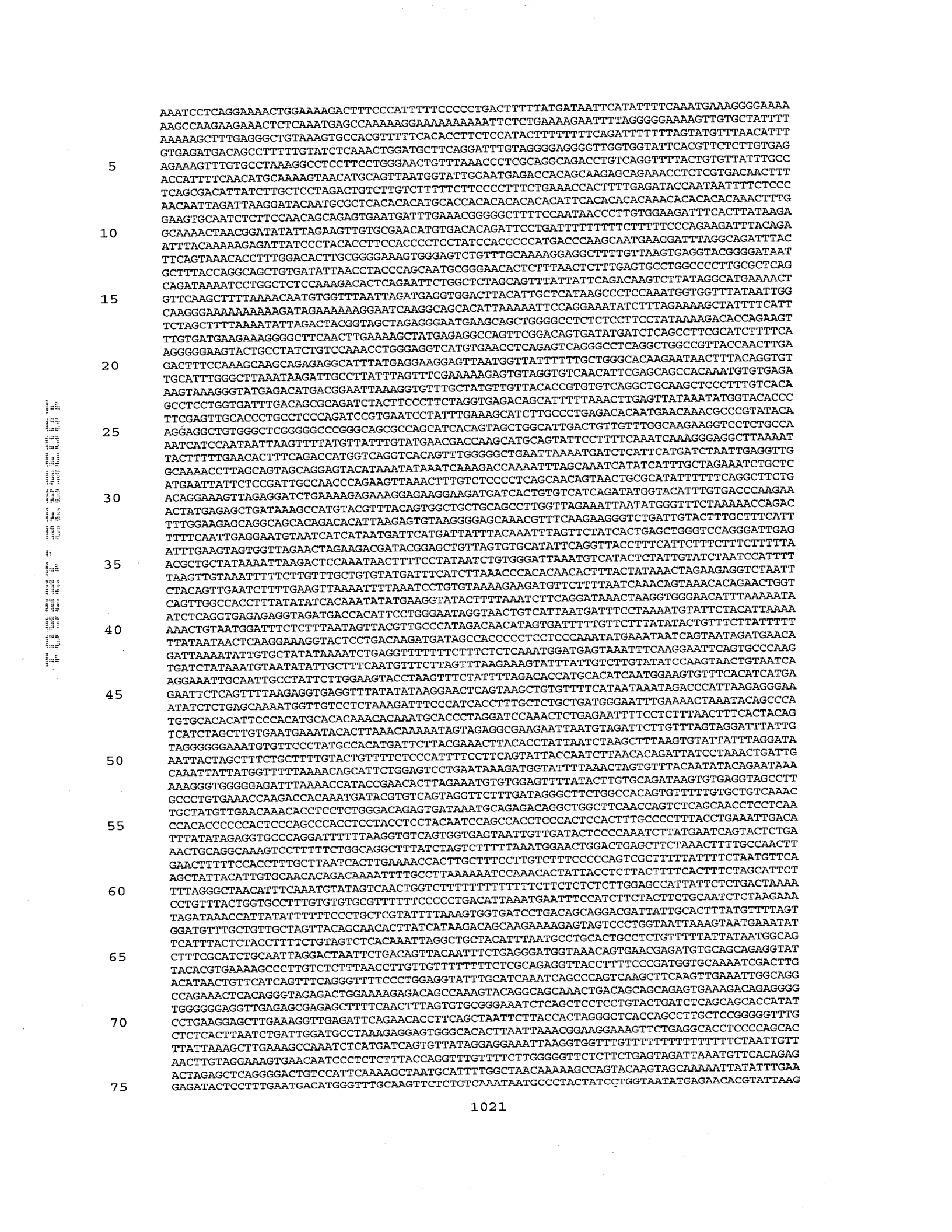


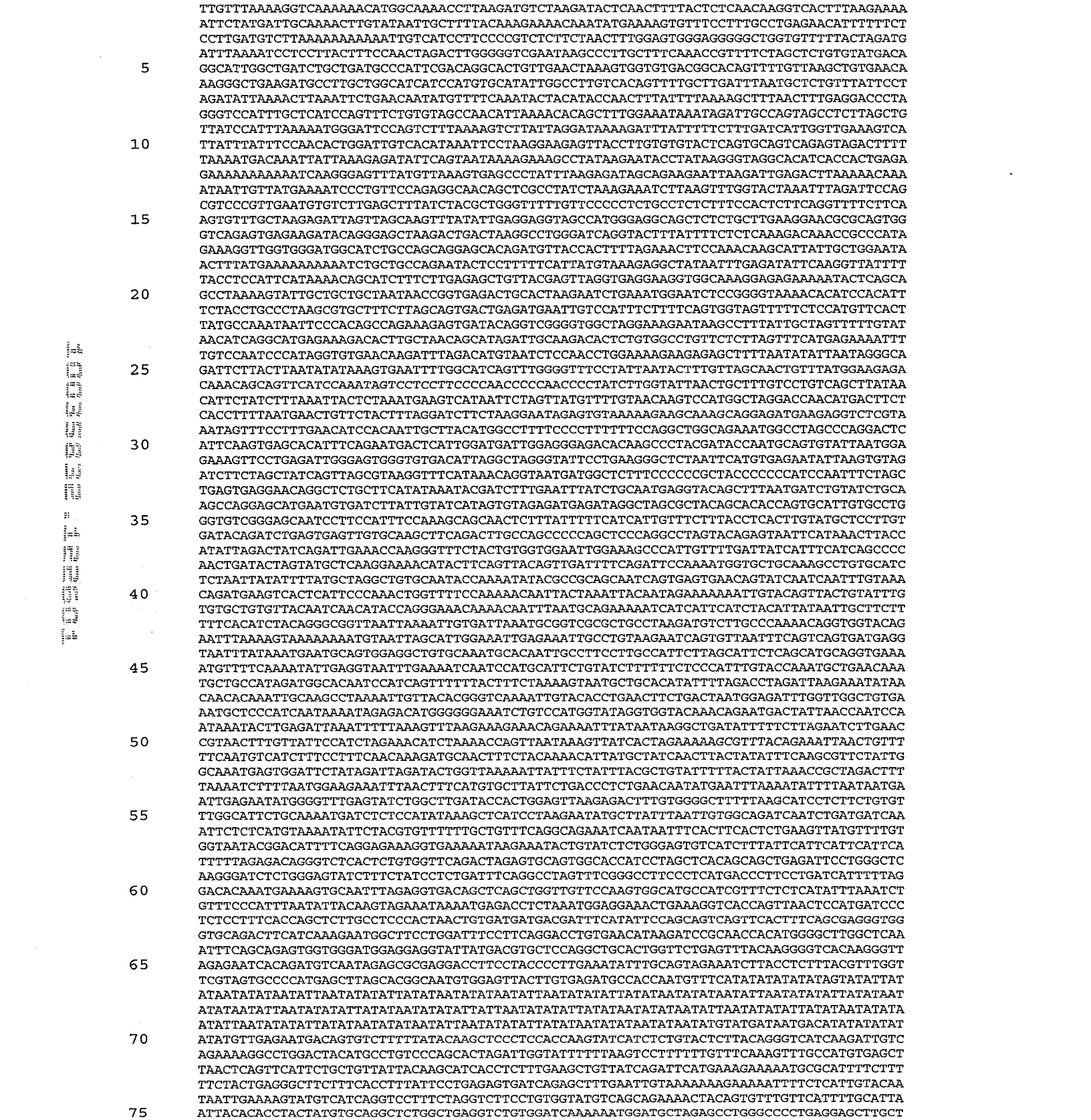


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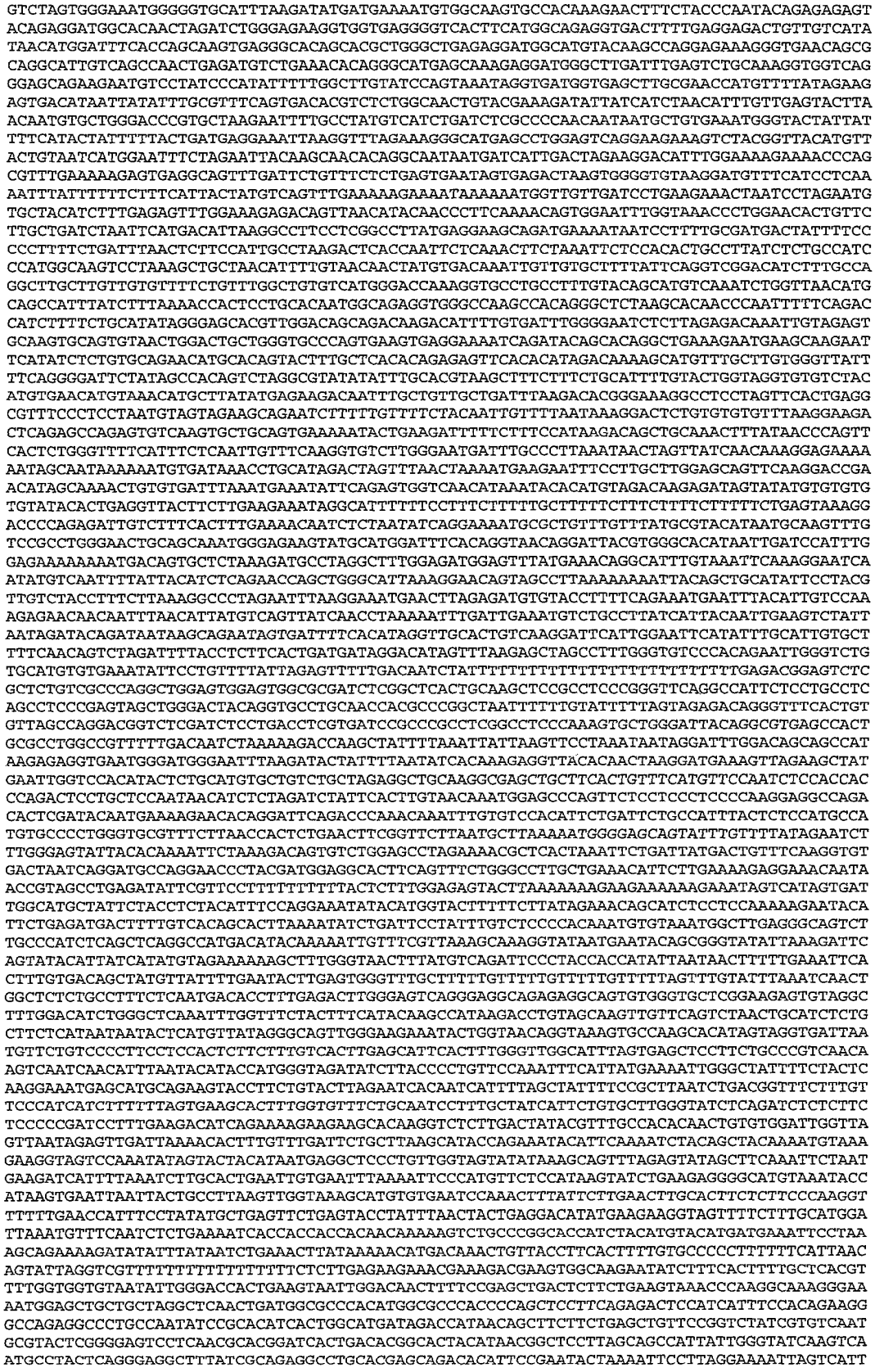
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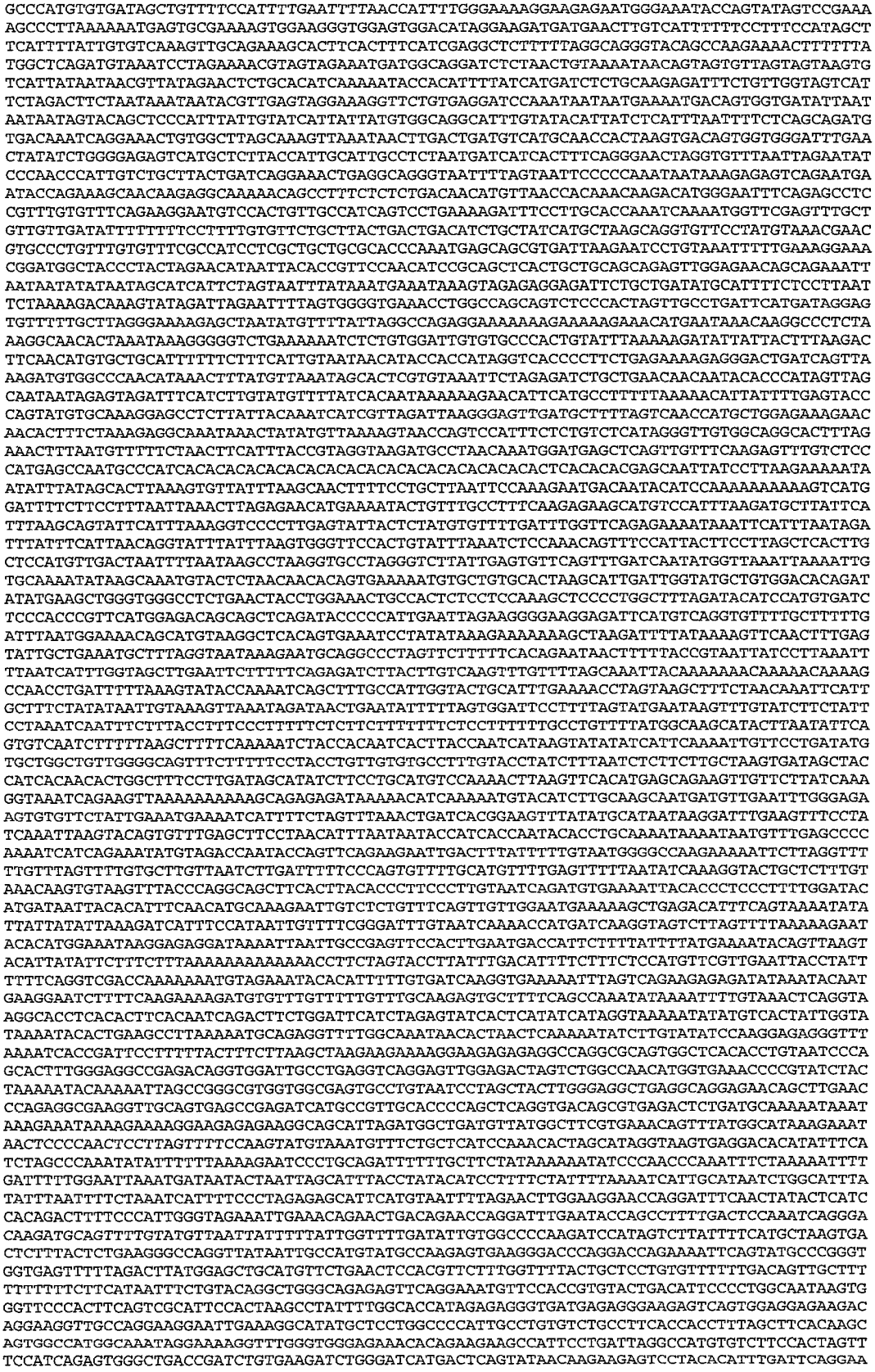
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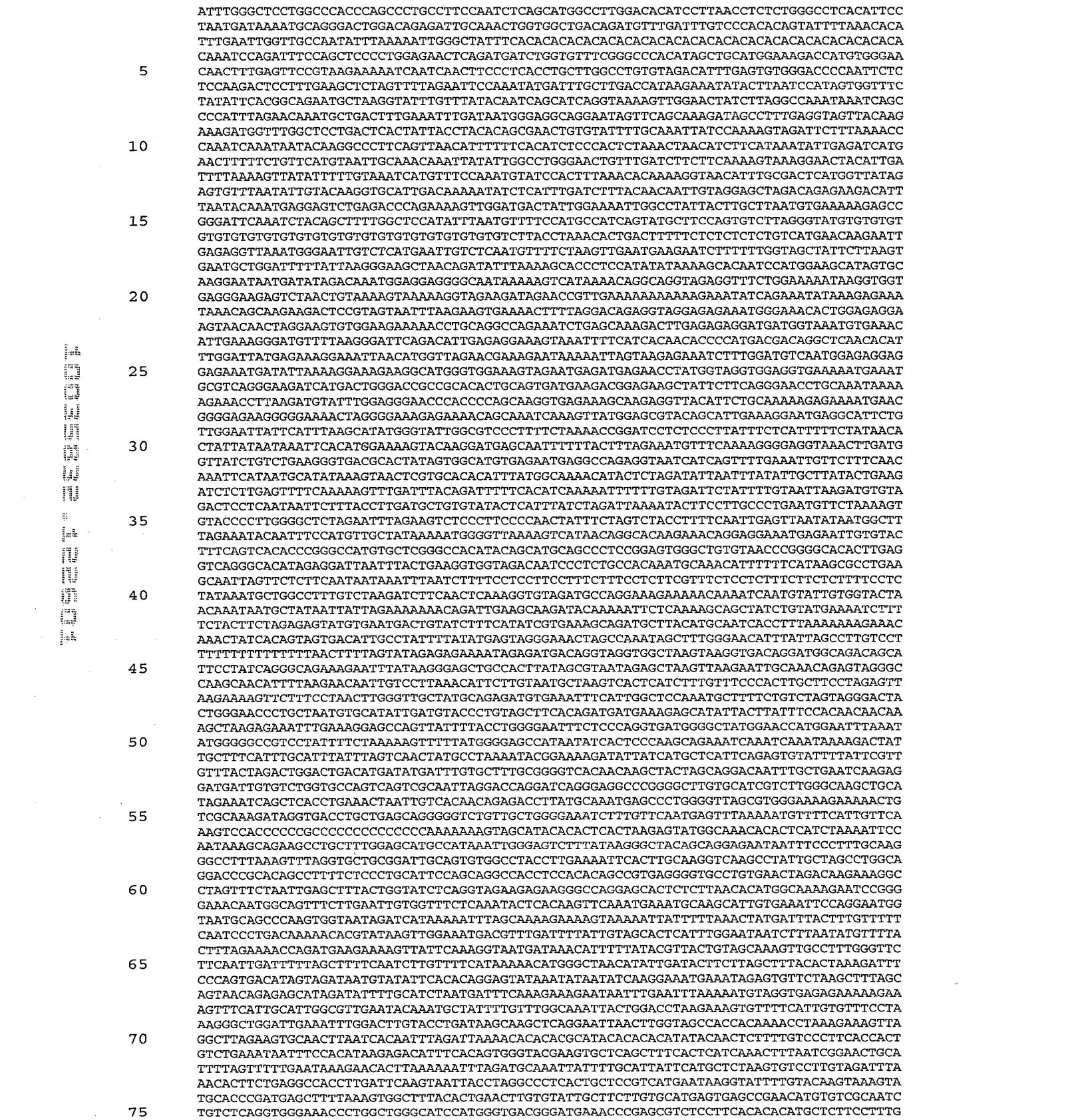


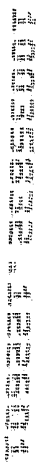


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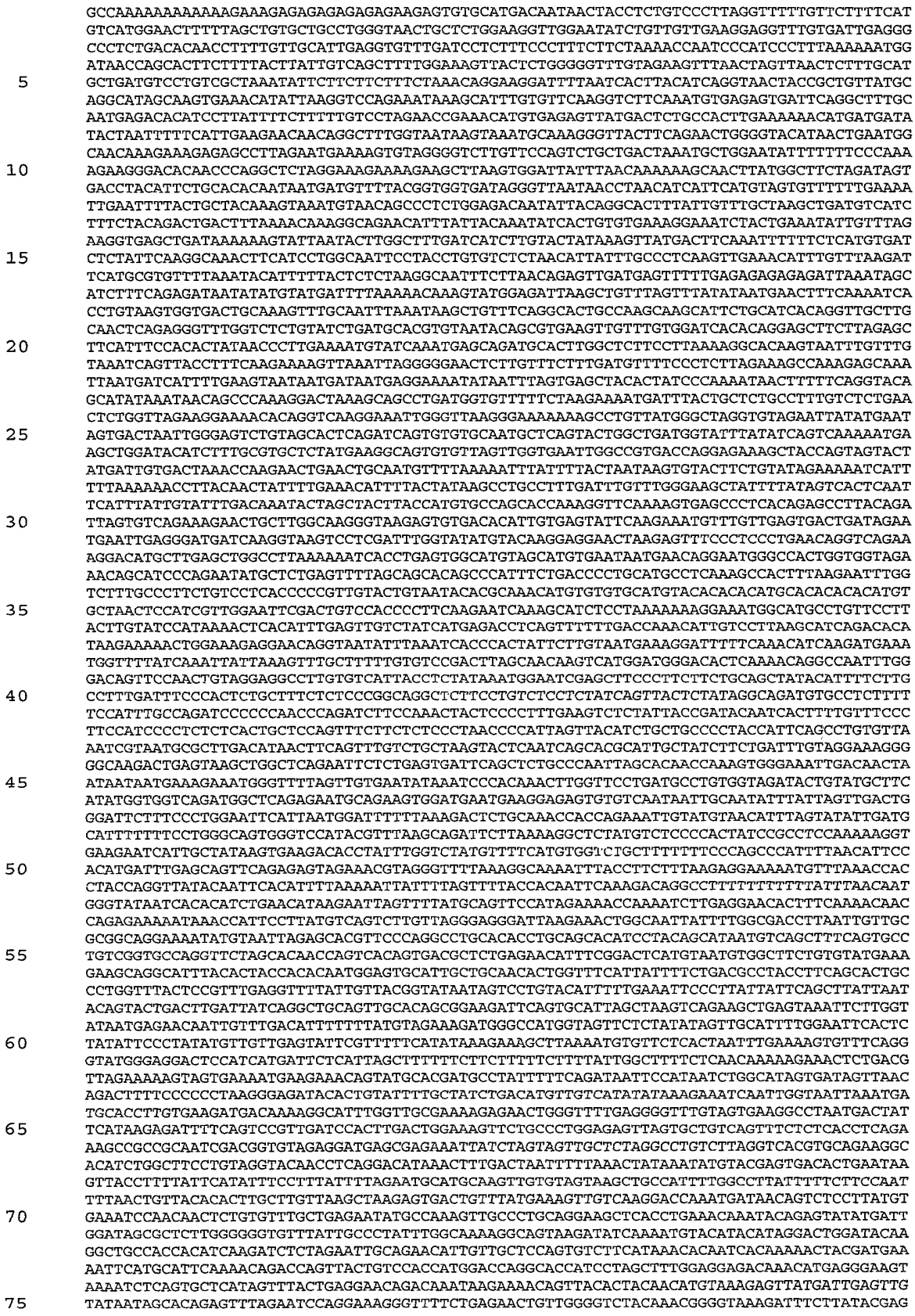


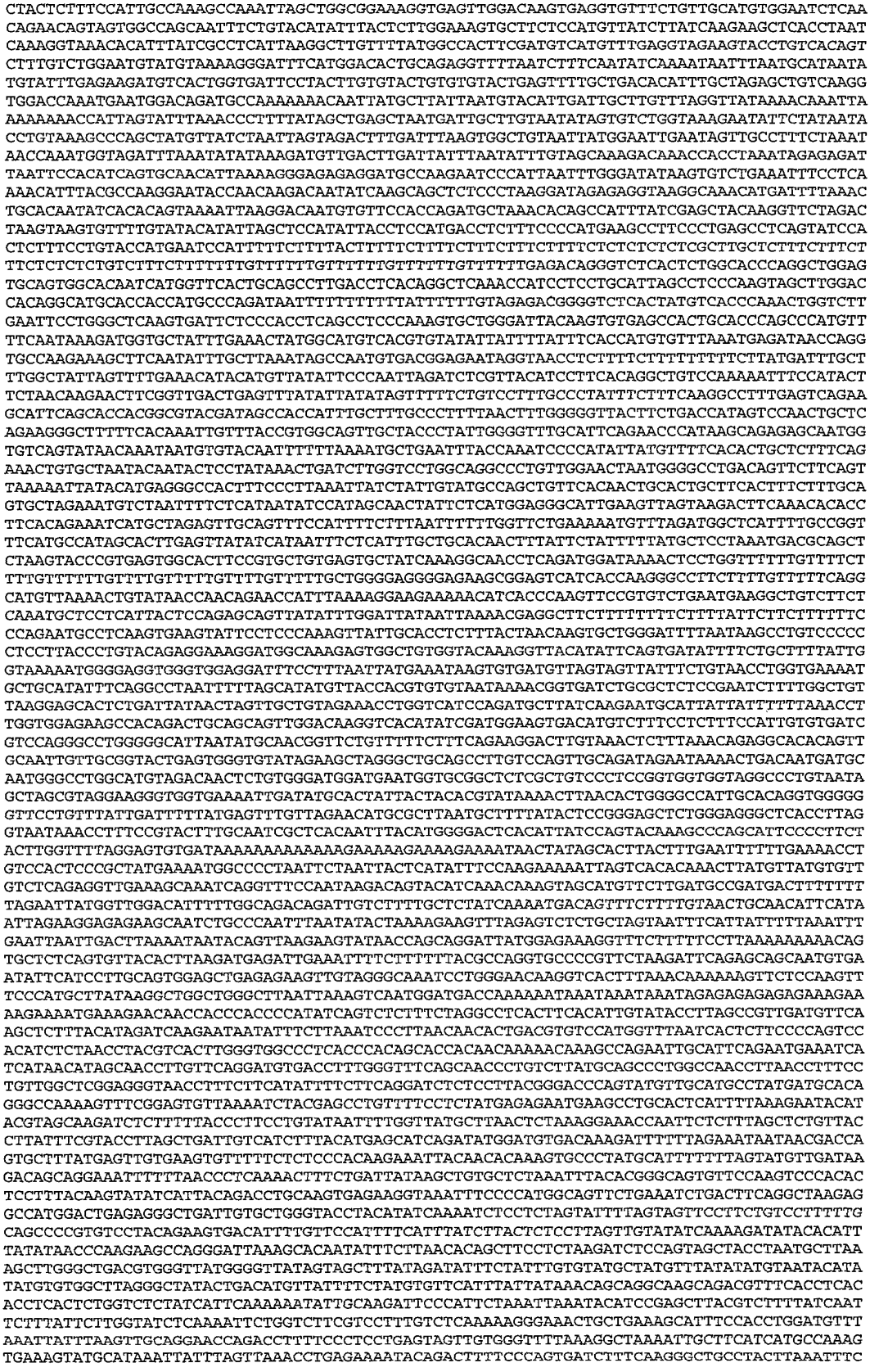


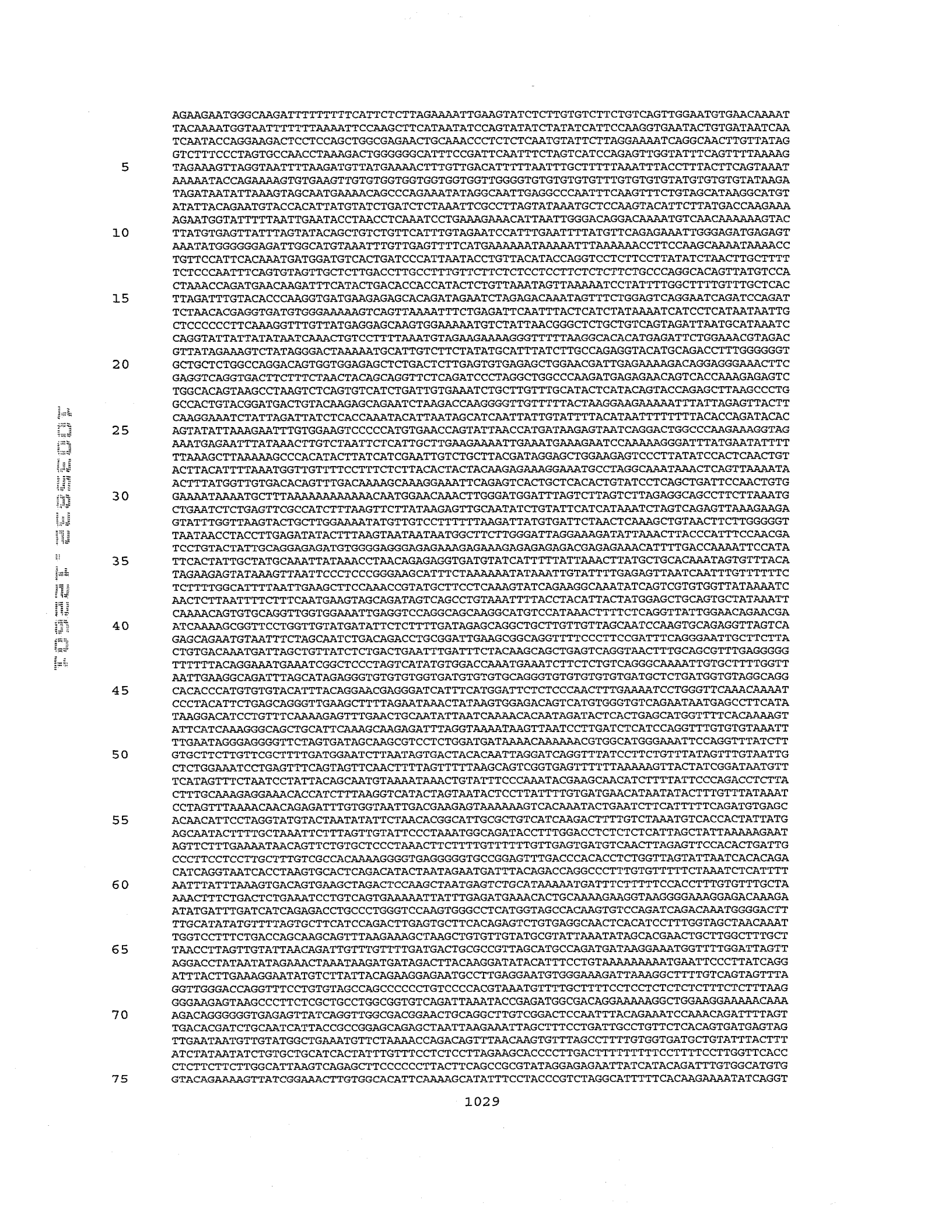




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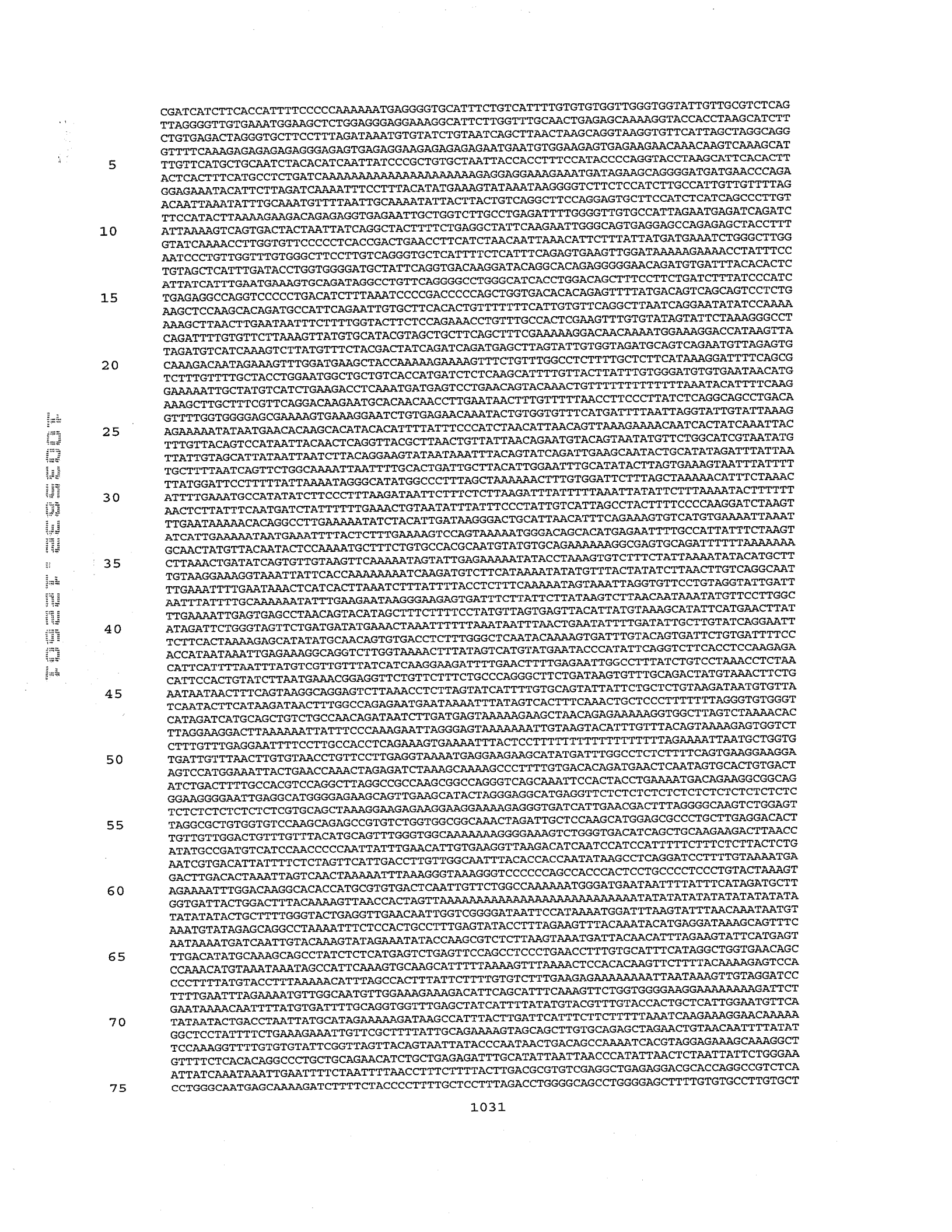




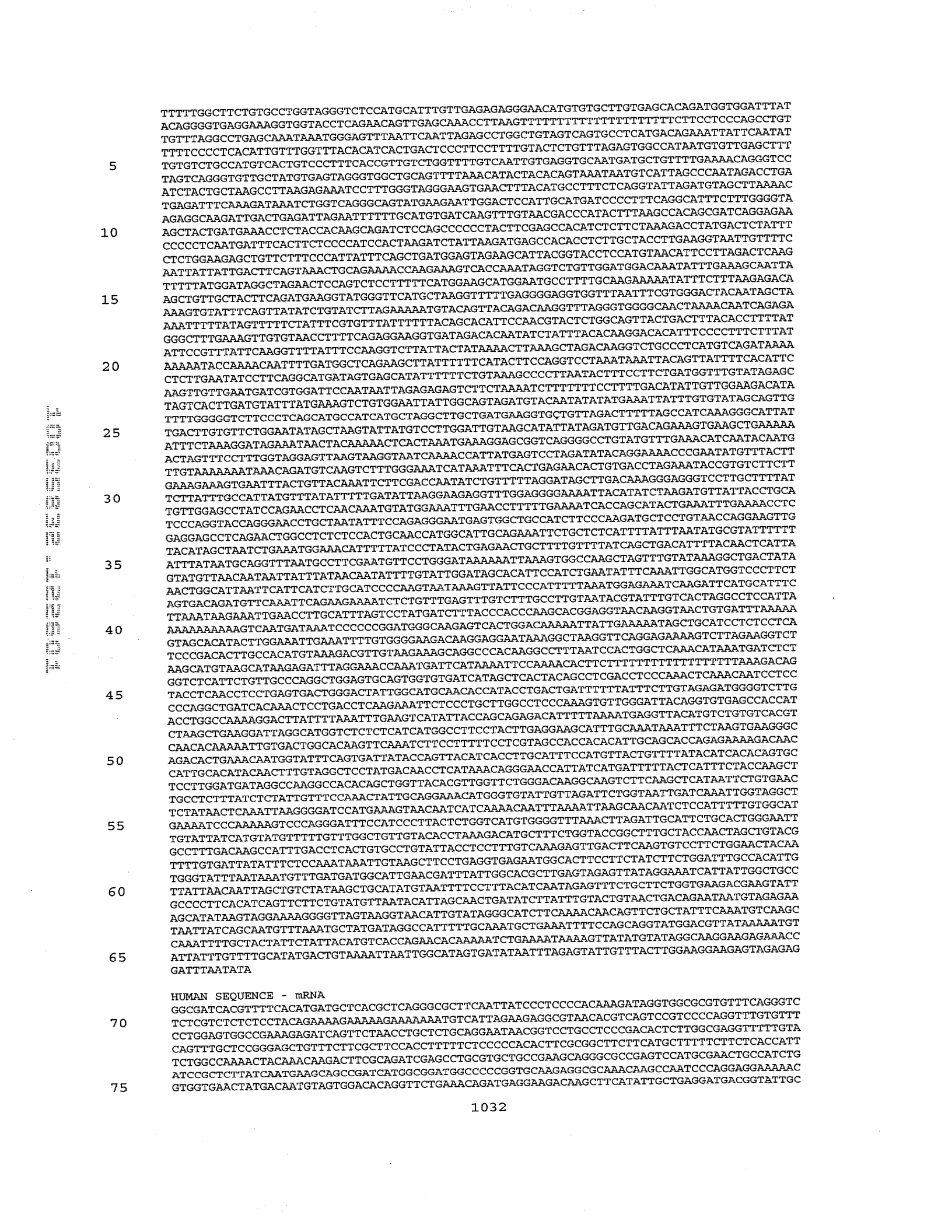


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HUMAN SEQUENCE - mRNA

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Table 49

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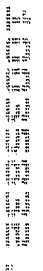
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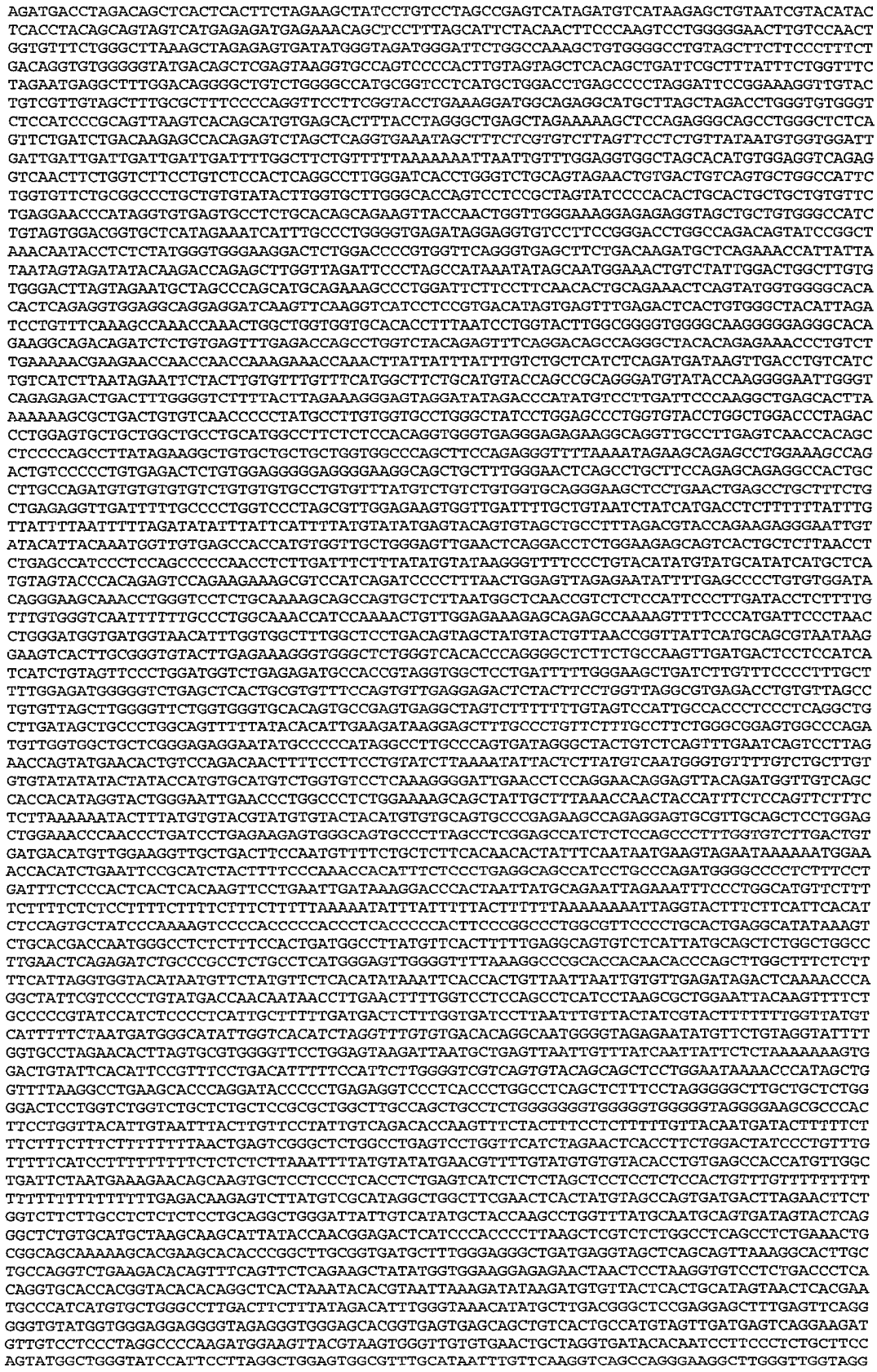
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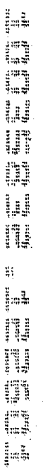
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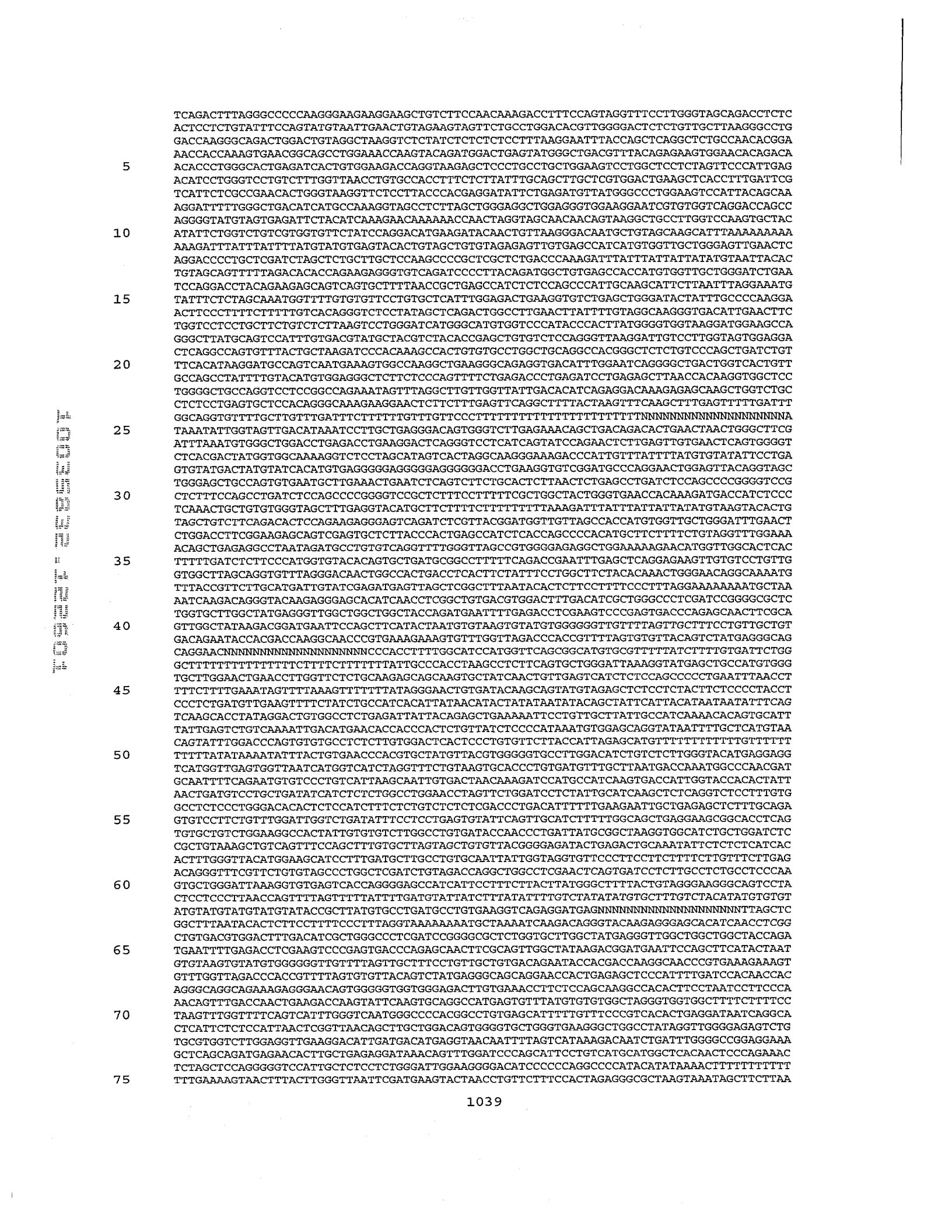
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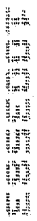




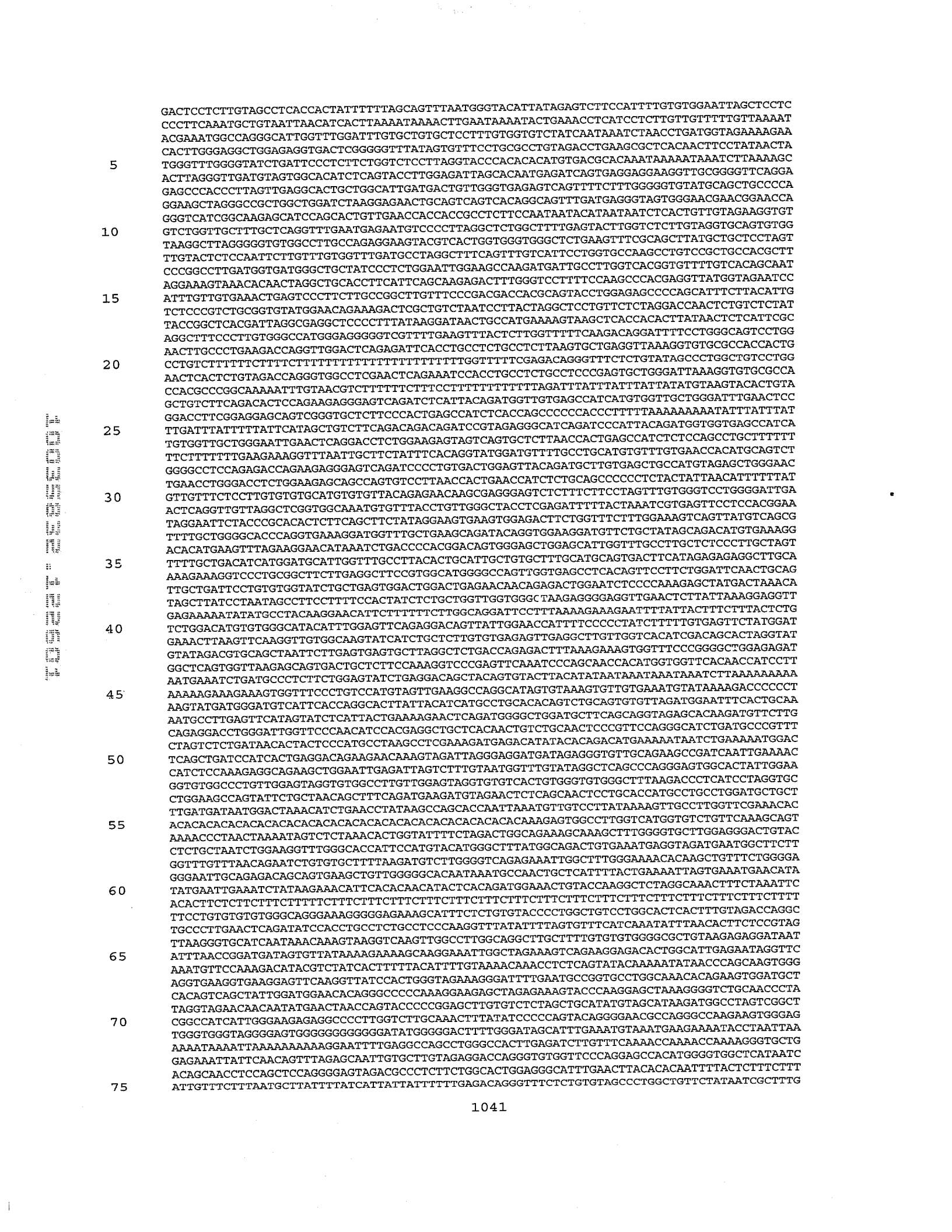
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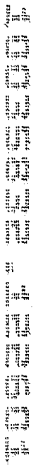
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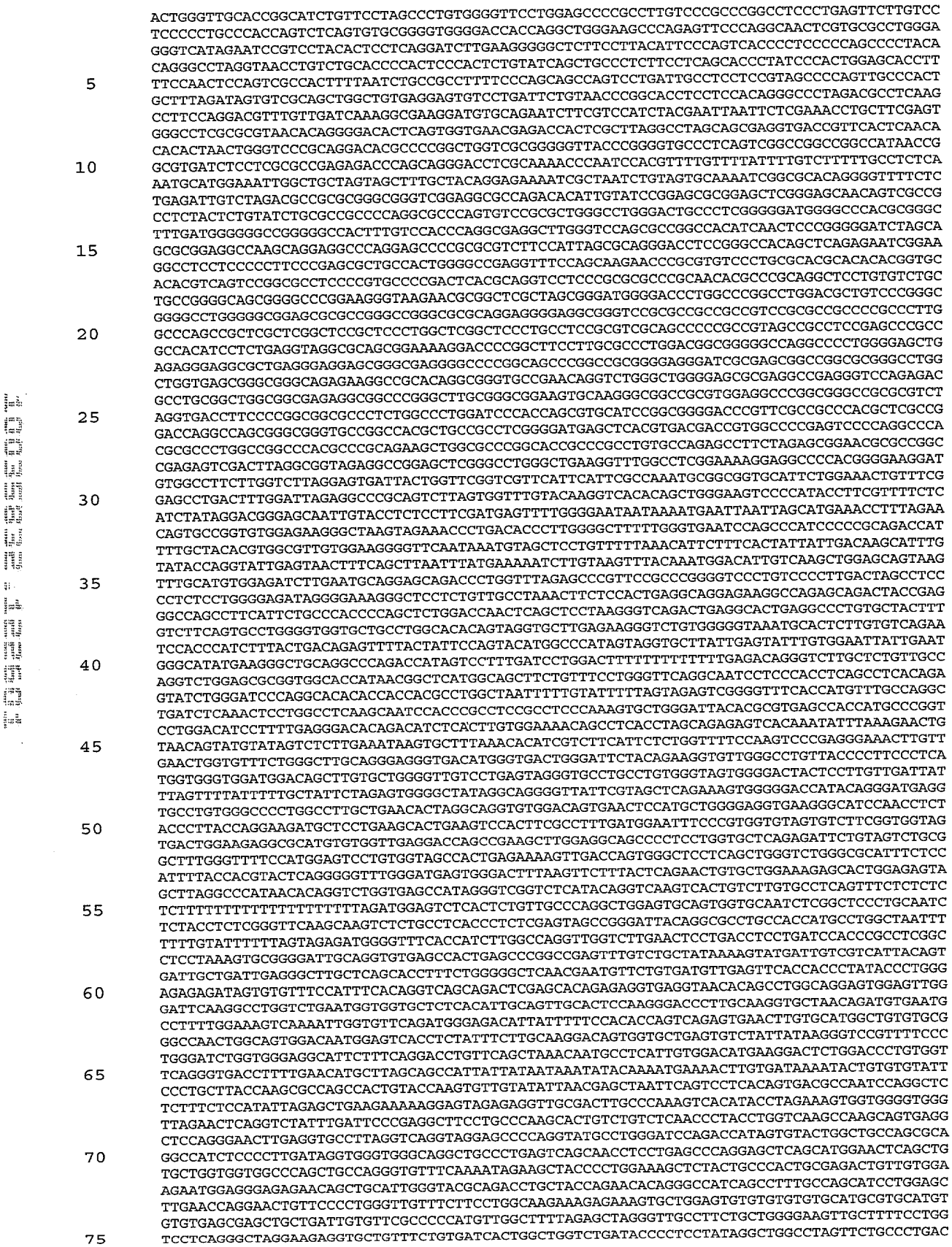
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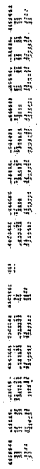
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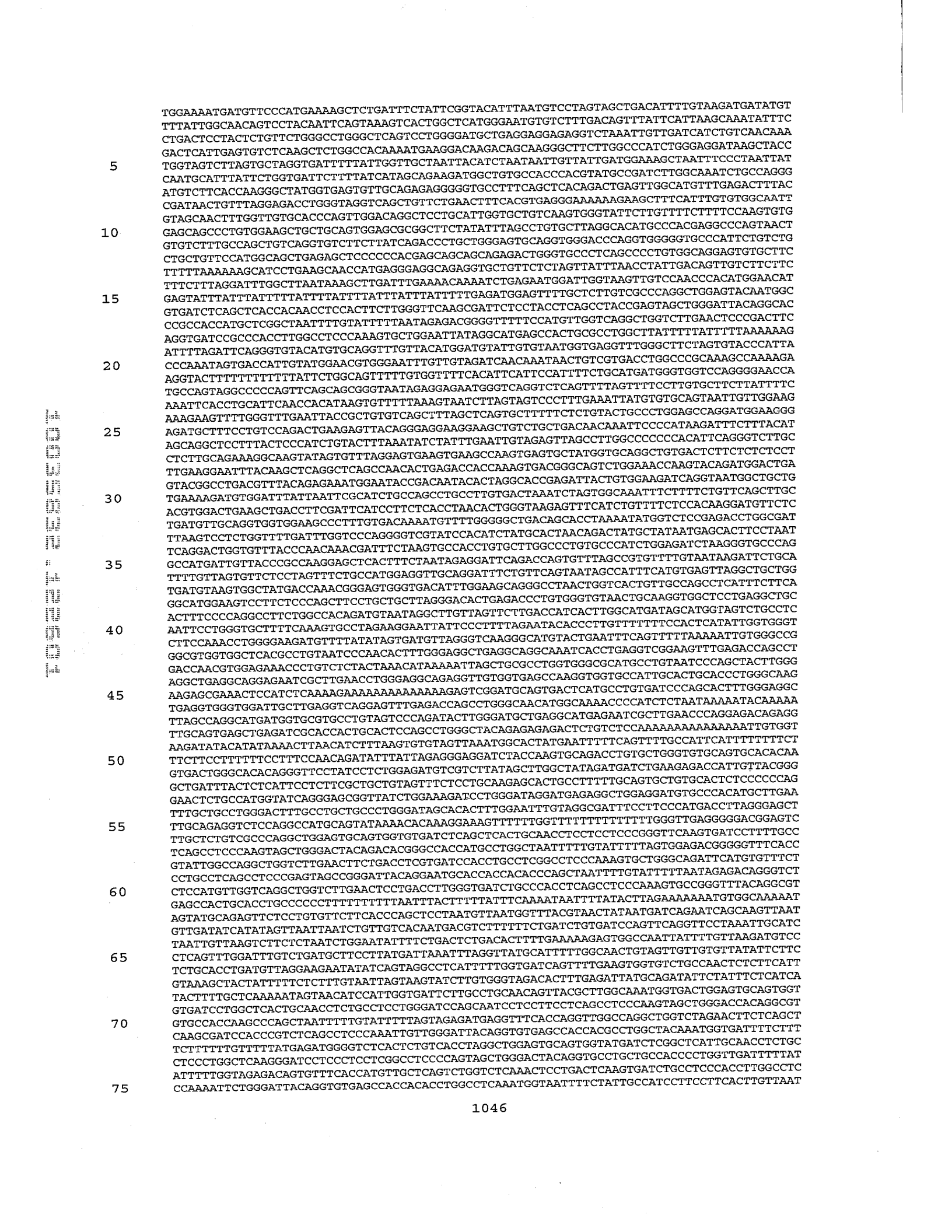


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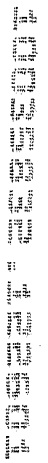


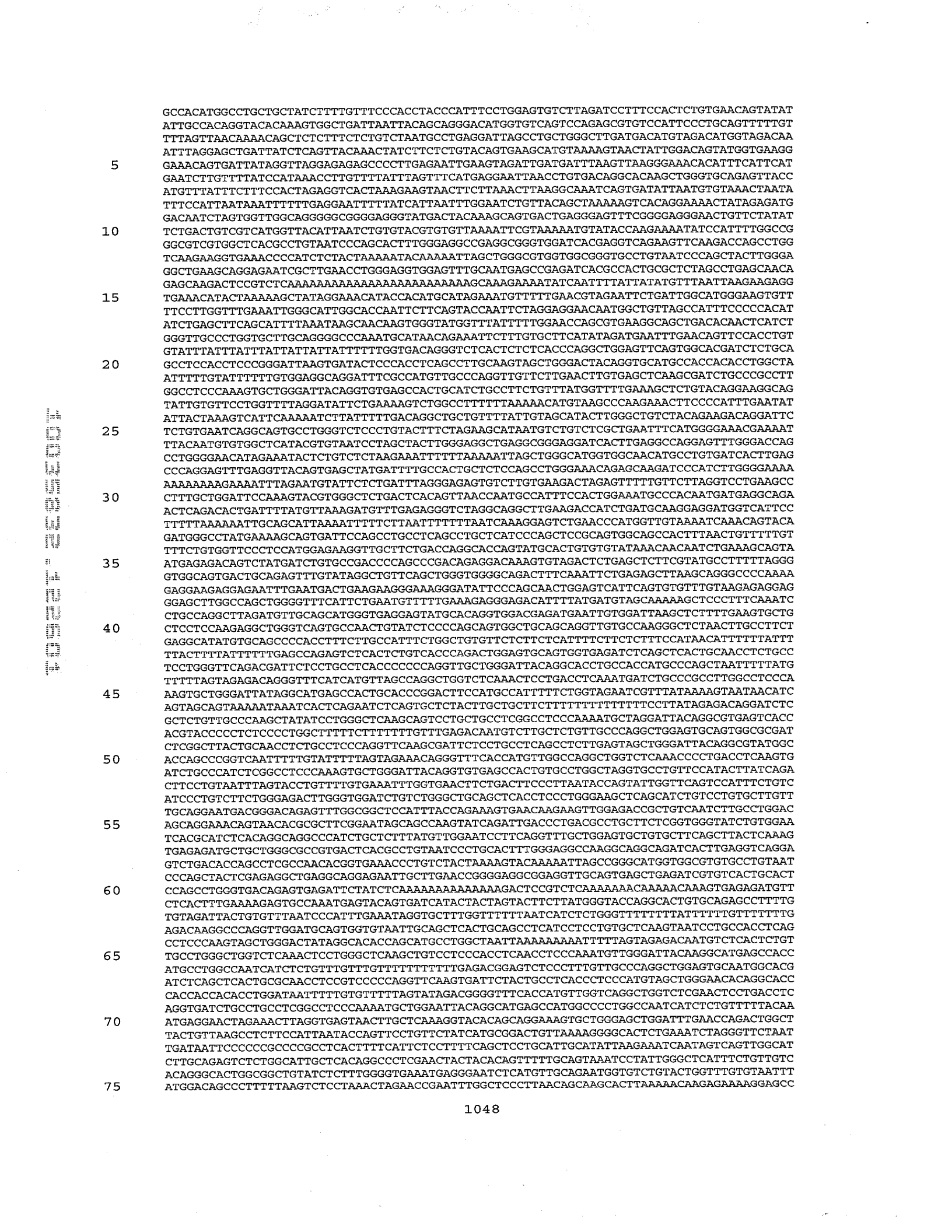


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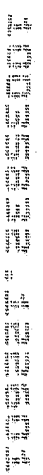


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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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Table 50

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ICSGNM Nfatc1

Celera mCG18180

HUMAN NOMENCLATURE

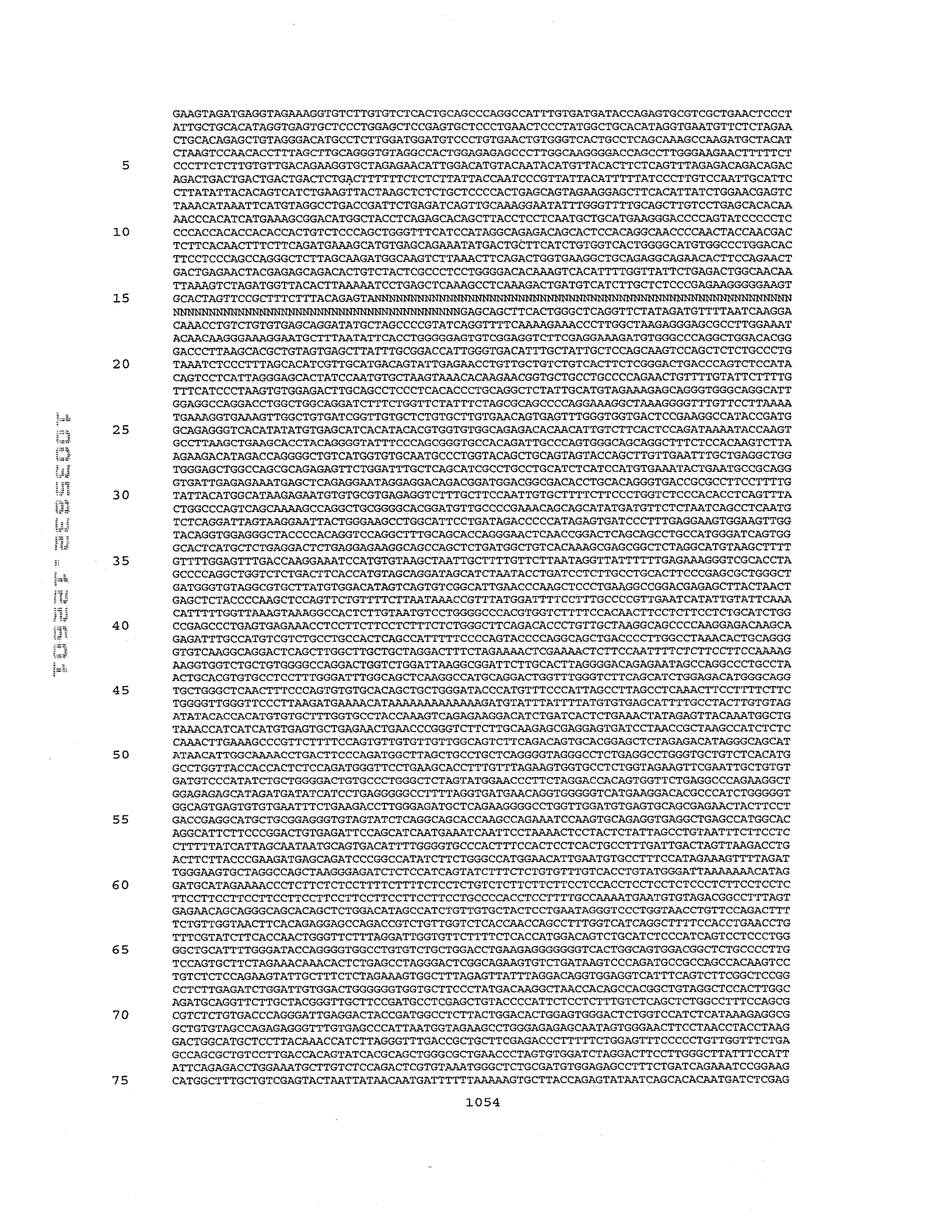
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MOUSE SEQUENCE - GENOMIC

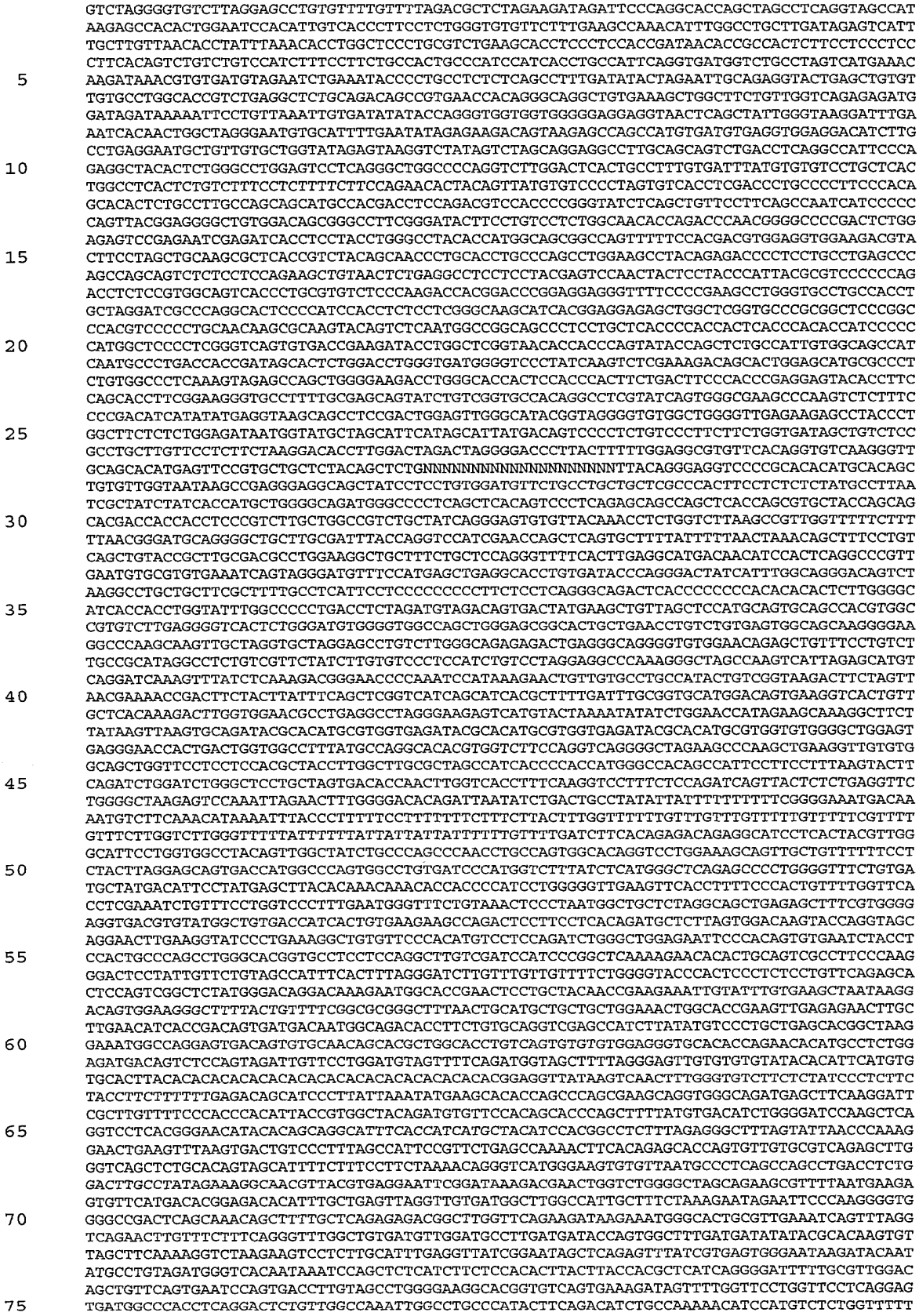
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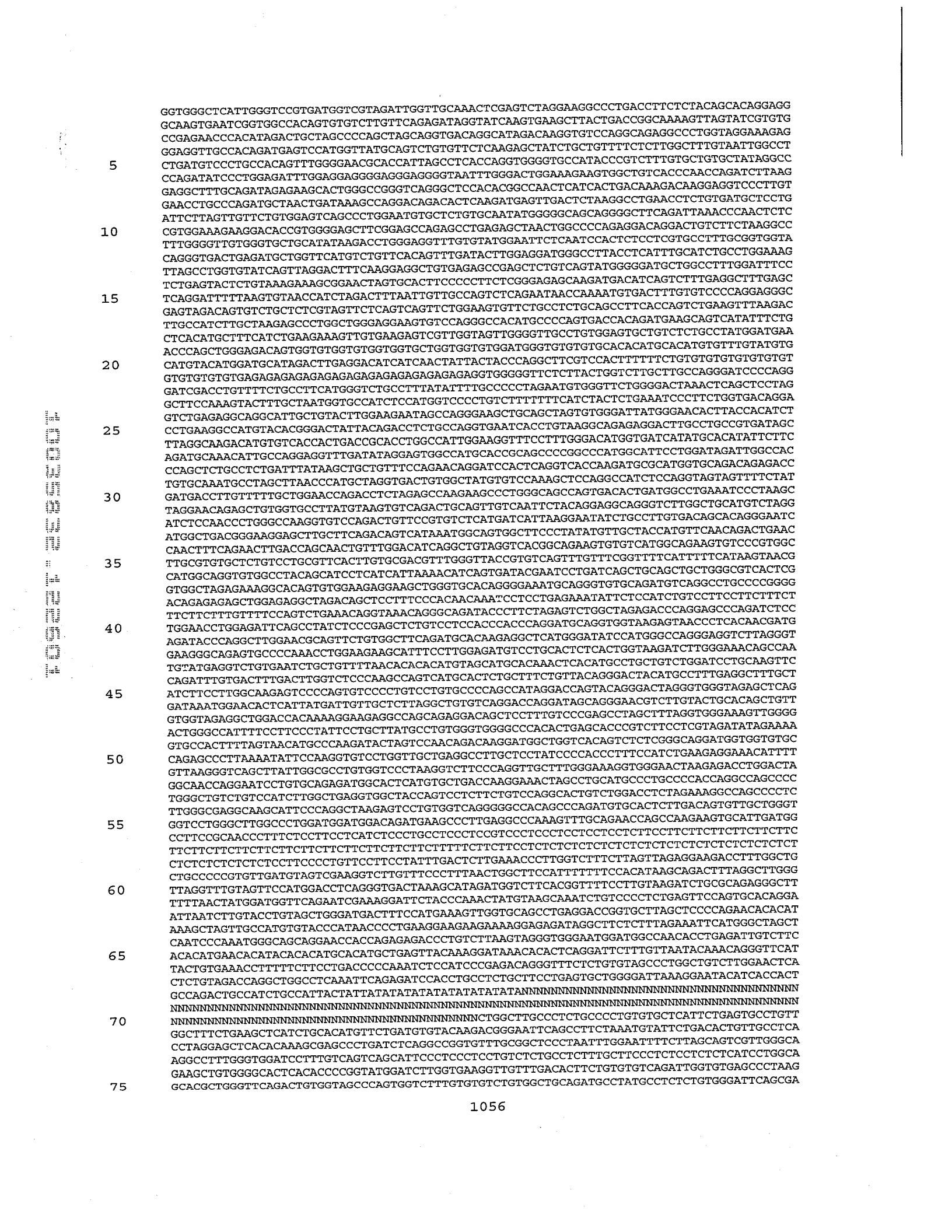
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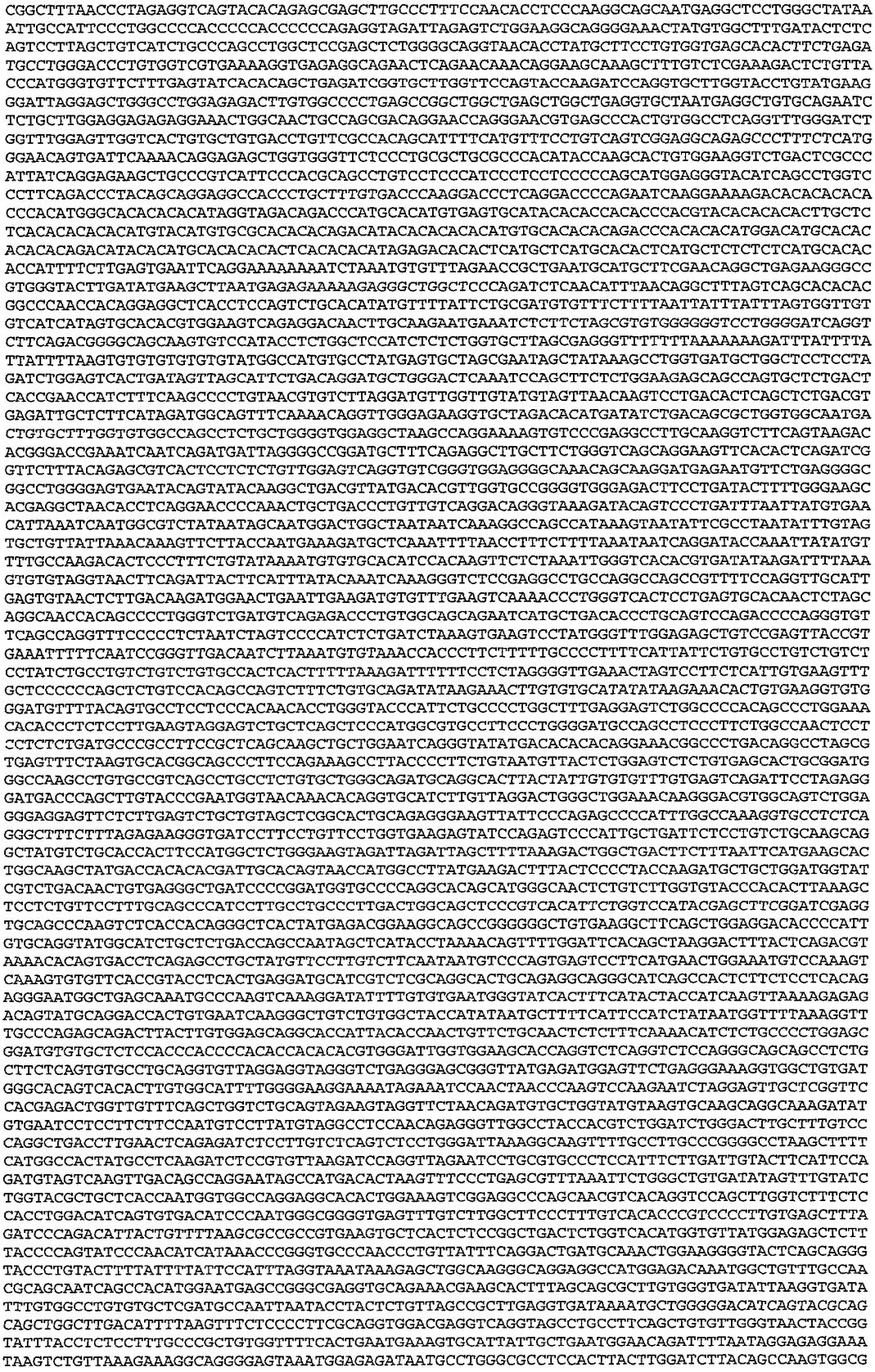
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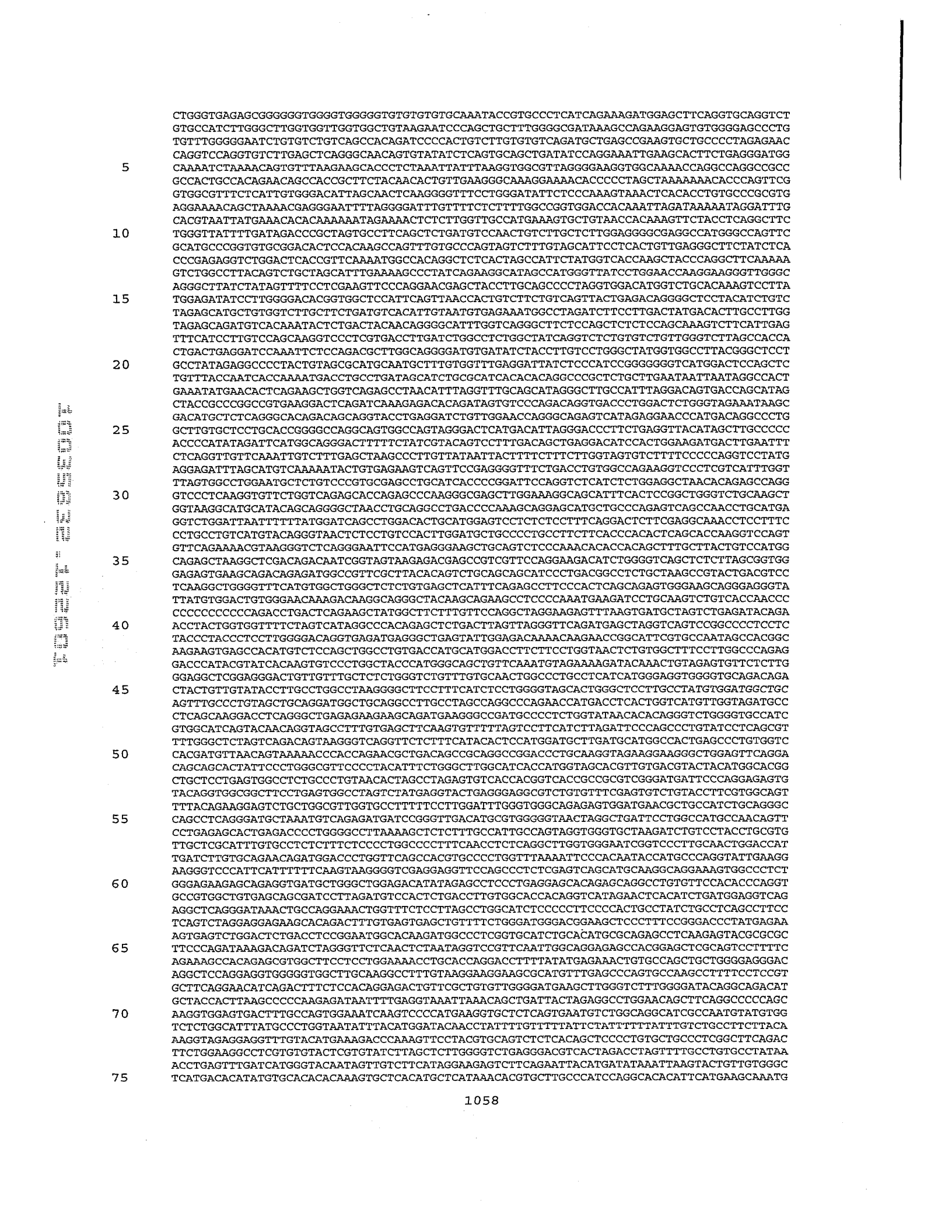
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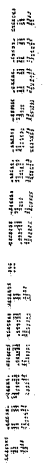


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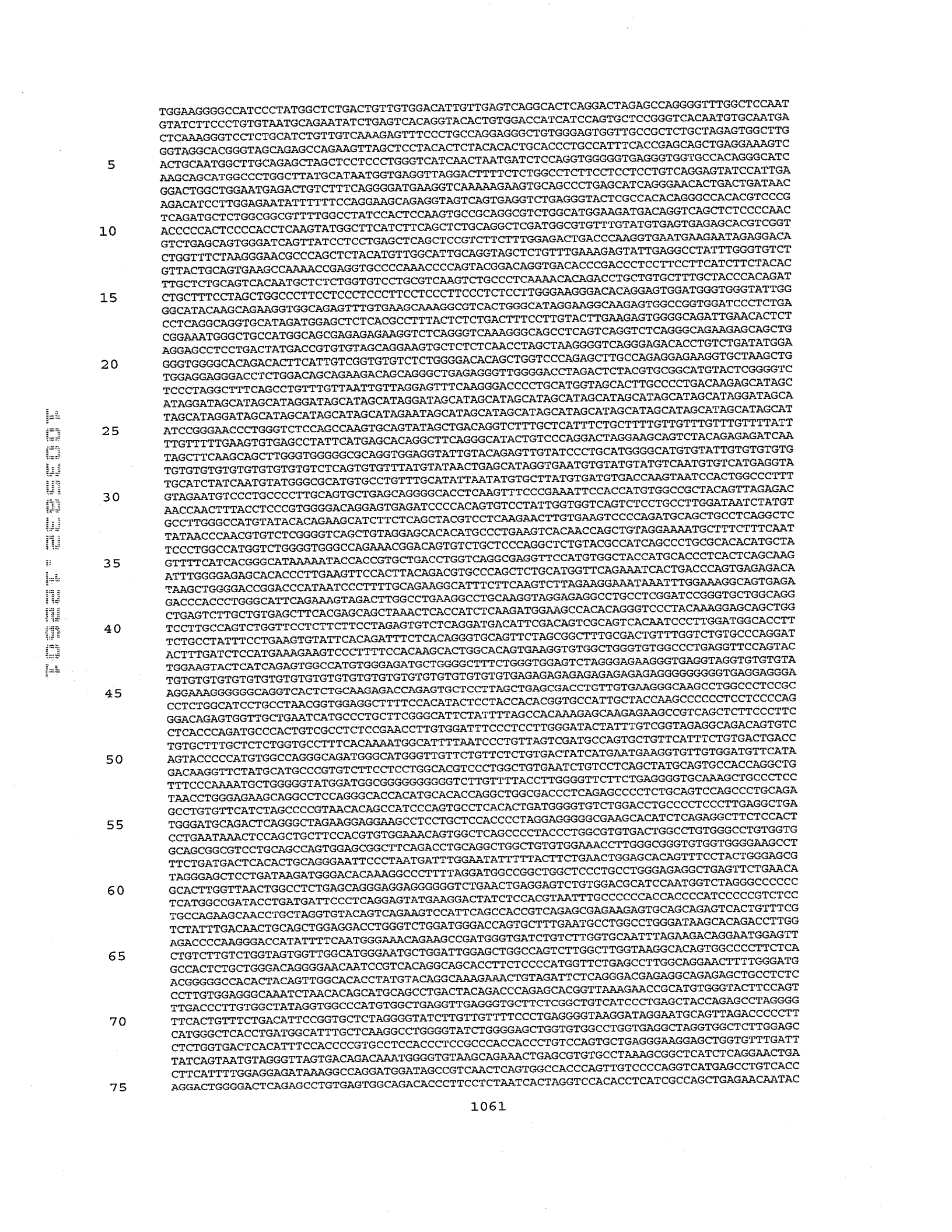


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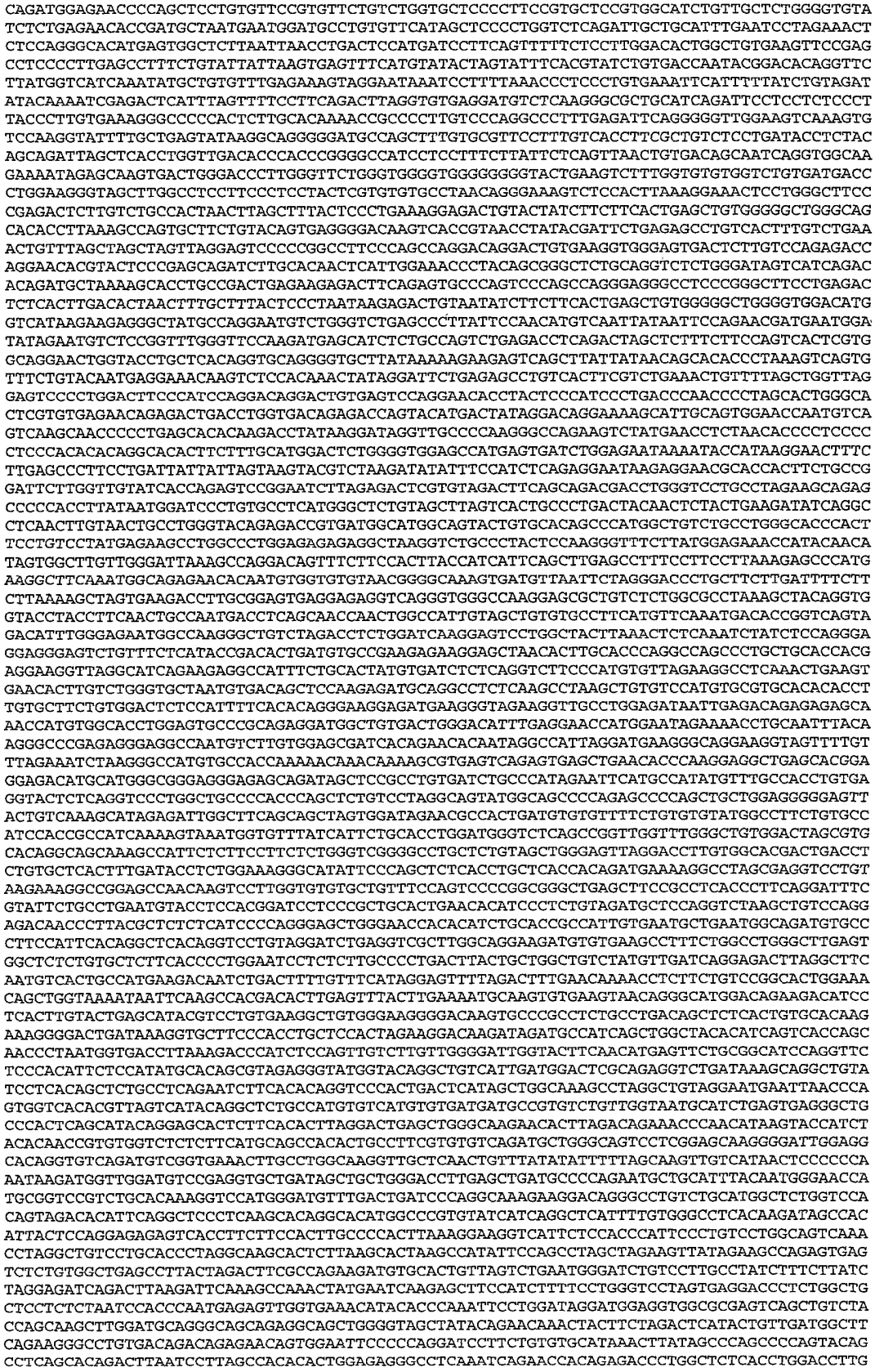
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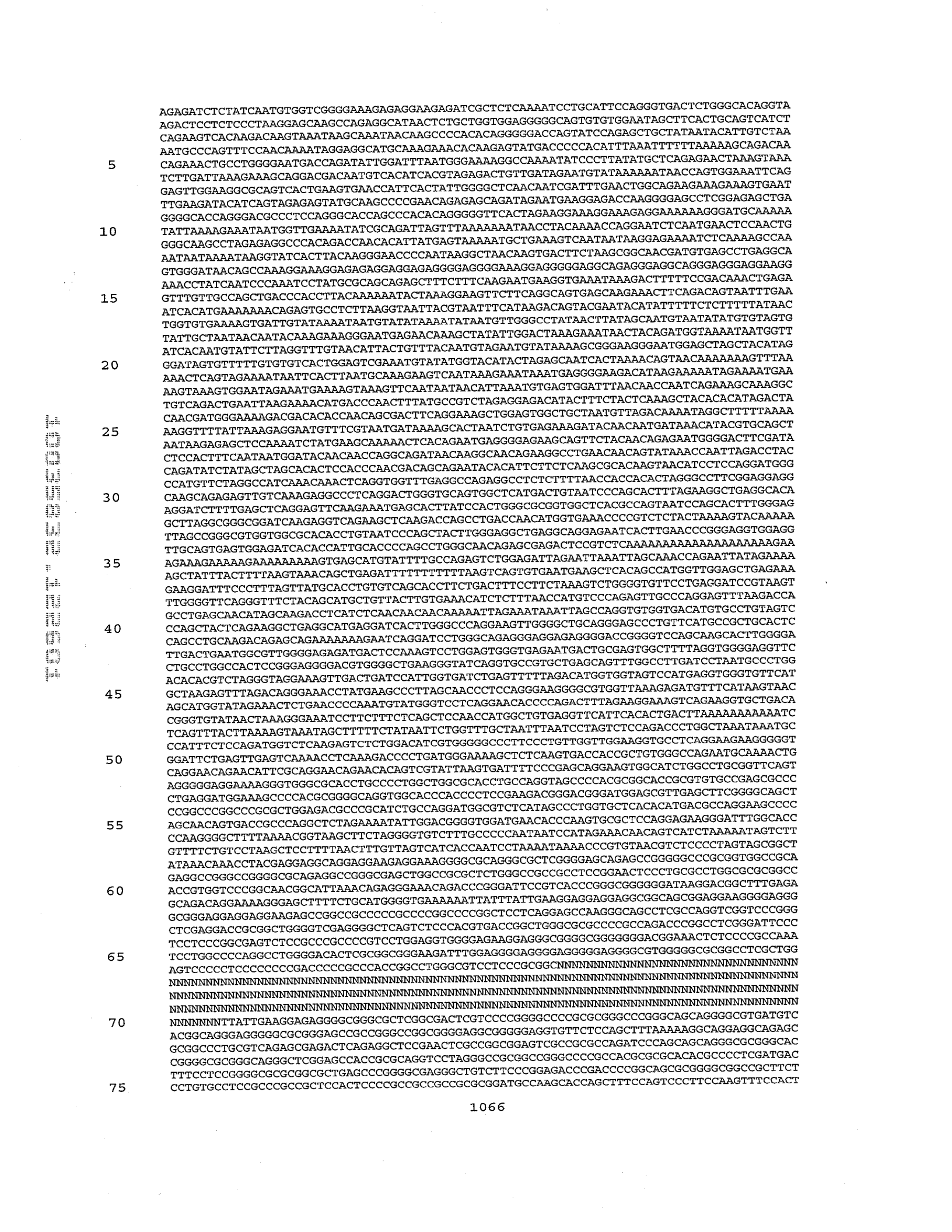
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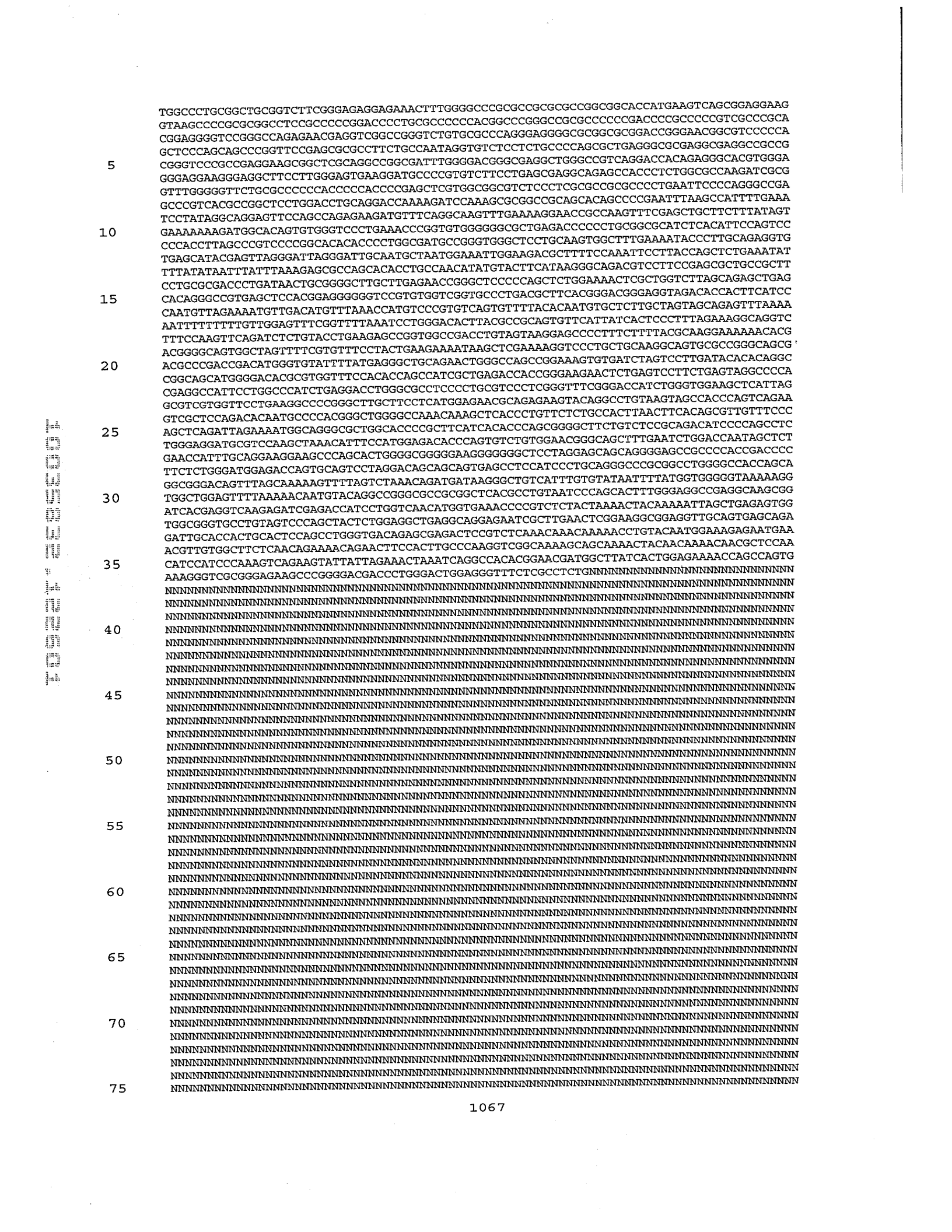
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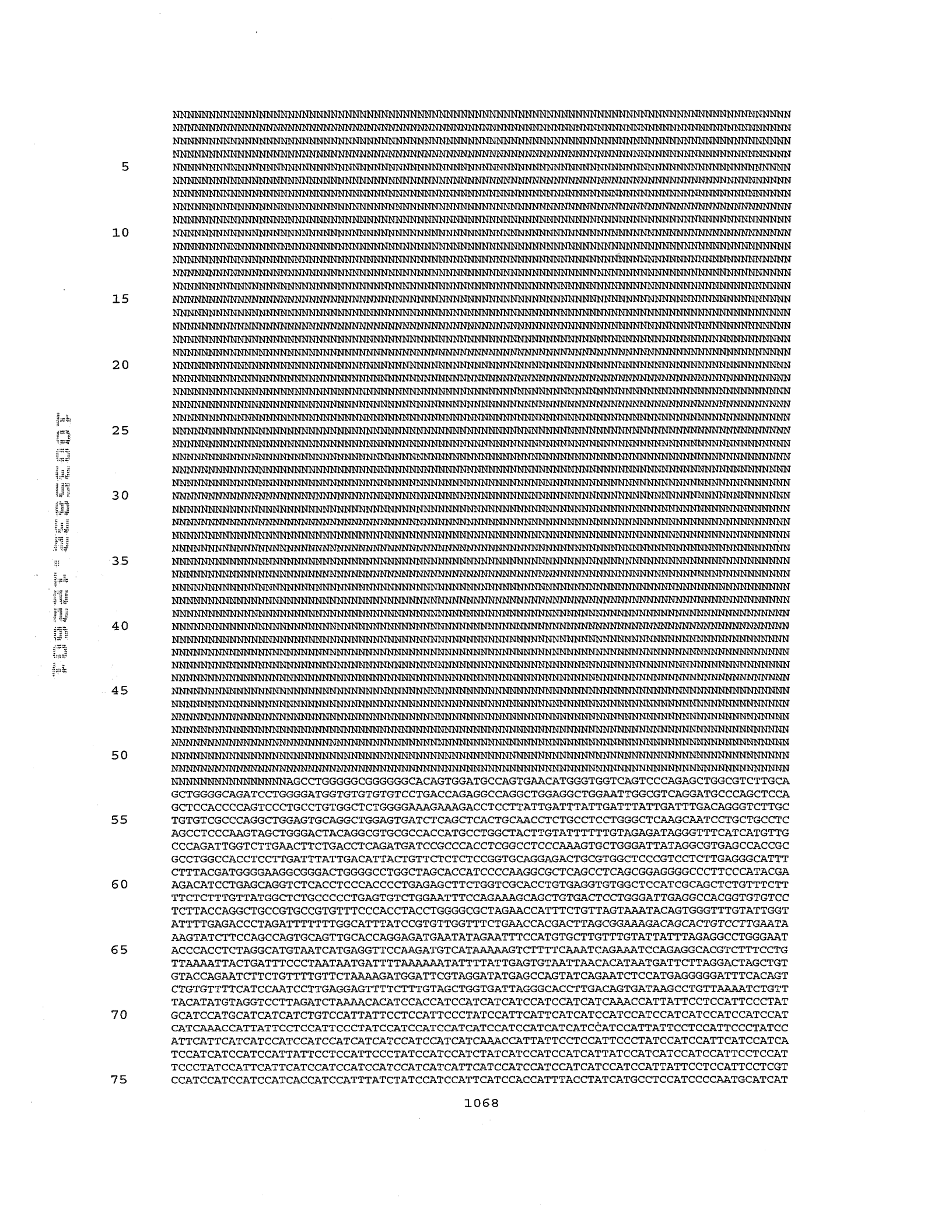
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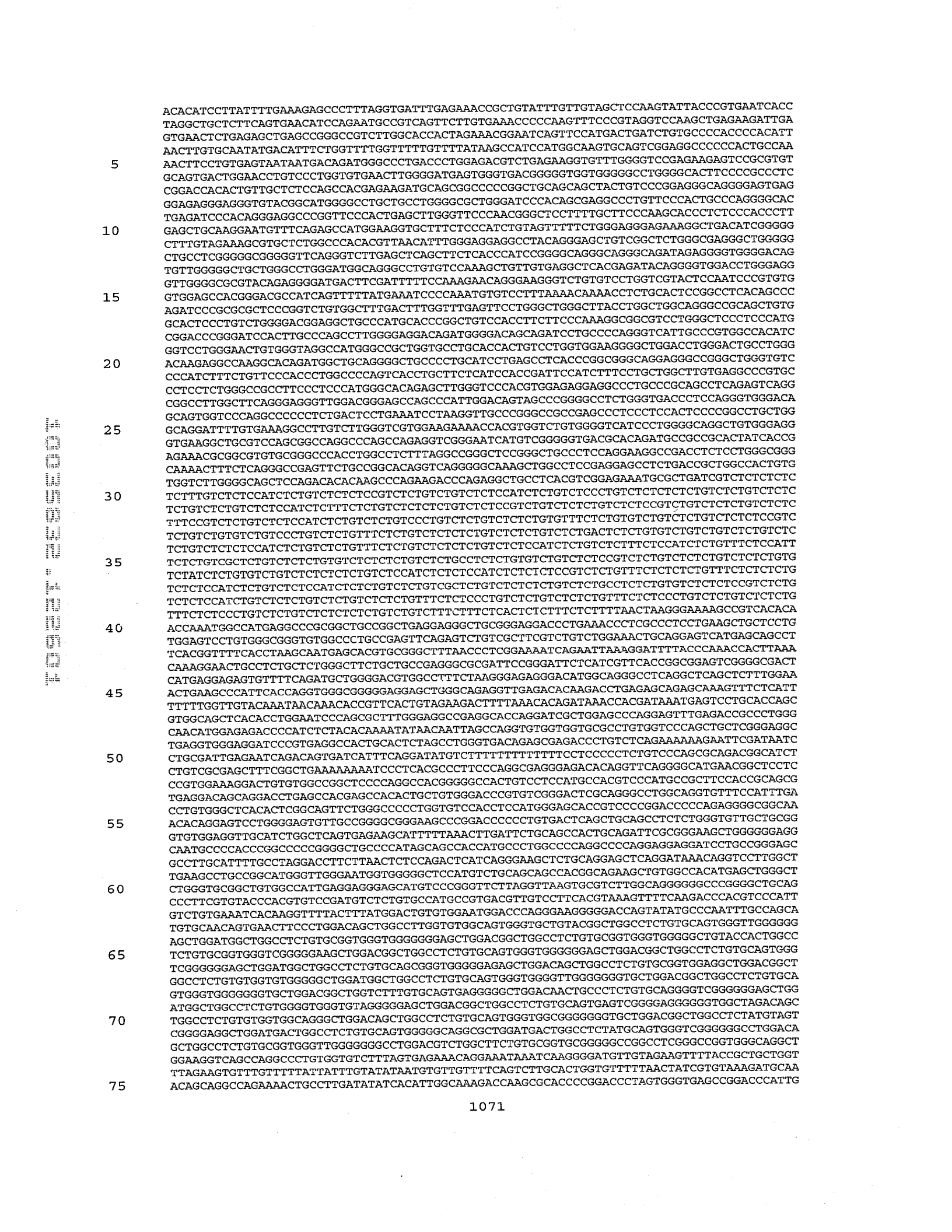


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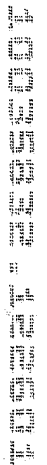
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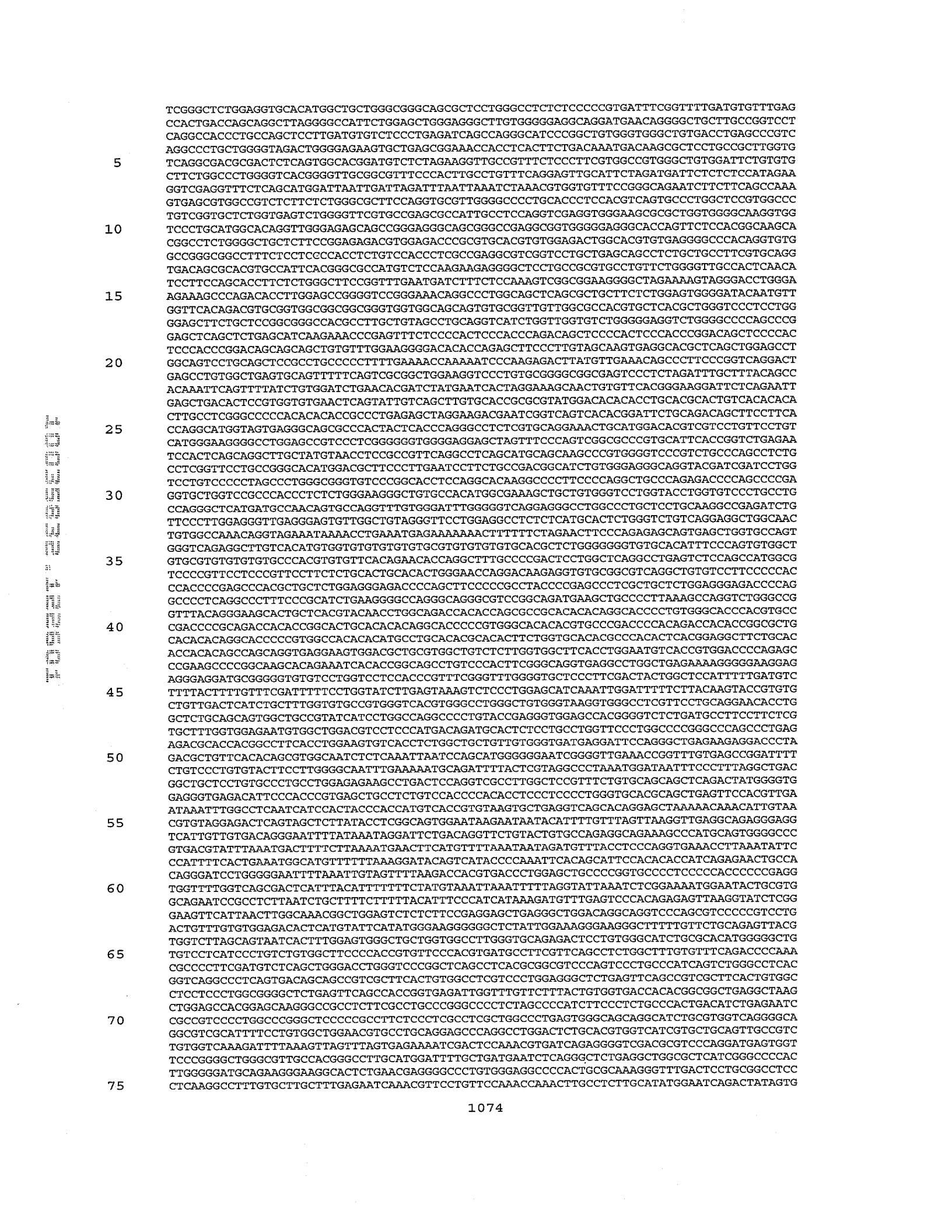


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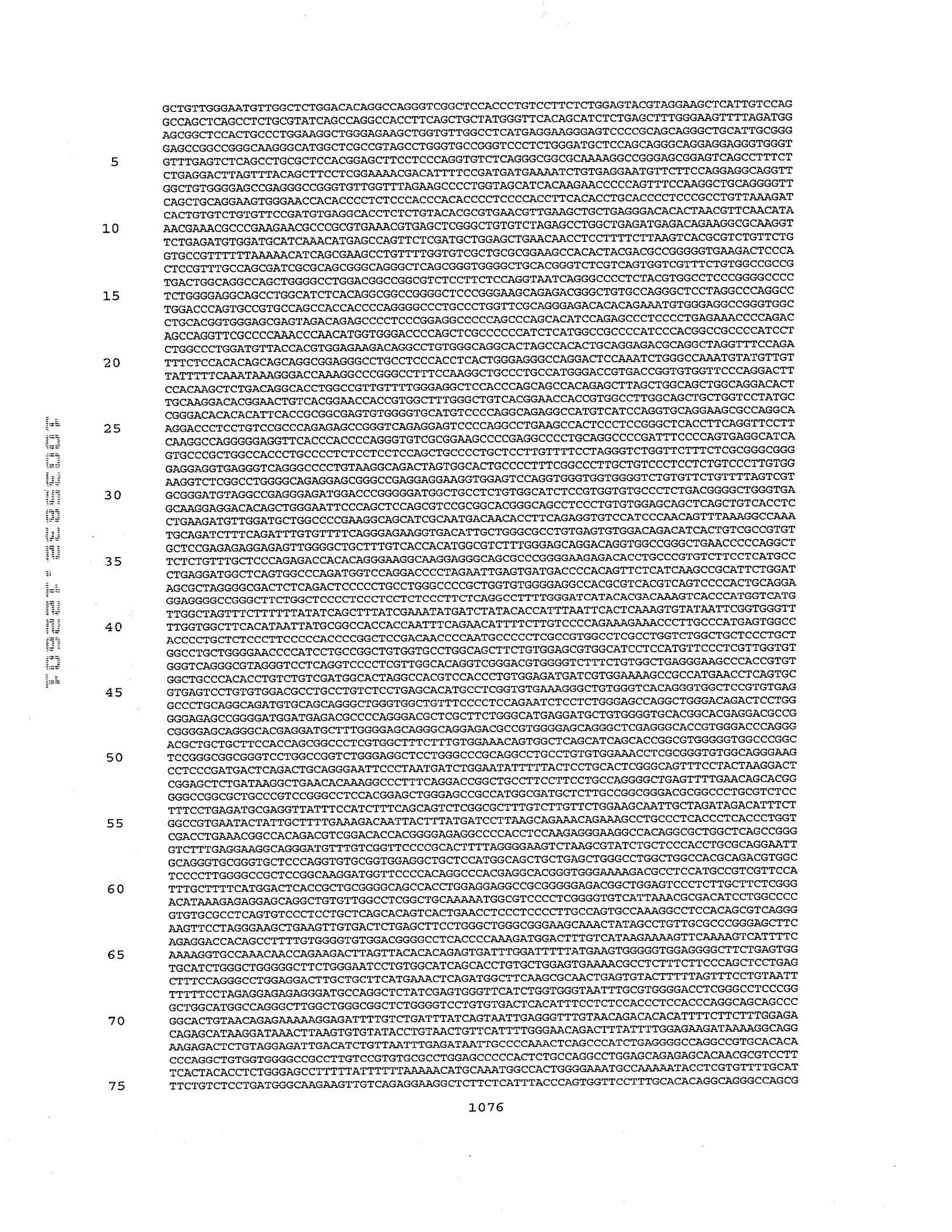


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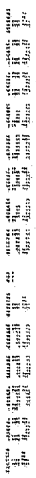


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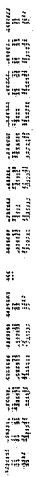
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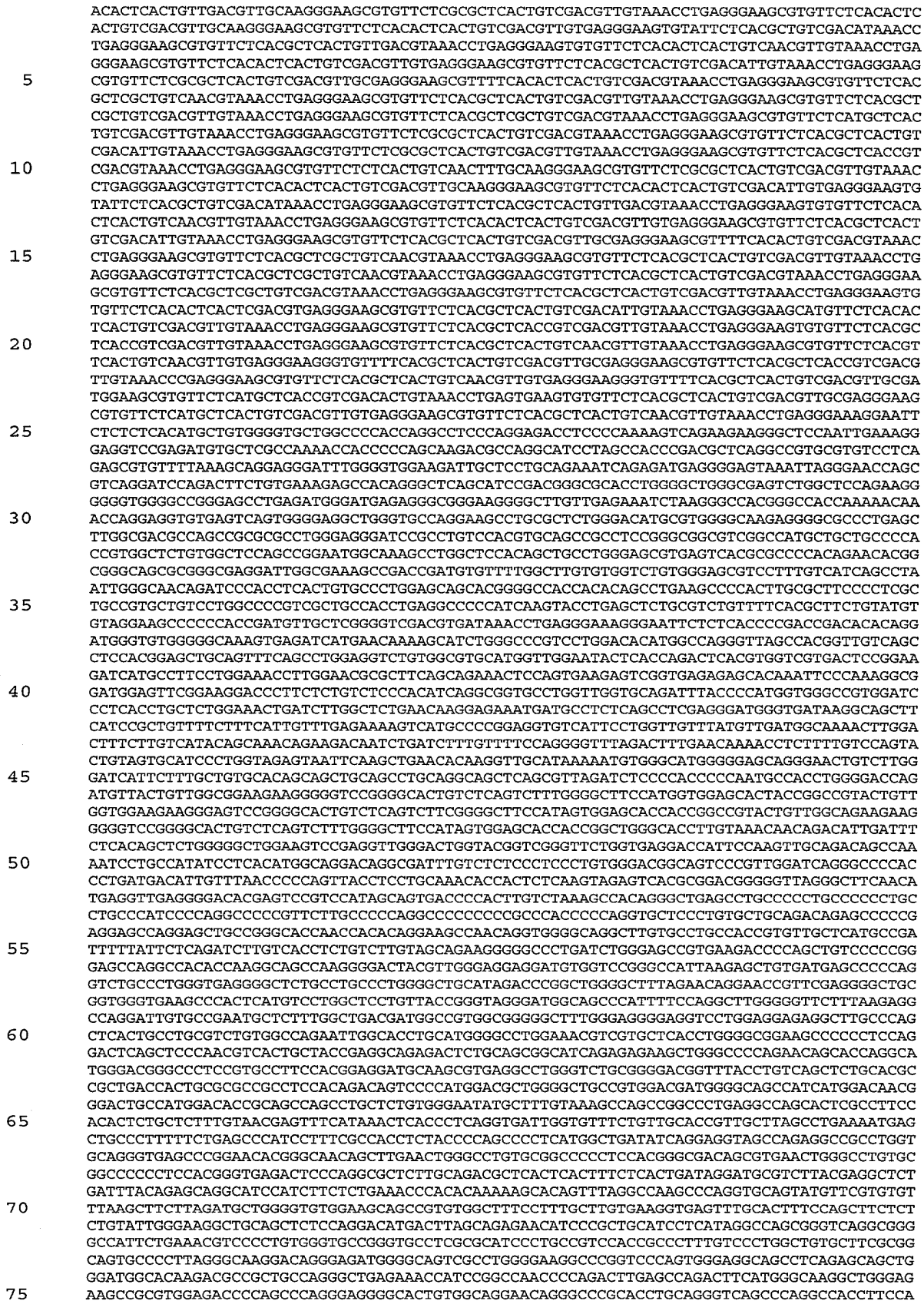


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HUMAN SEQUENCE - mRNA
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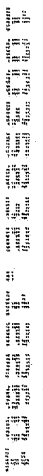
Table 51

MOUSE NOMENCLATURE
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Celera mCG3409

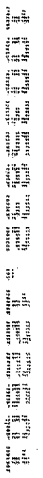
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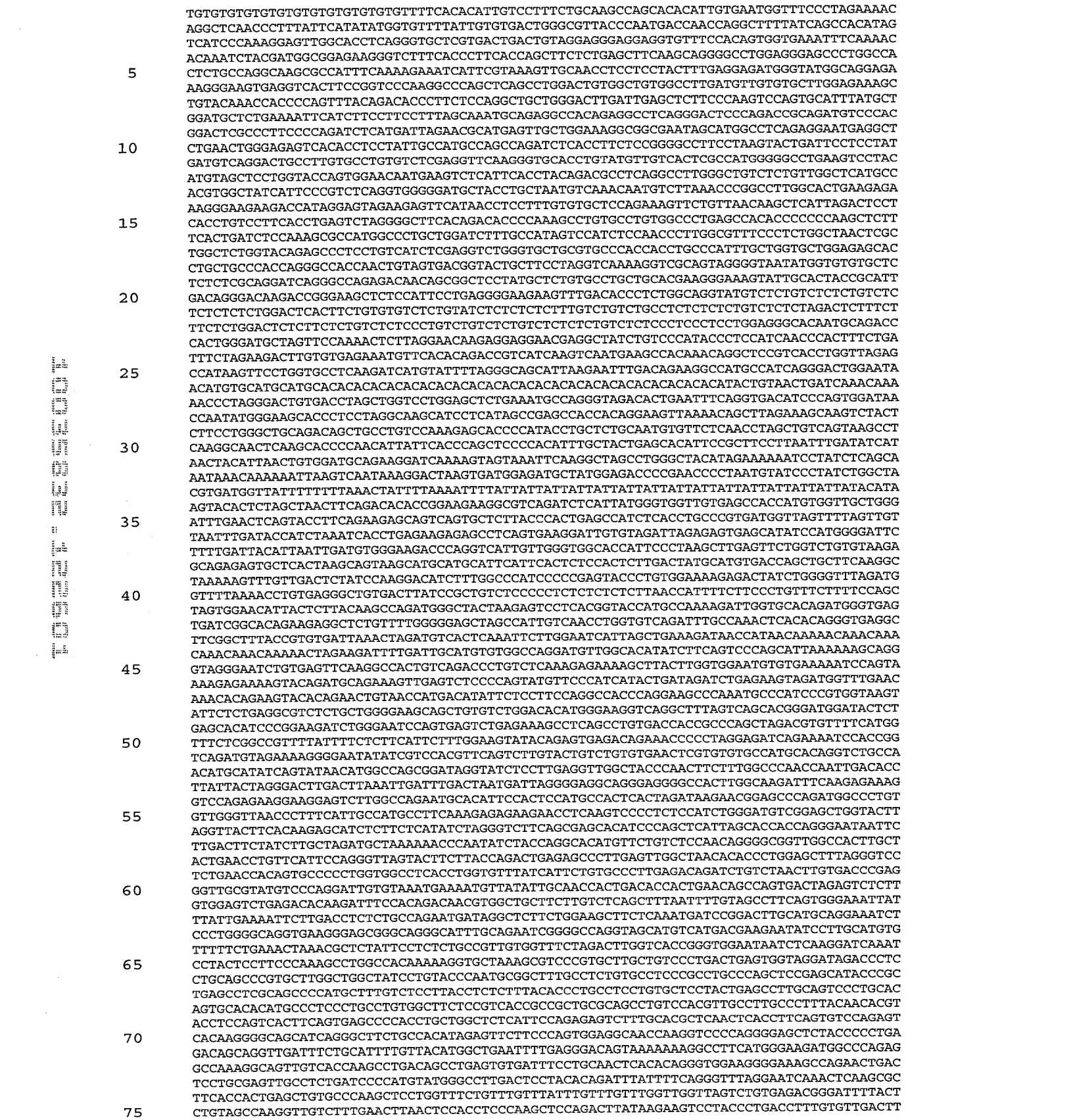
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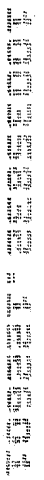


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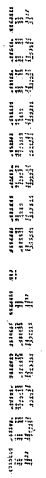


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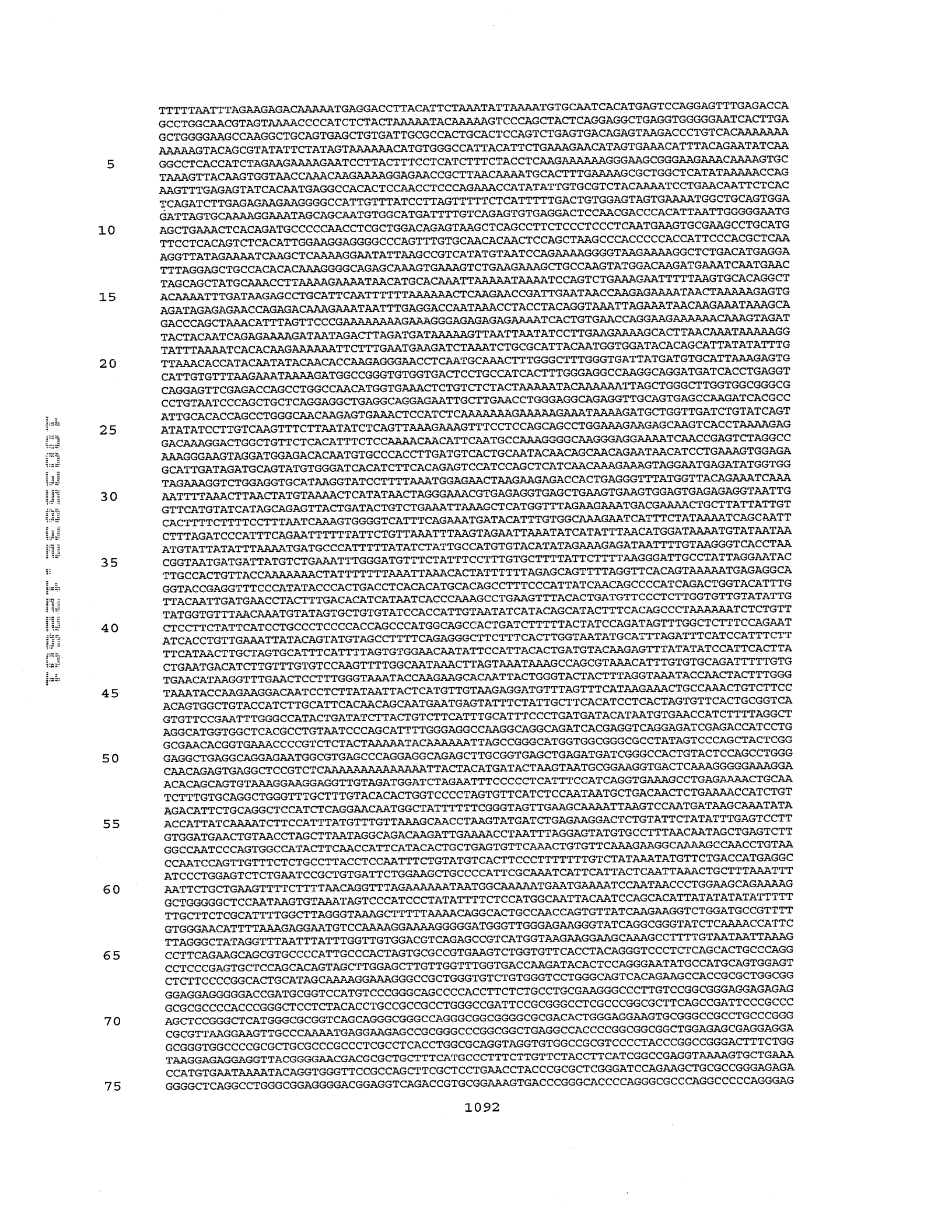
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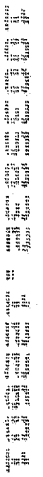
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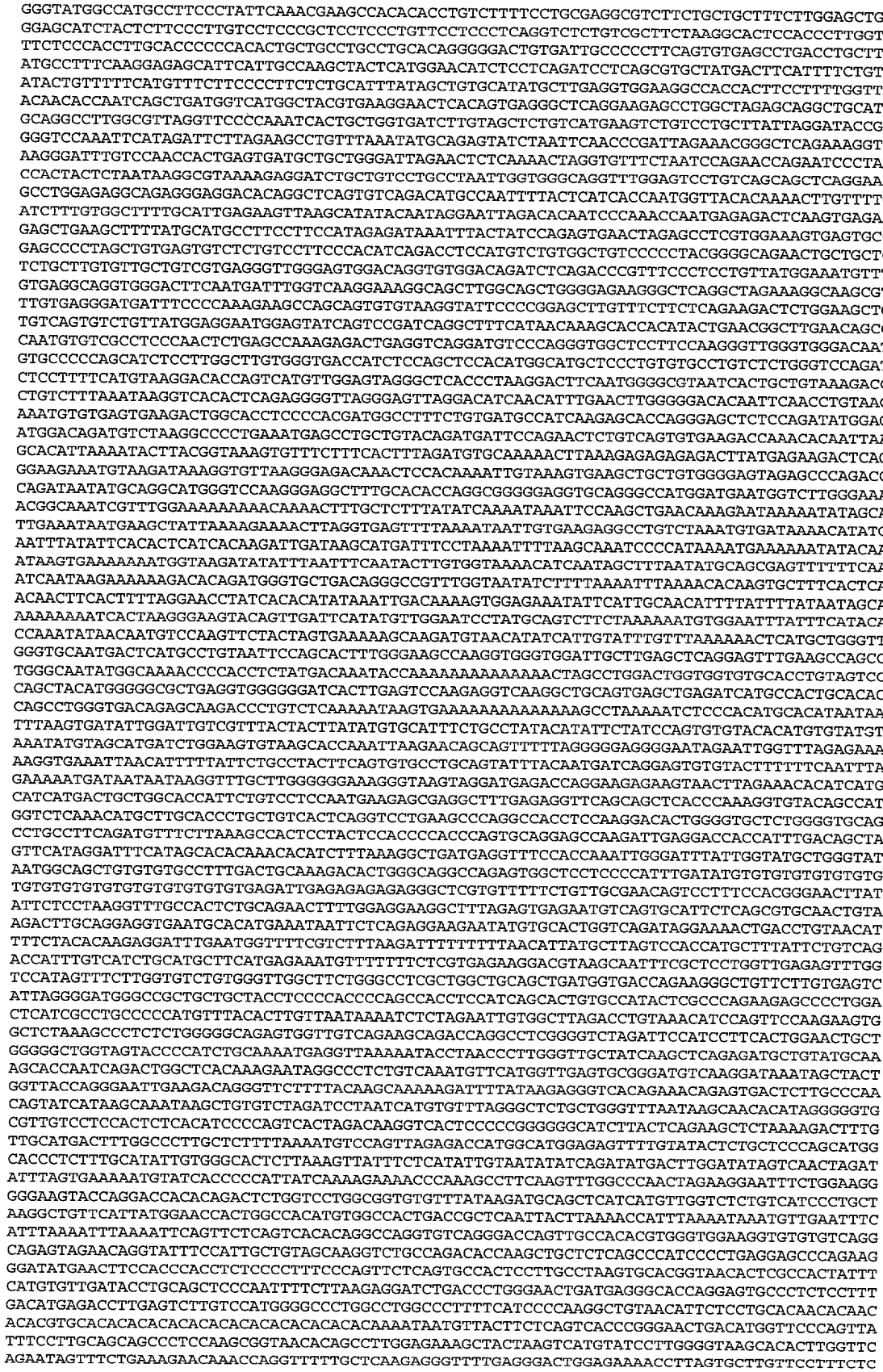
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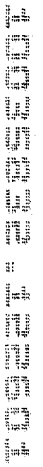


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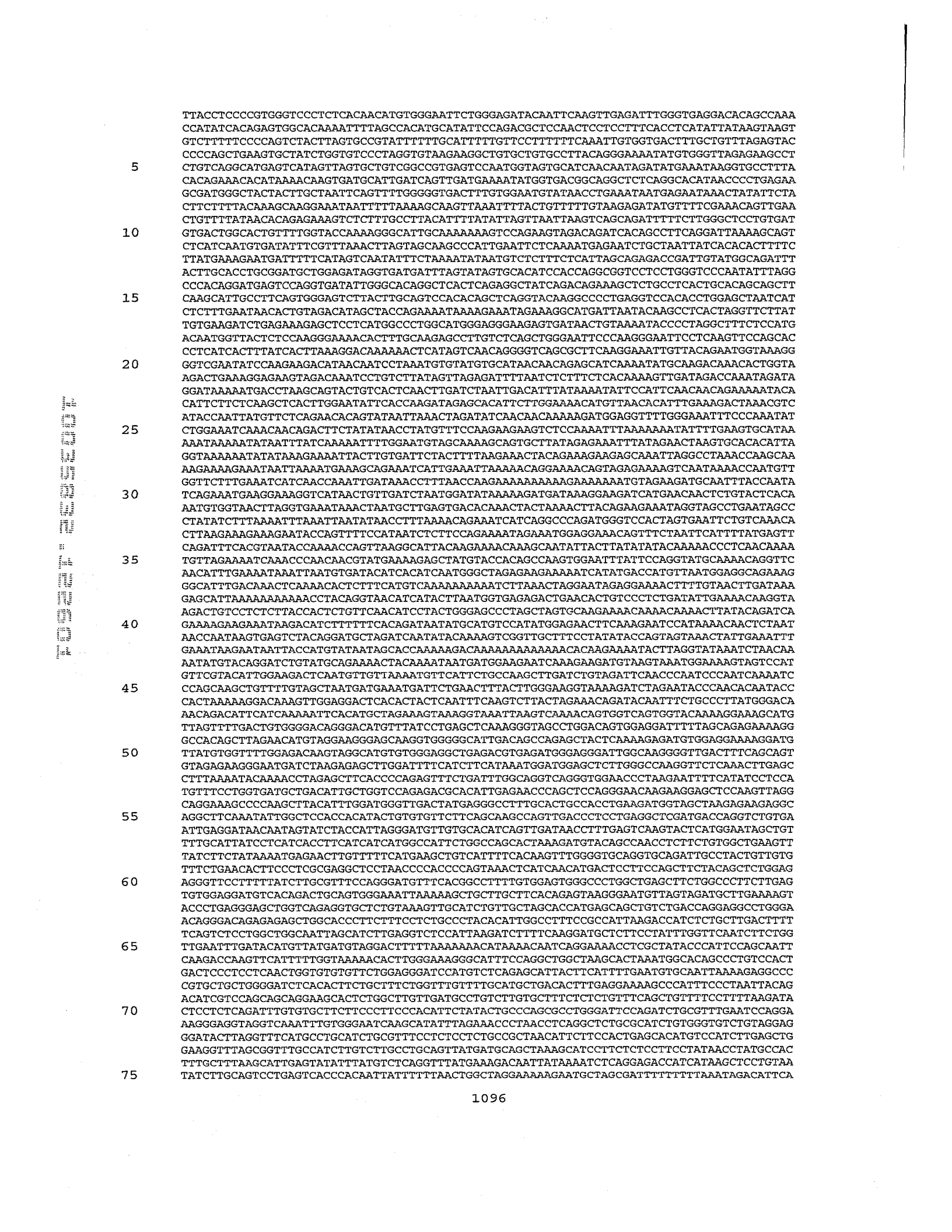


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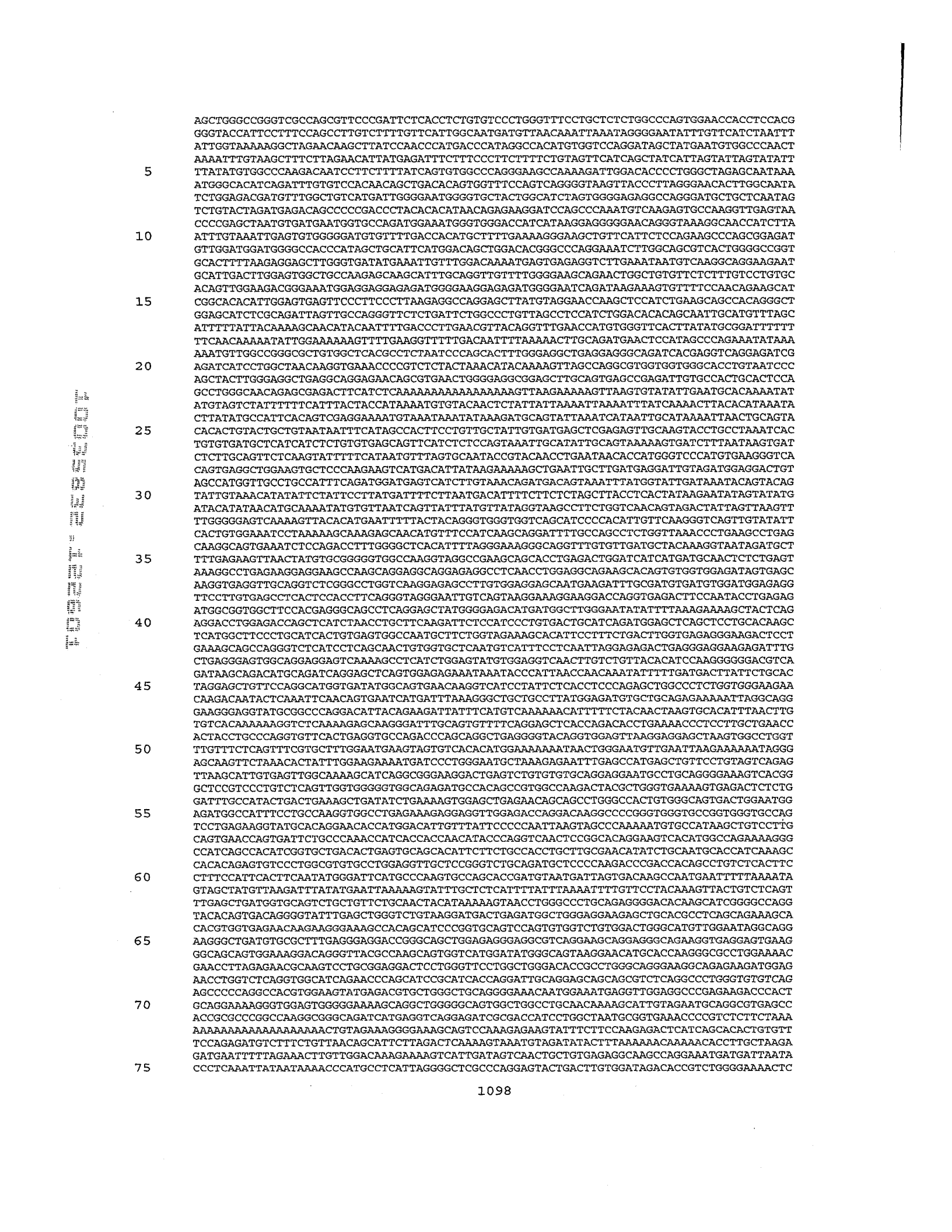




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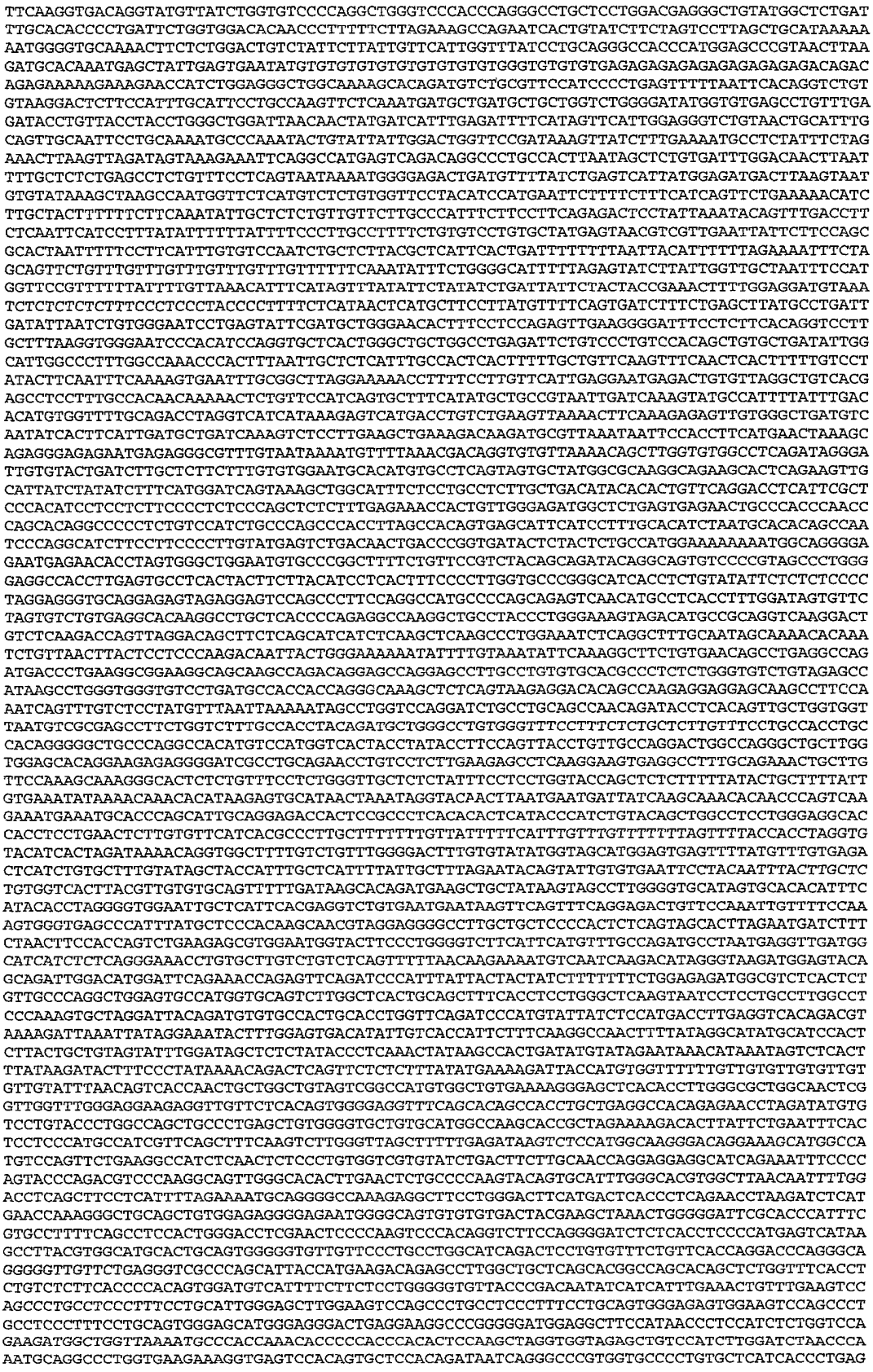


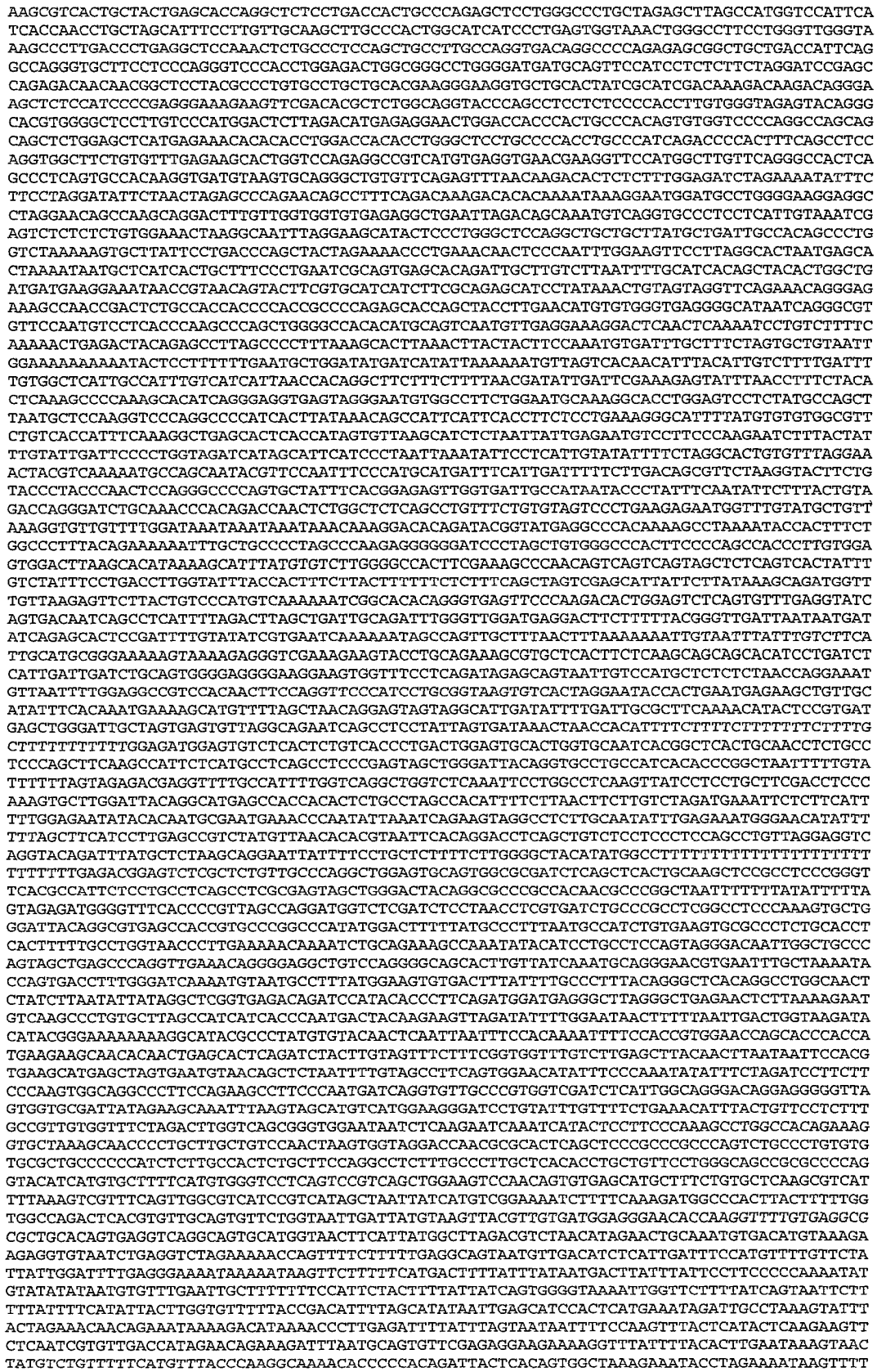
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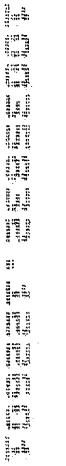
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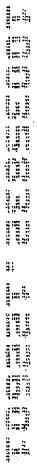




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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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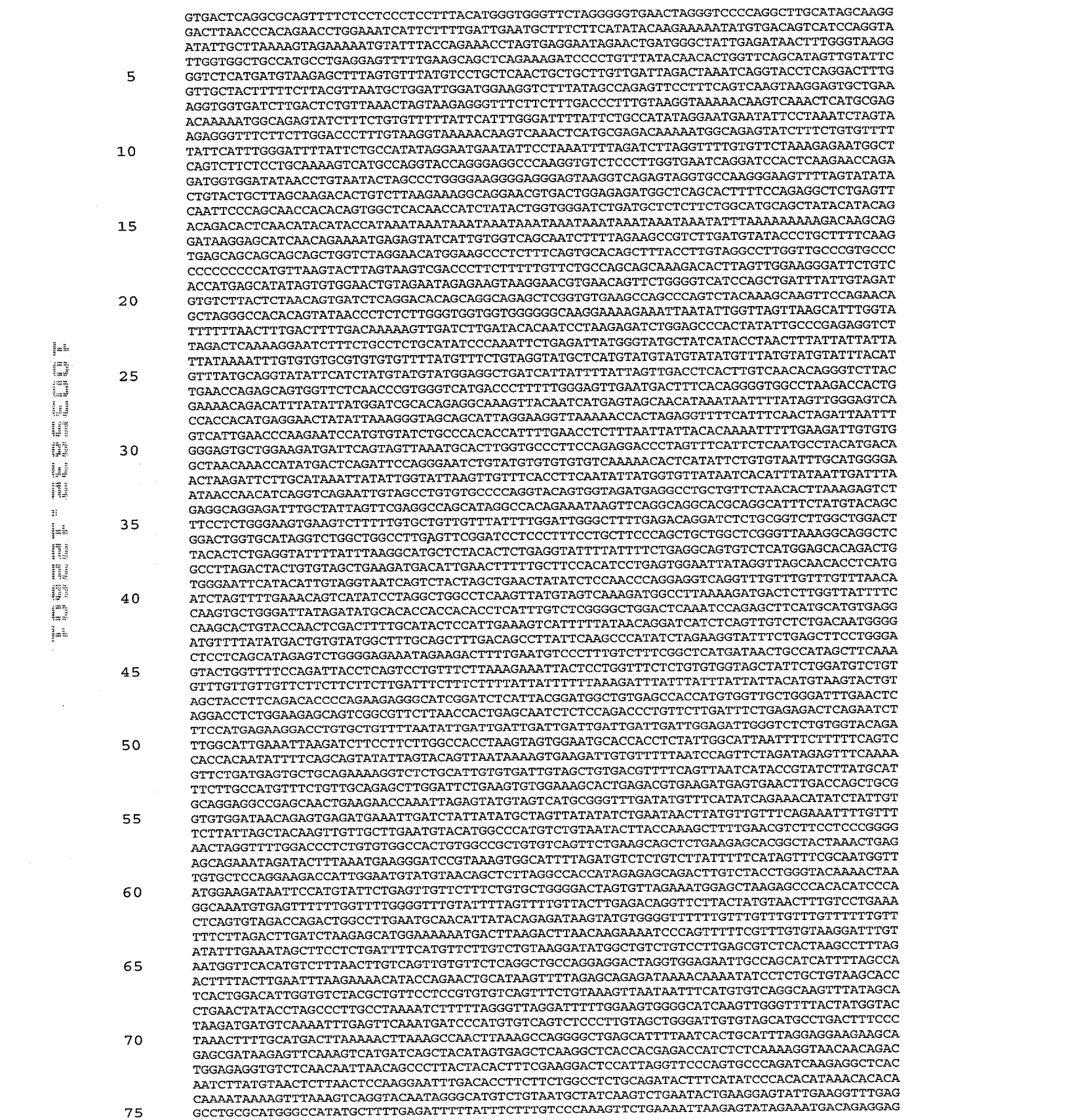
Table 52

MOUSE NOMENCLATURE
ICSGNM Gnb1
Celera mCG23363

HUMAN NOMENCLATURE
HGNC GNB1
Celera hCG23470

MOUSE SEQUENCE - GENOMIC

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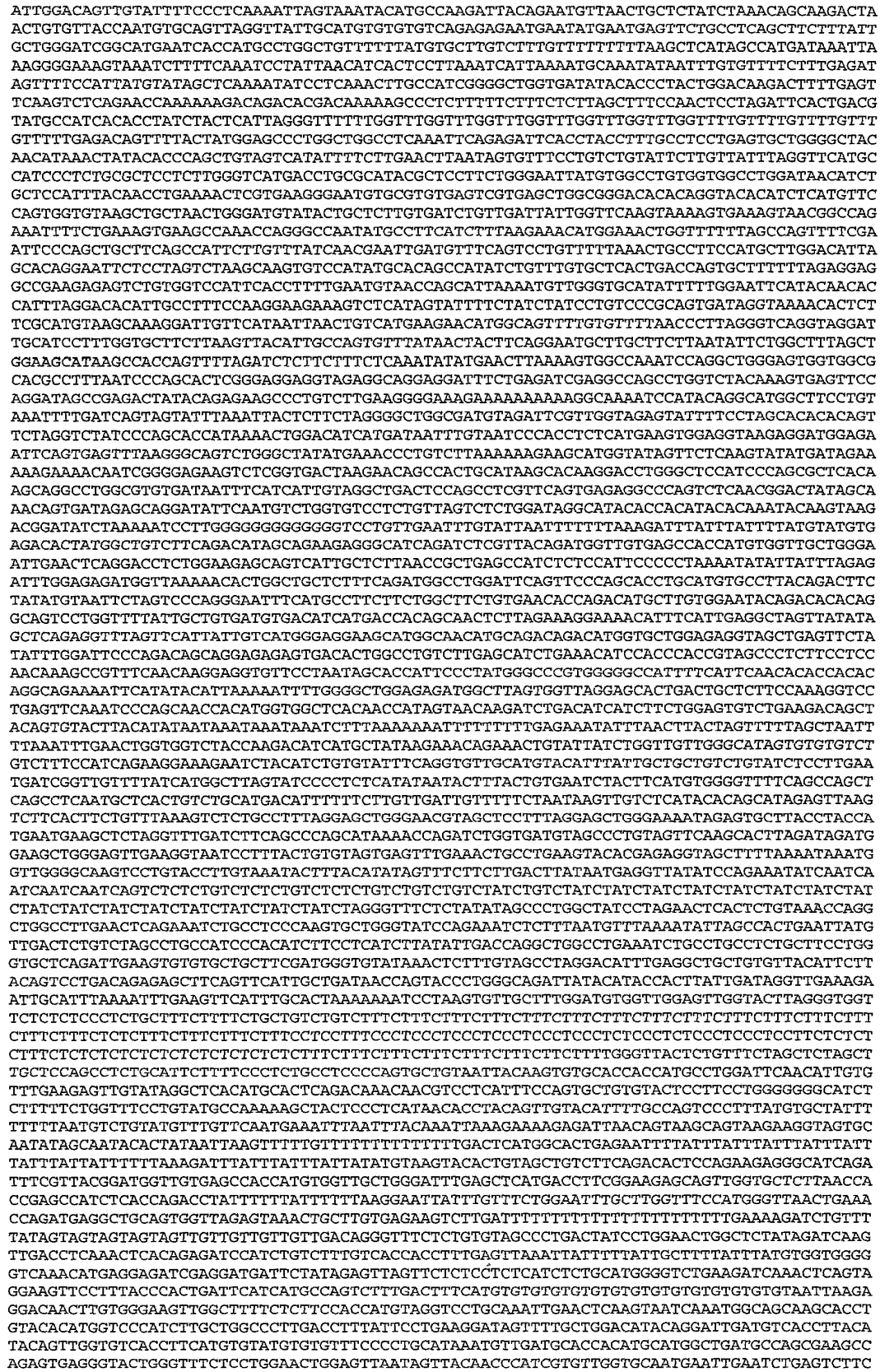
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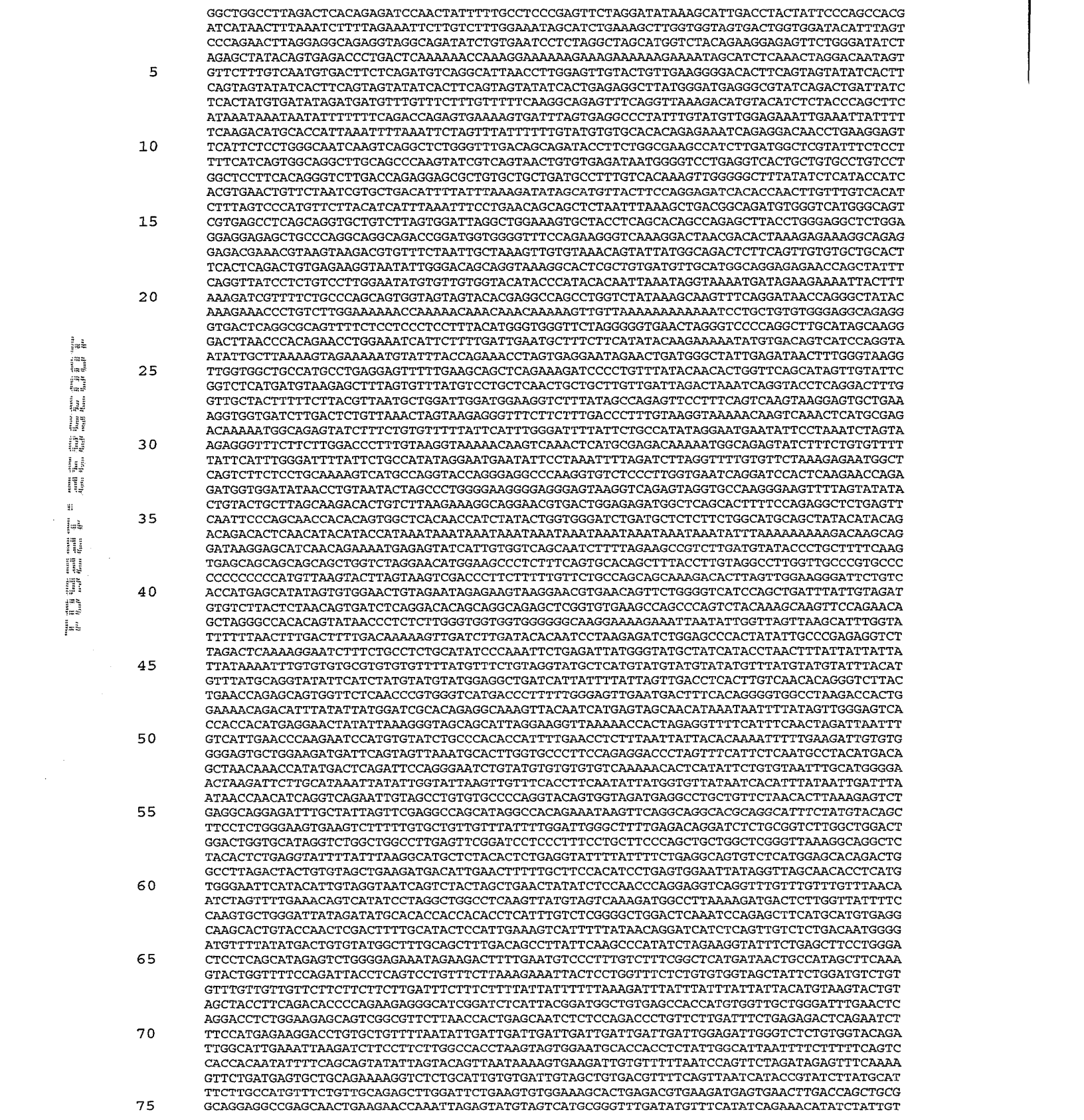
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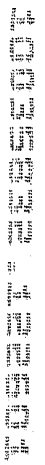
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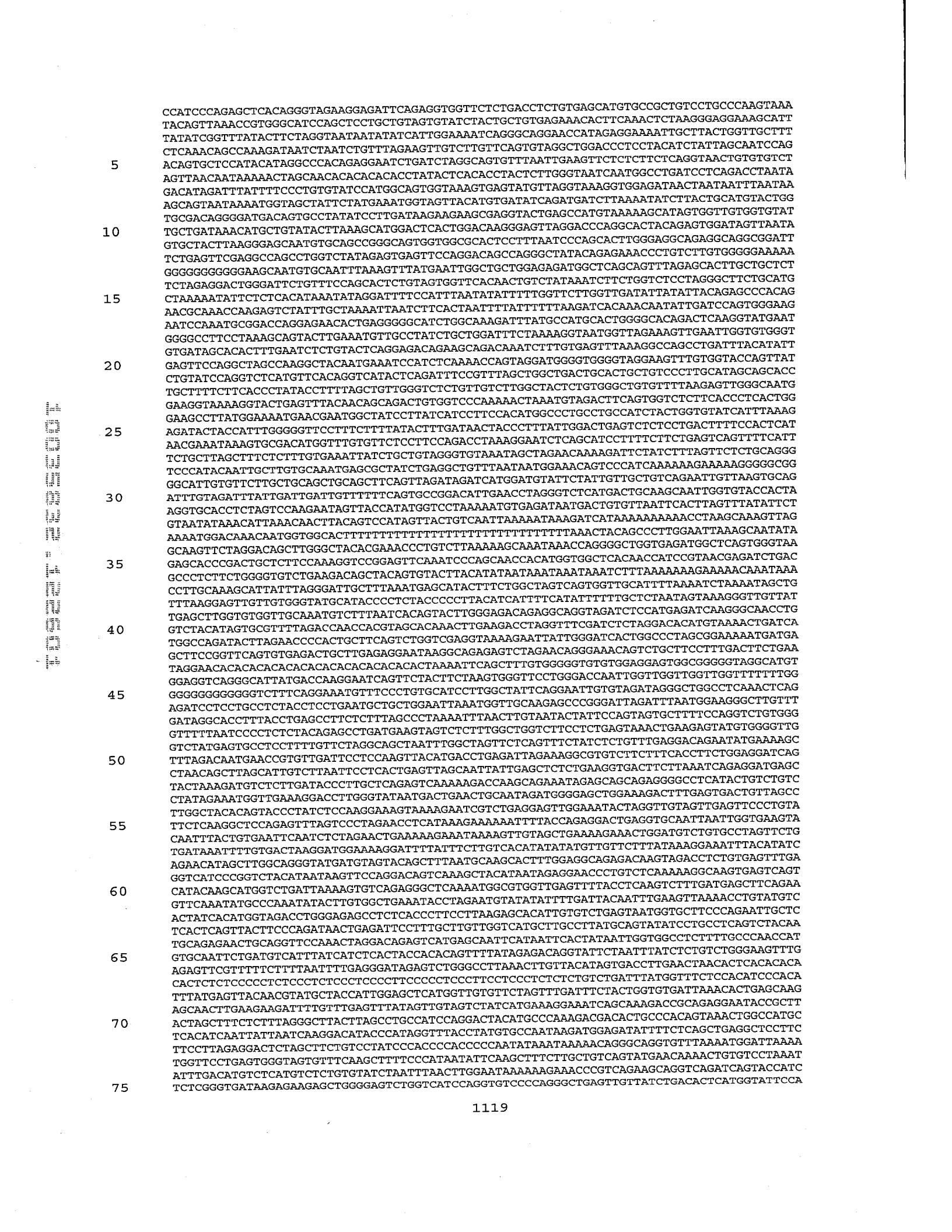
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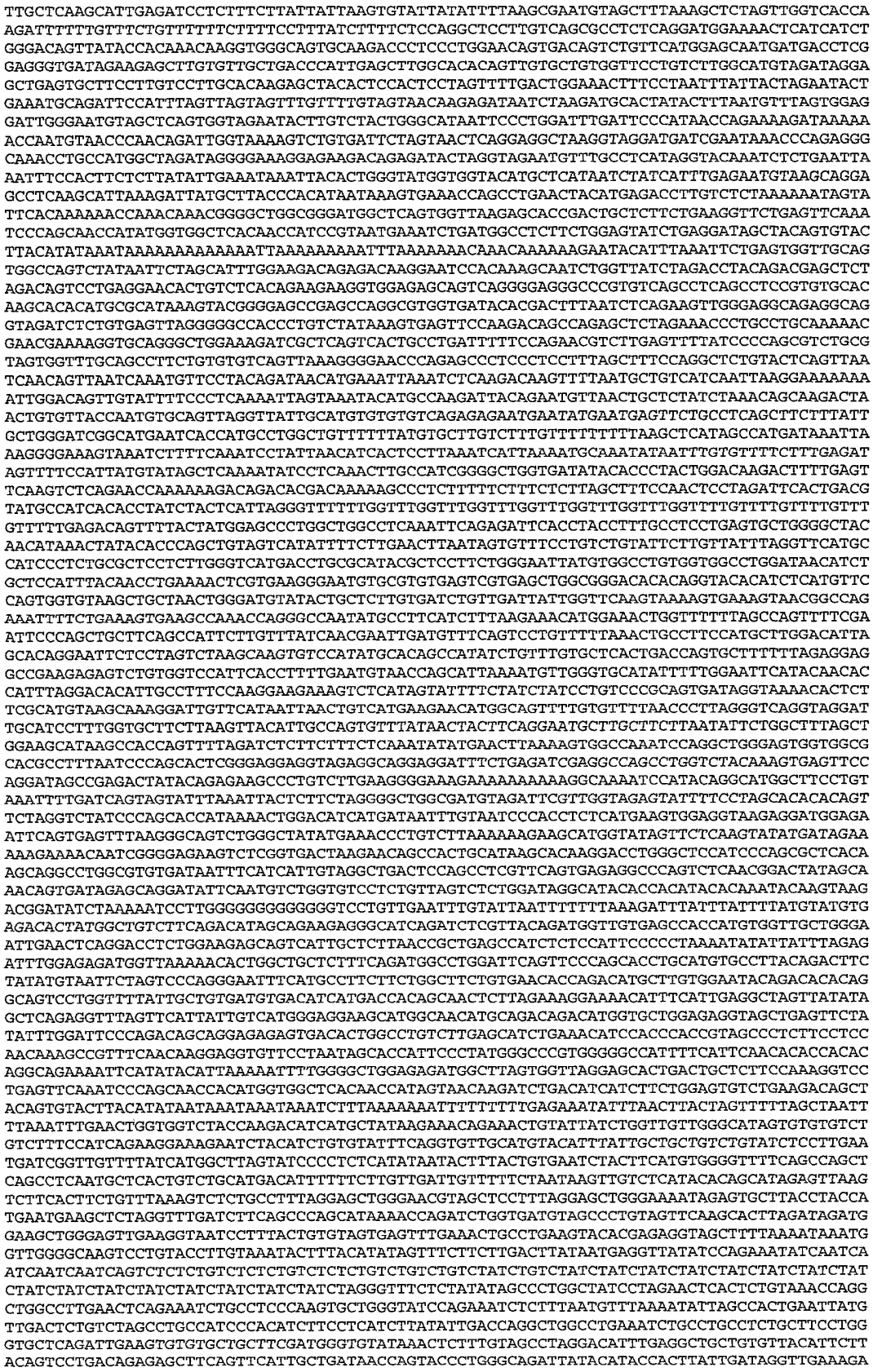




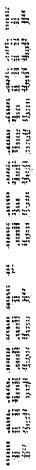
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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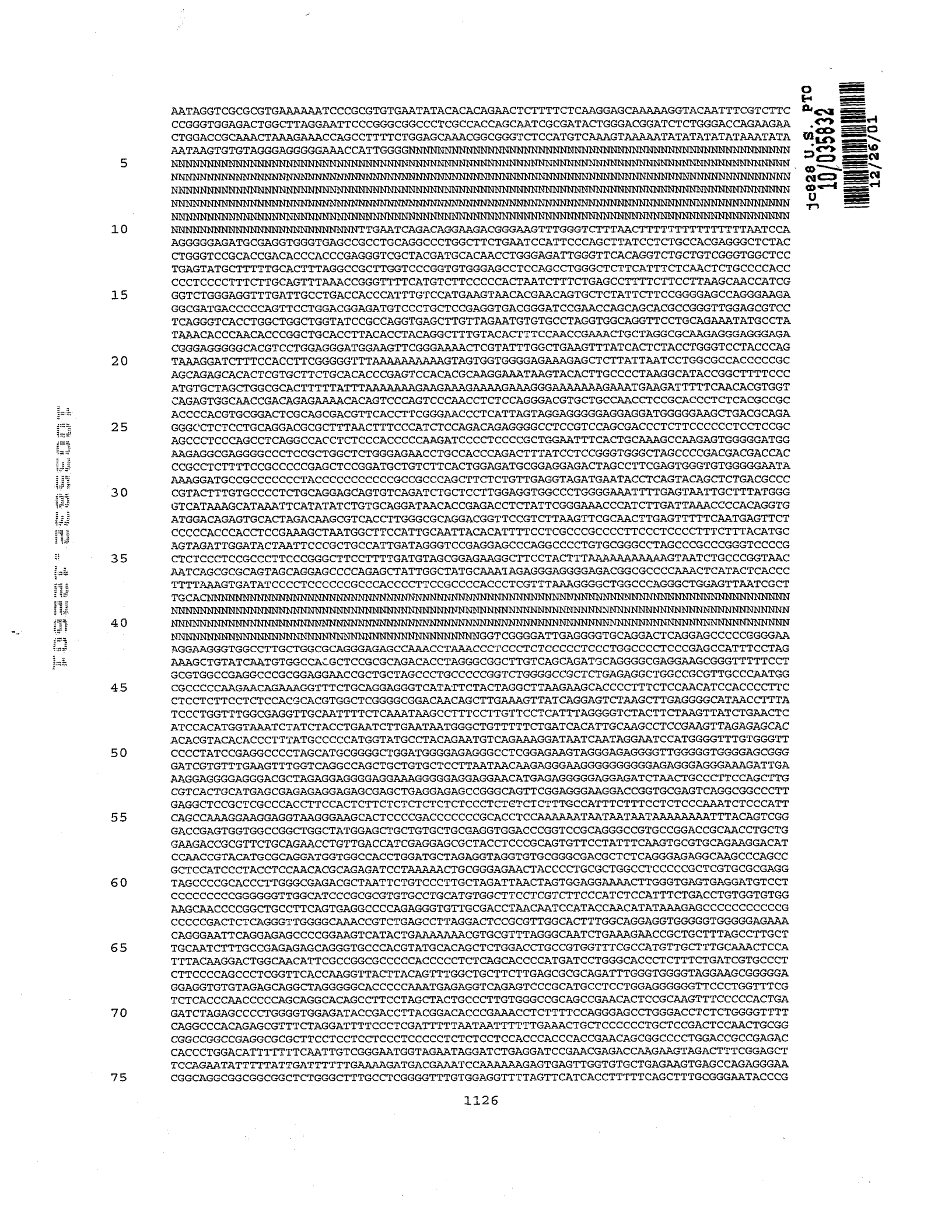
Table 53

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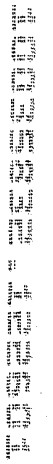
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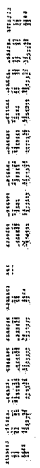
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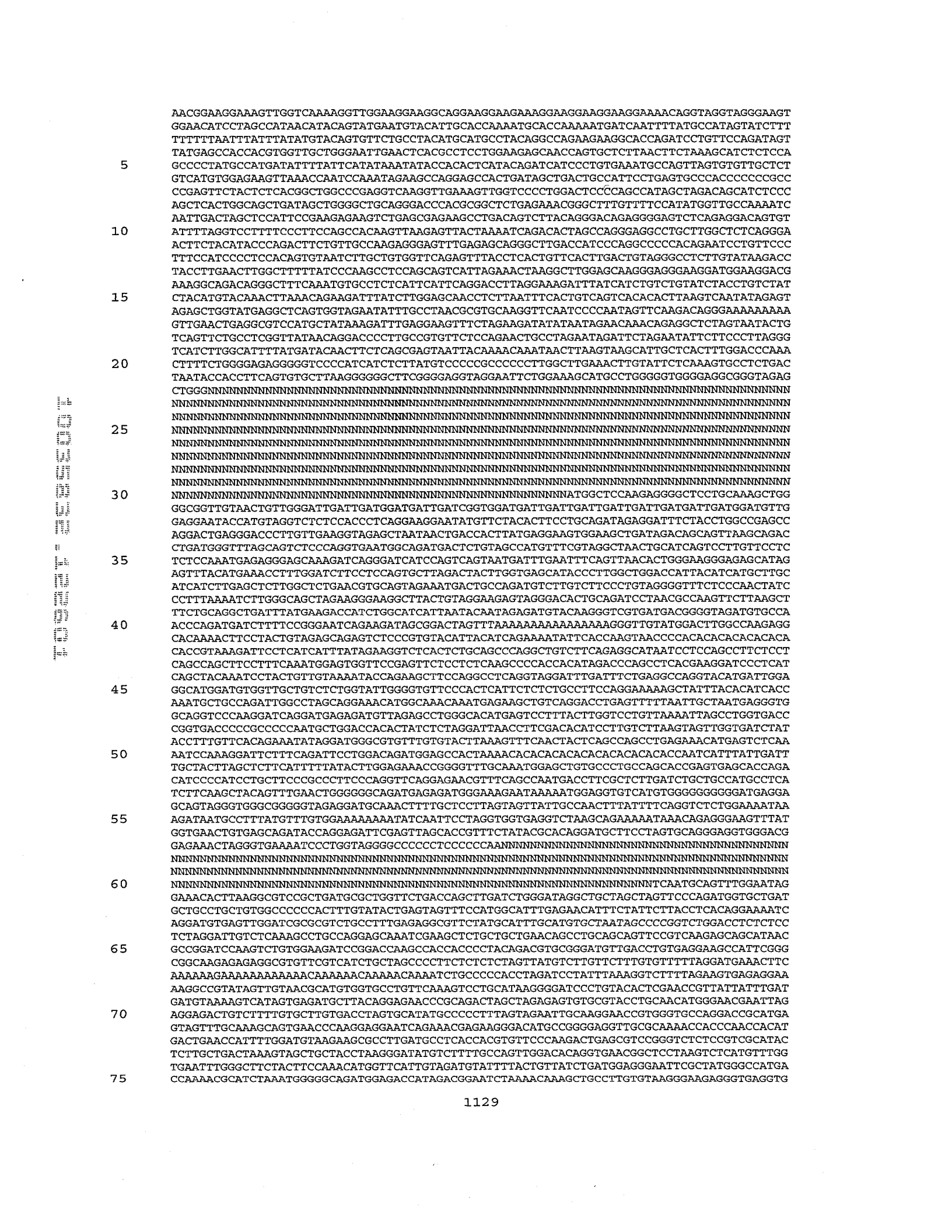
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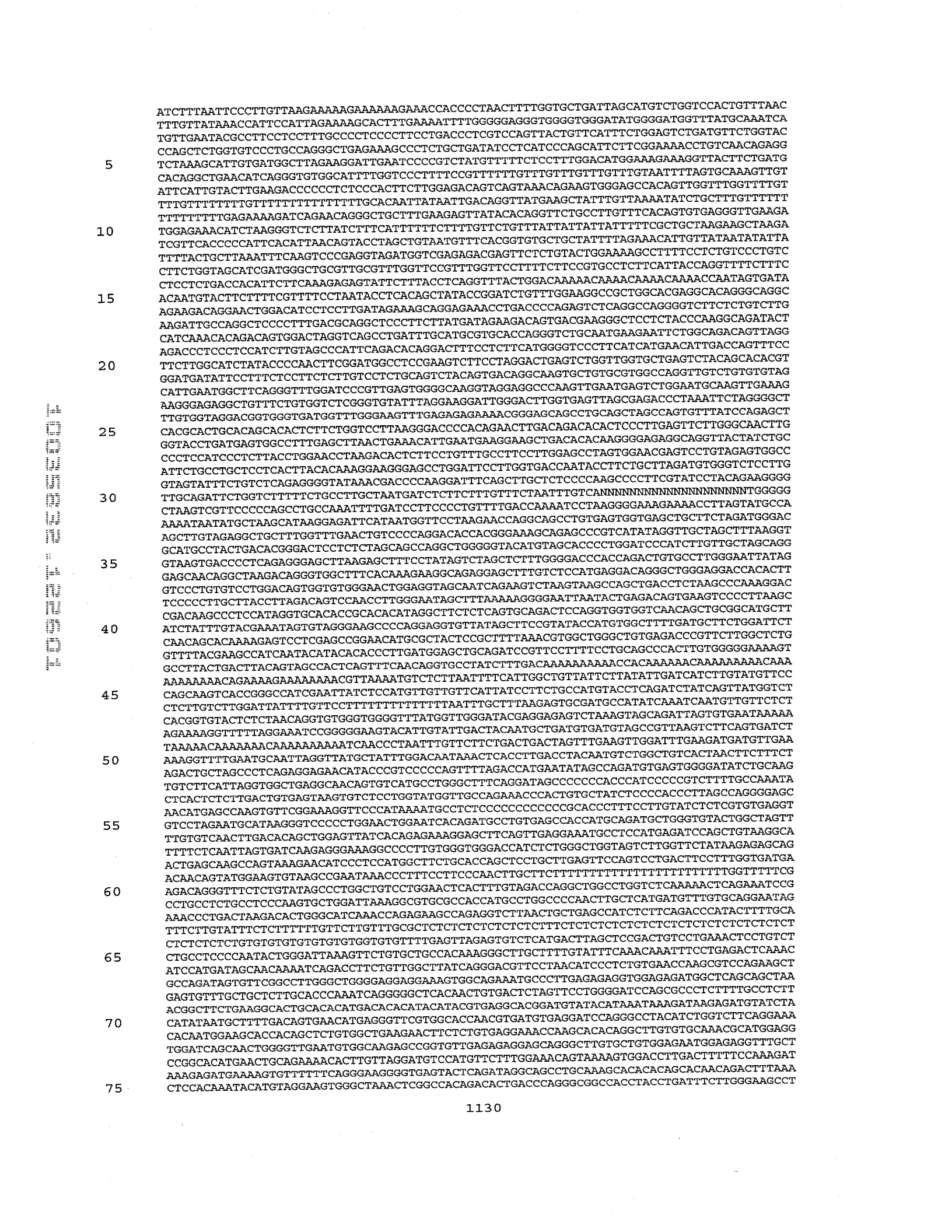


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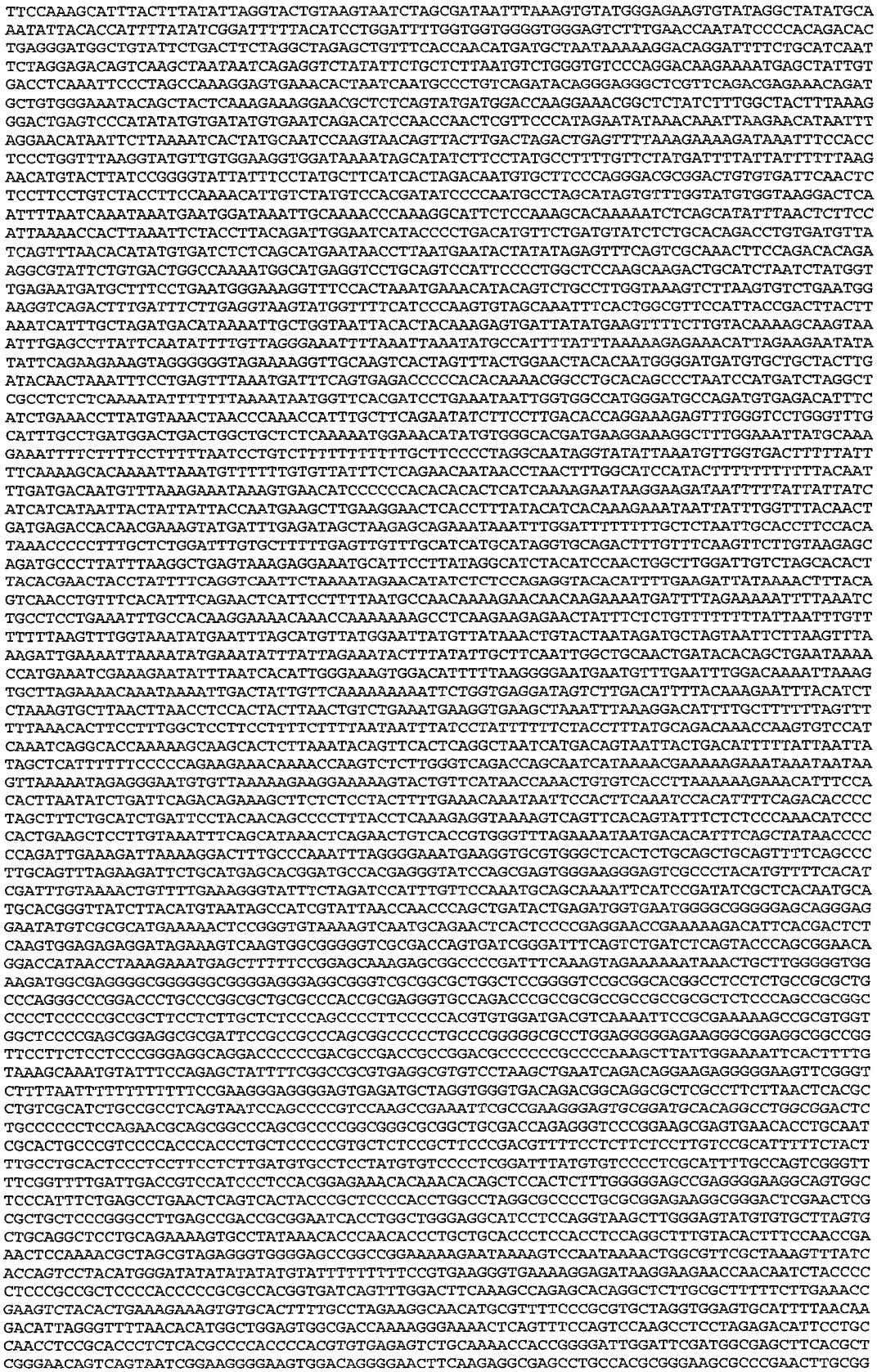
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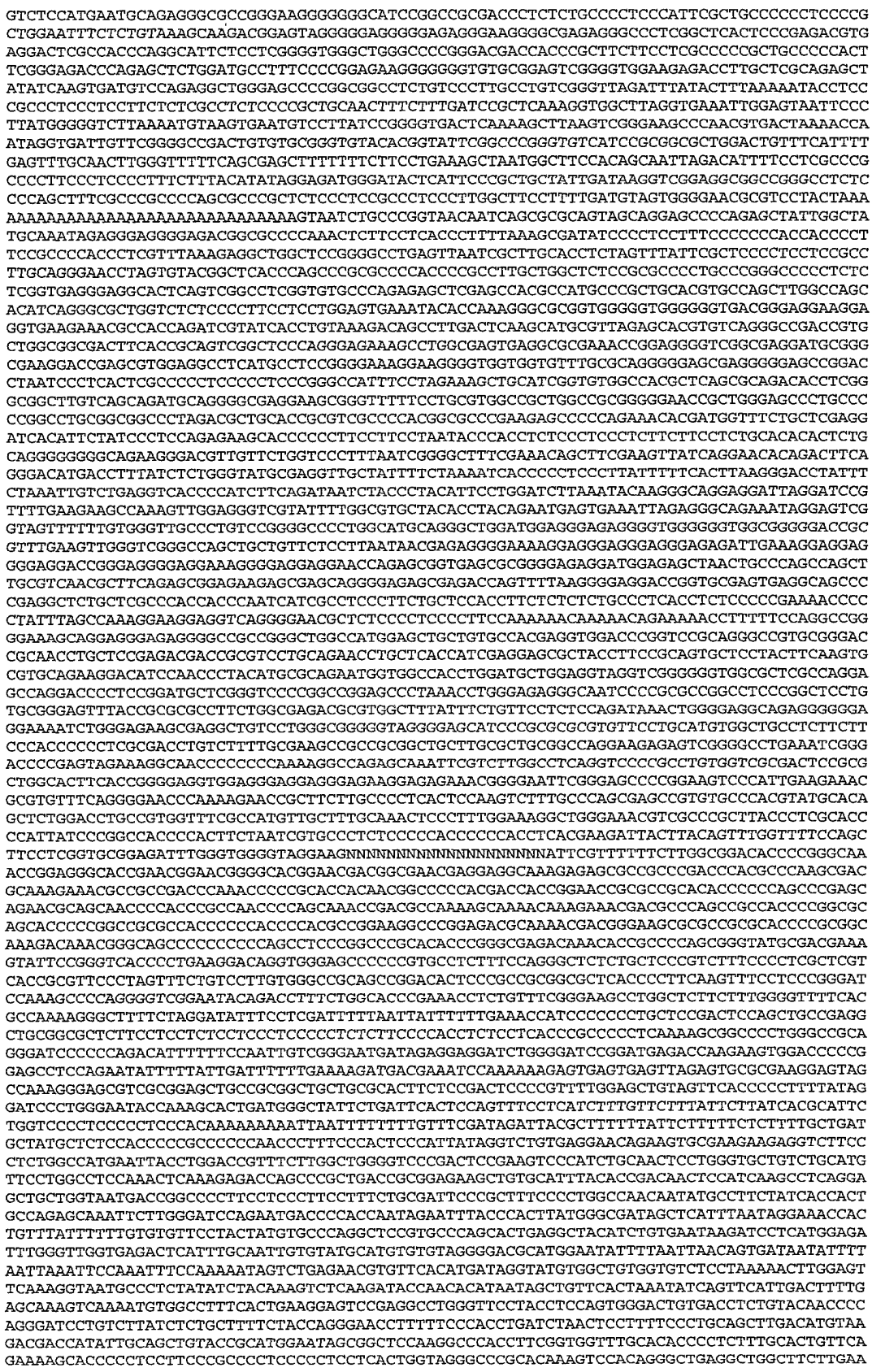
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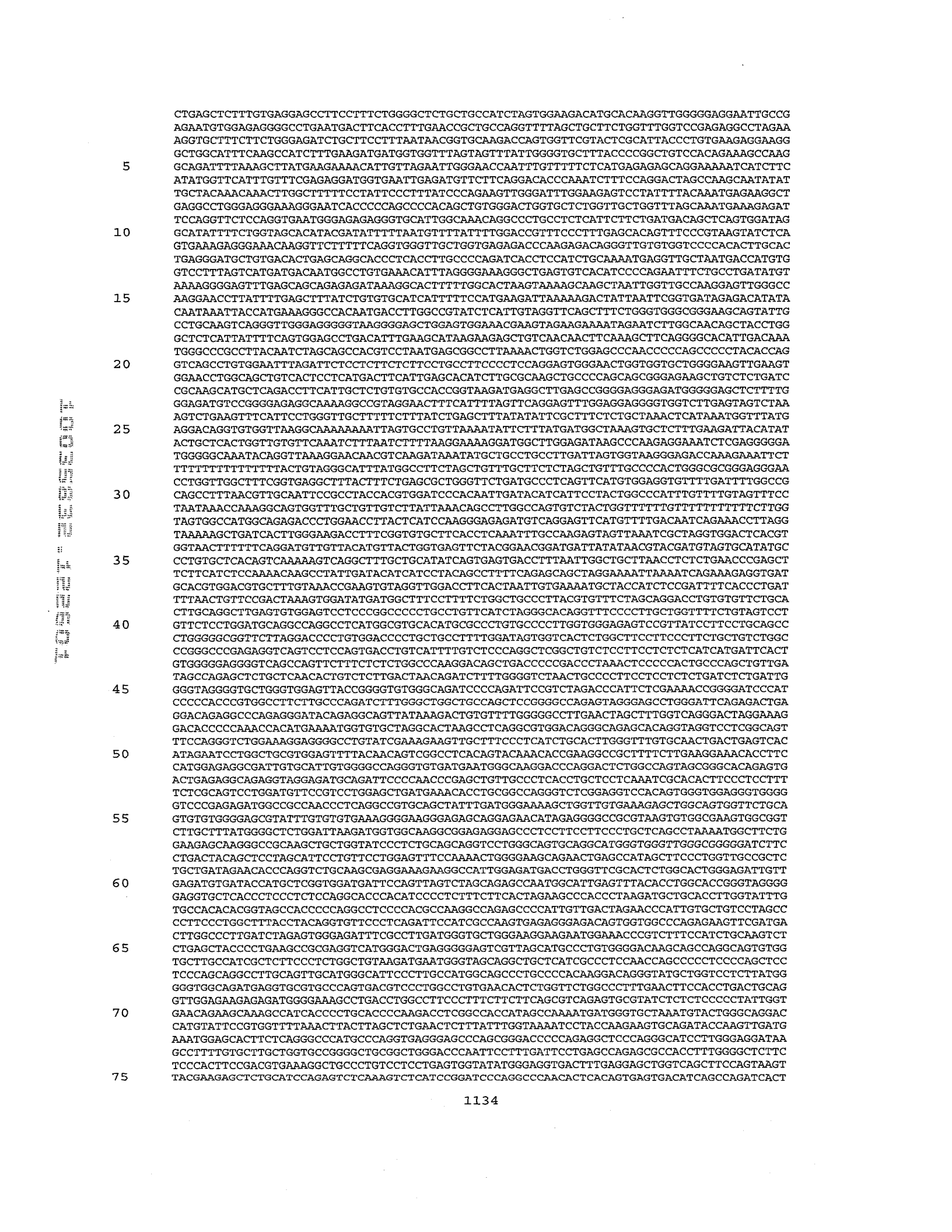
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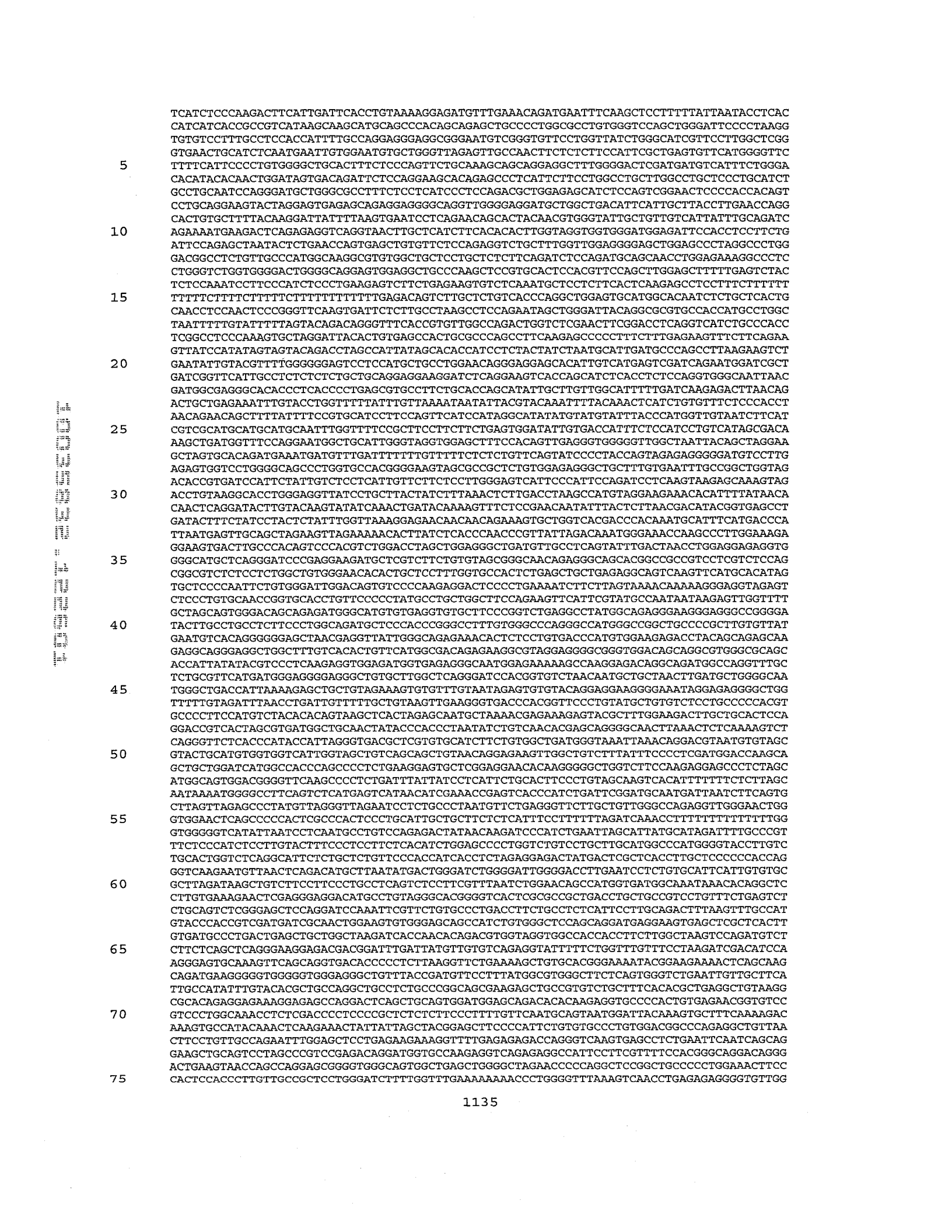
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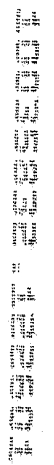
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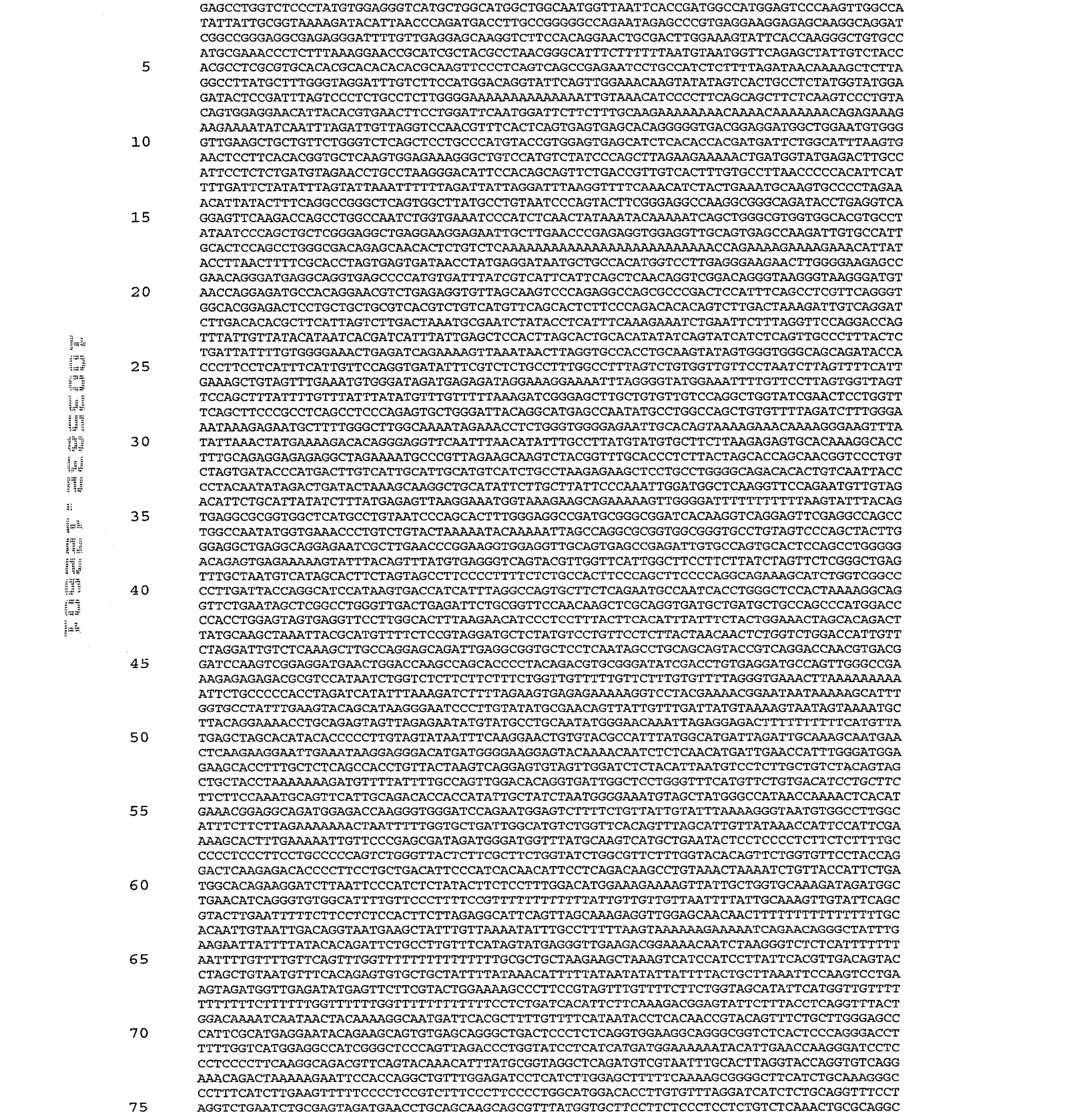


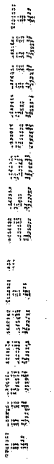






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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 54

MOUSE NOMENCLATURE

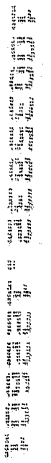
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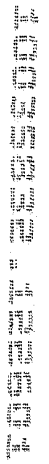
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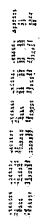


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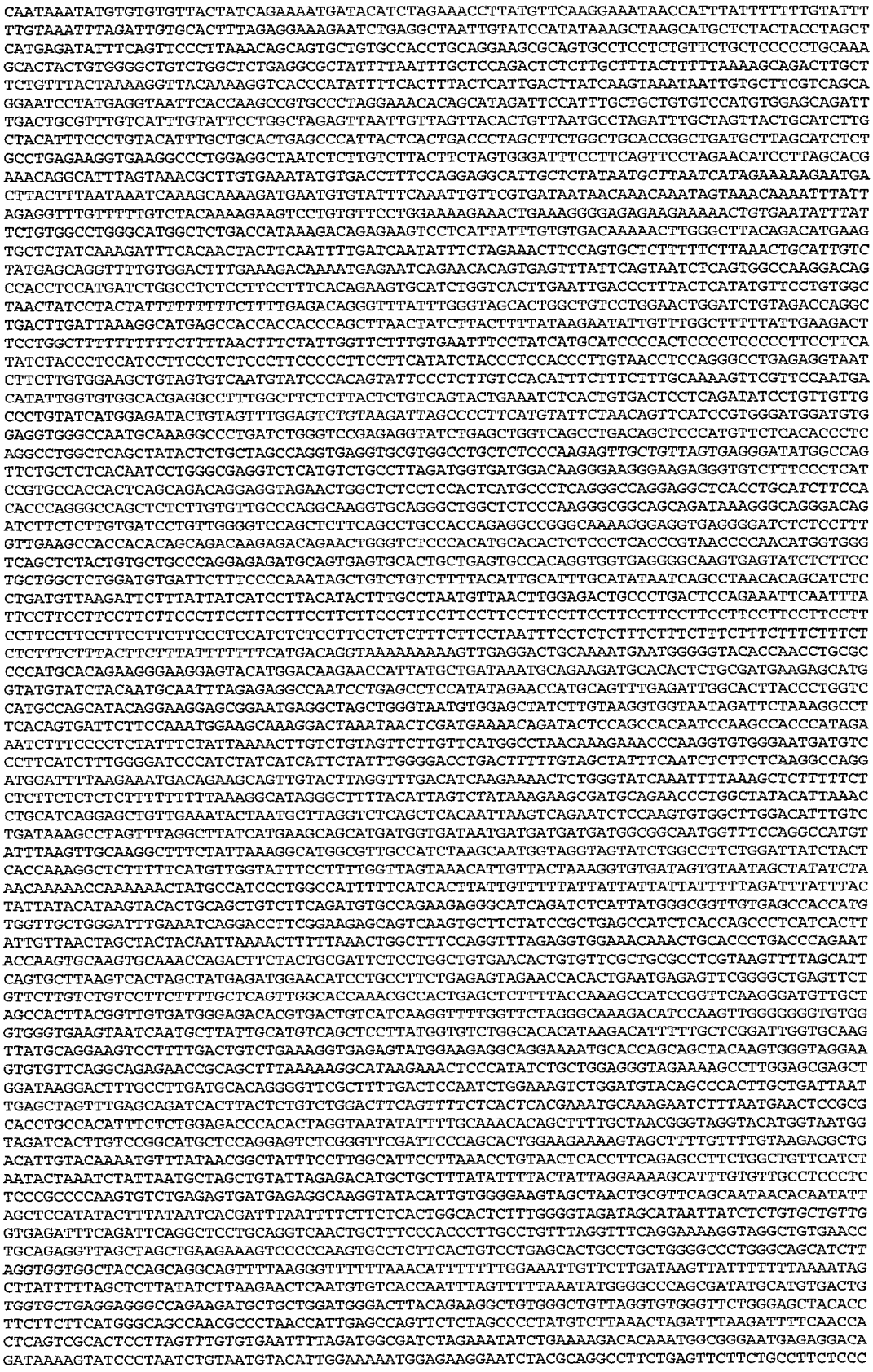


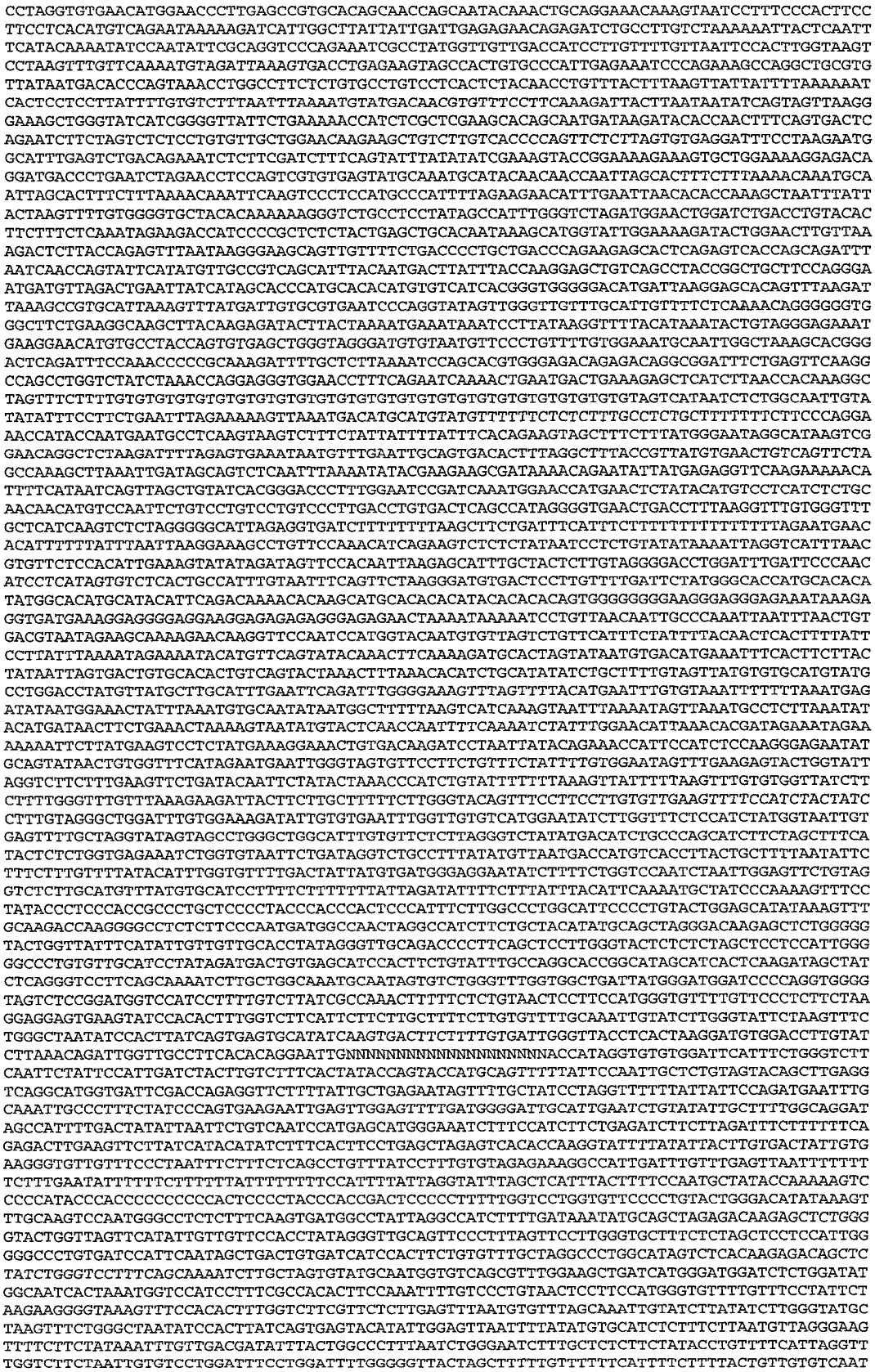
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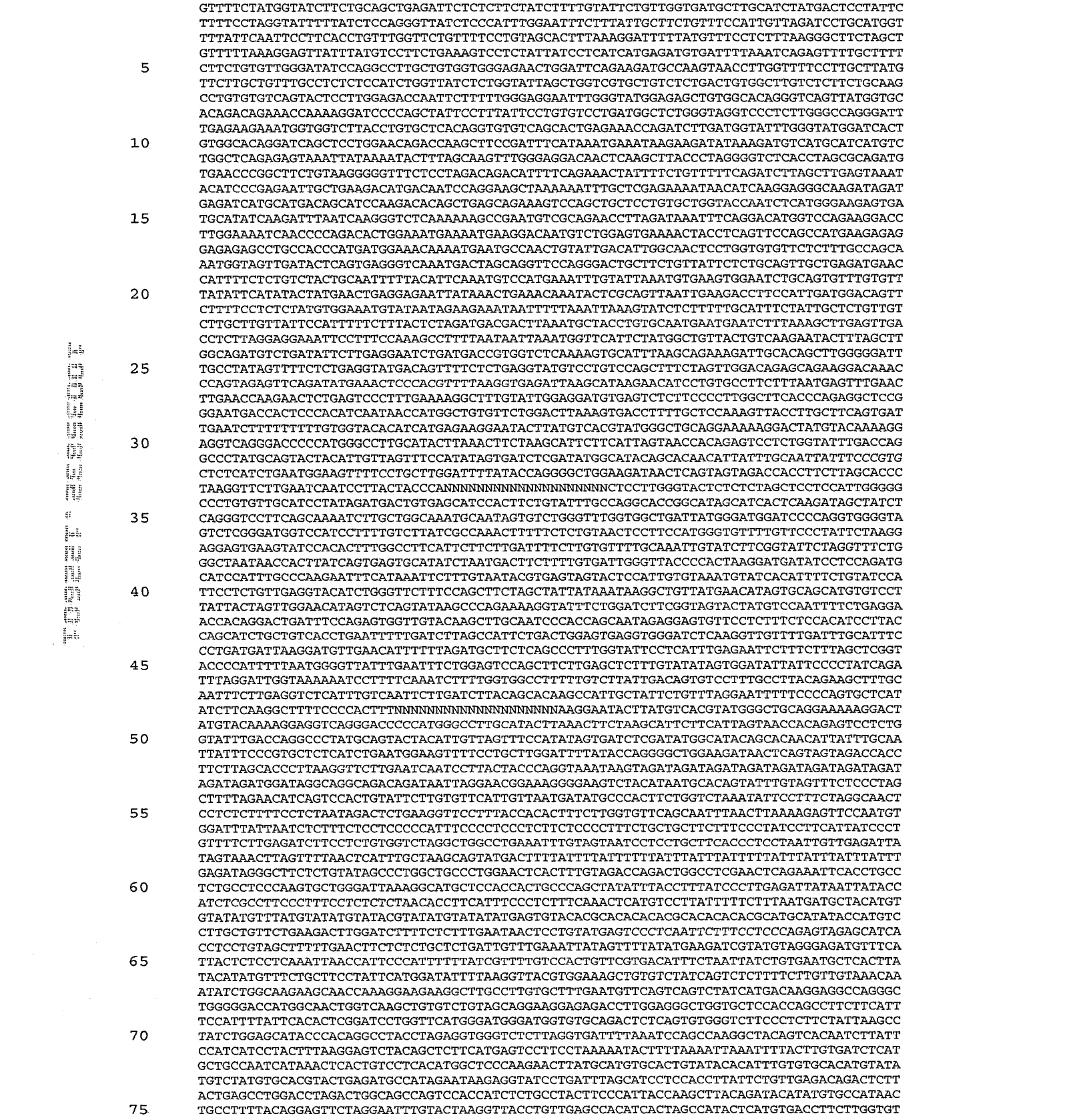
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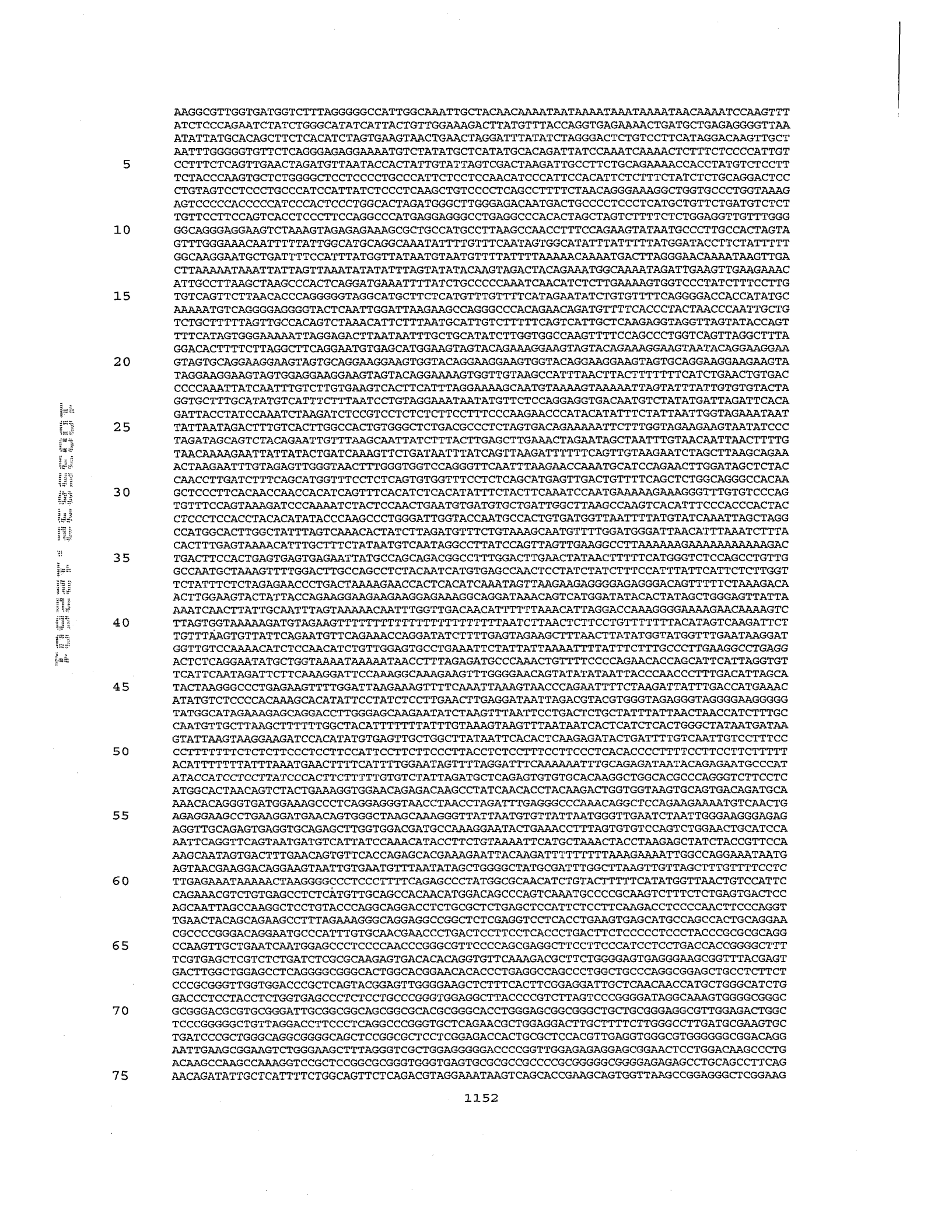
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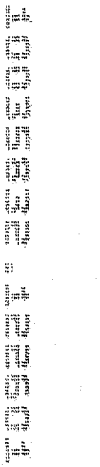
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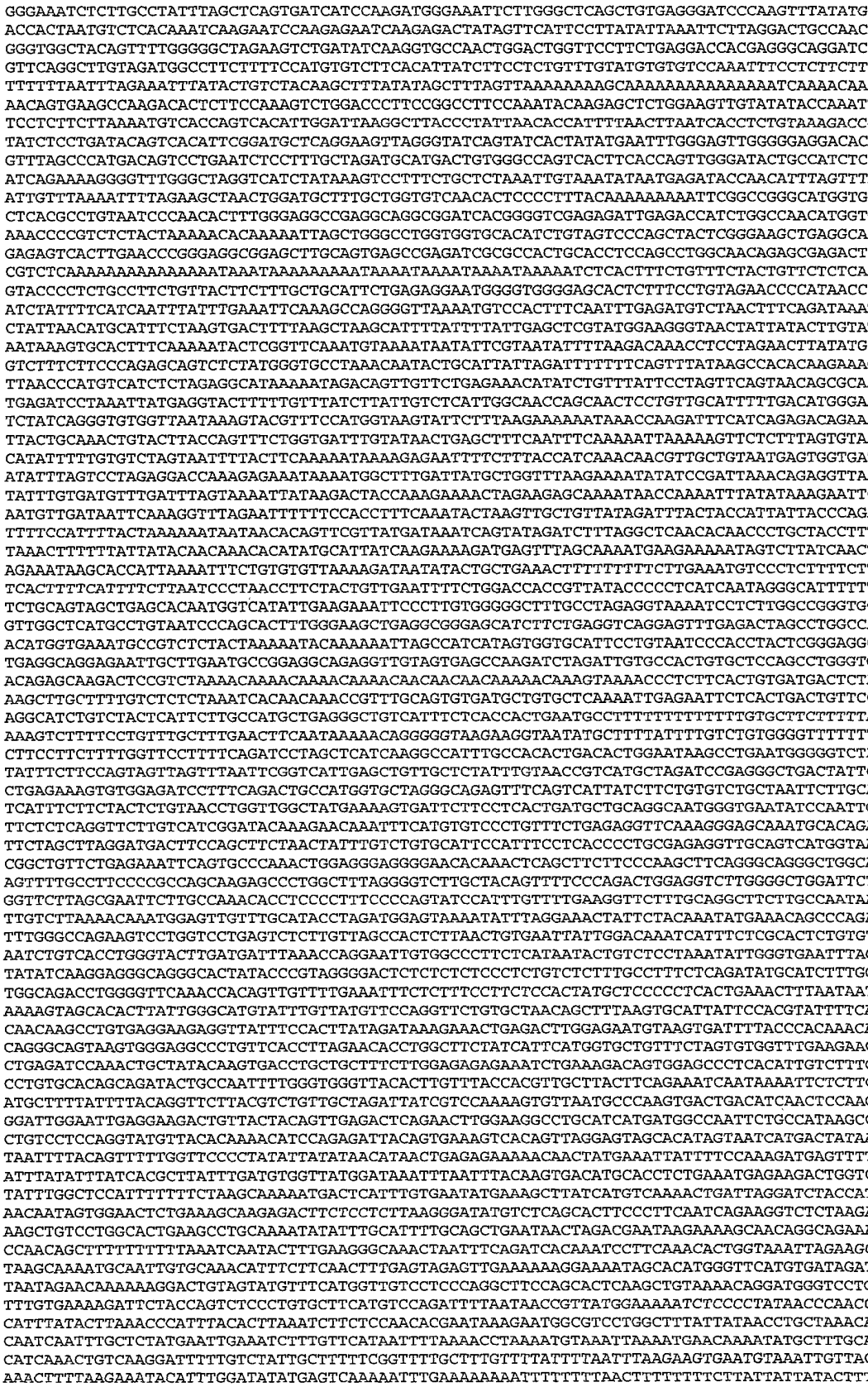
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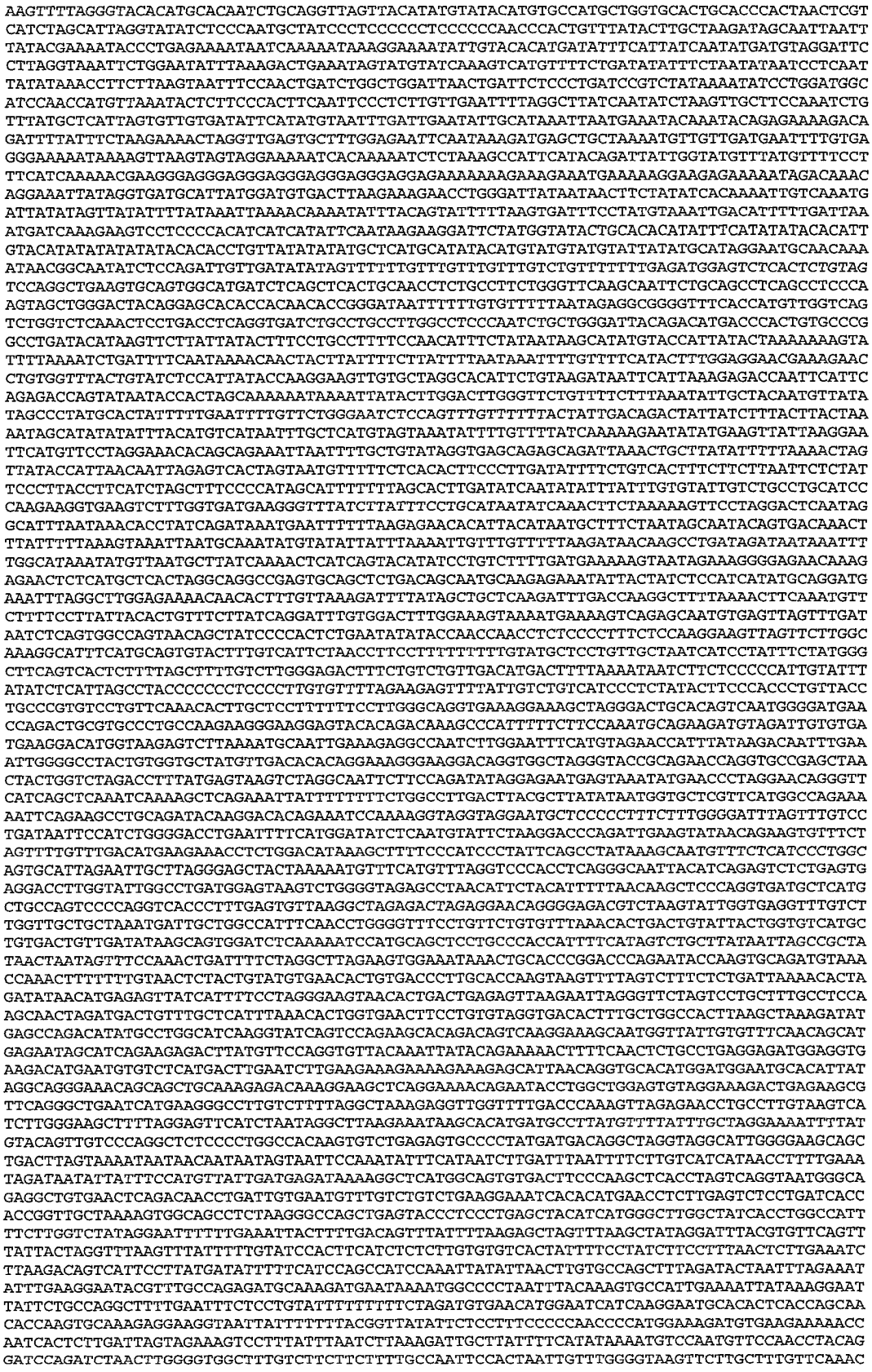
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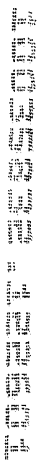






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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 55

MOUSE NOMENCLATURE
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Celera mCG1847

HUMAN NOMENCLATURE
HGNC IRF2
Celera hCG16244

MOUSE SEQUENCE - GENOMIC

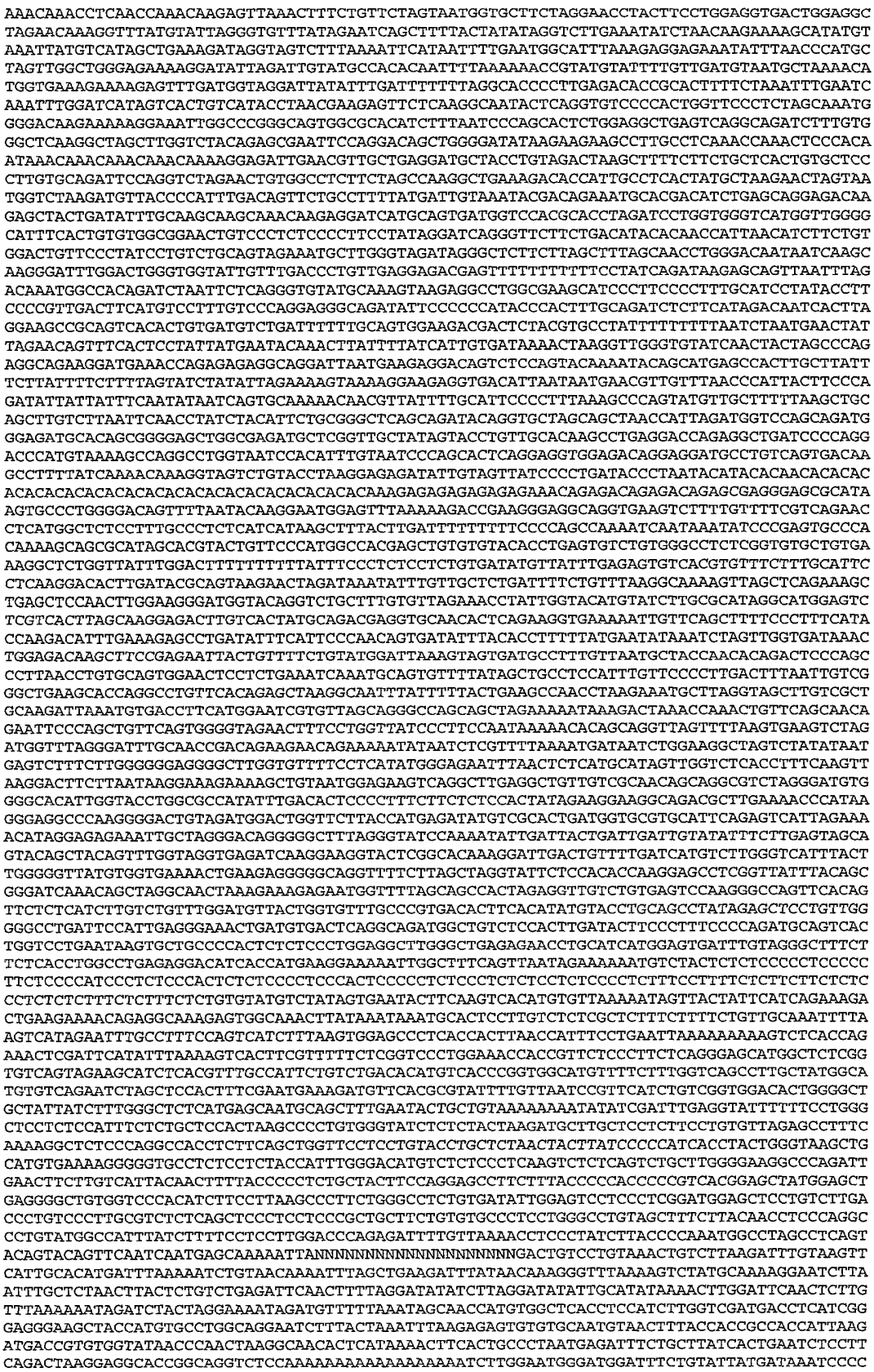
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Feb 22, 2005 4:50:50 PM

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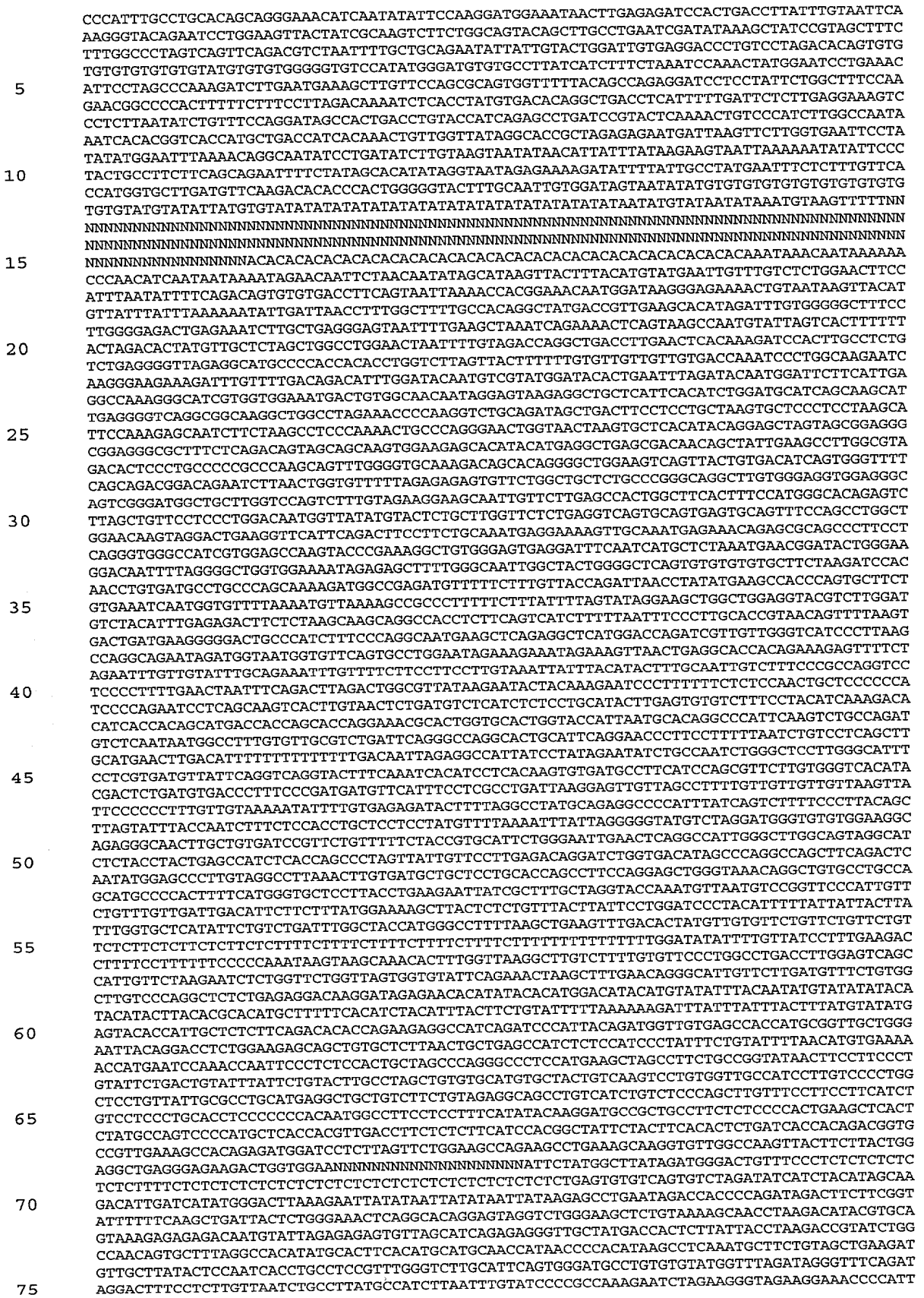
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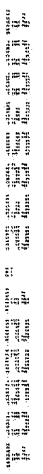


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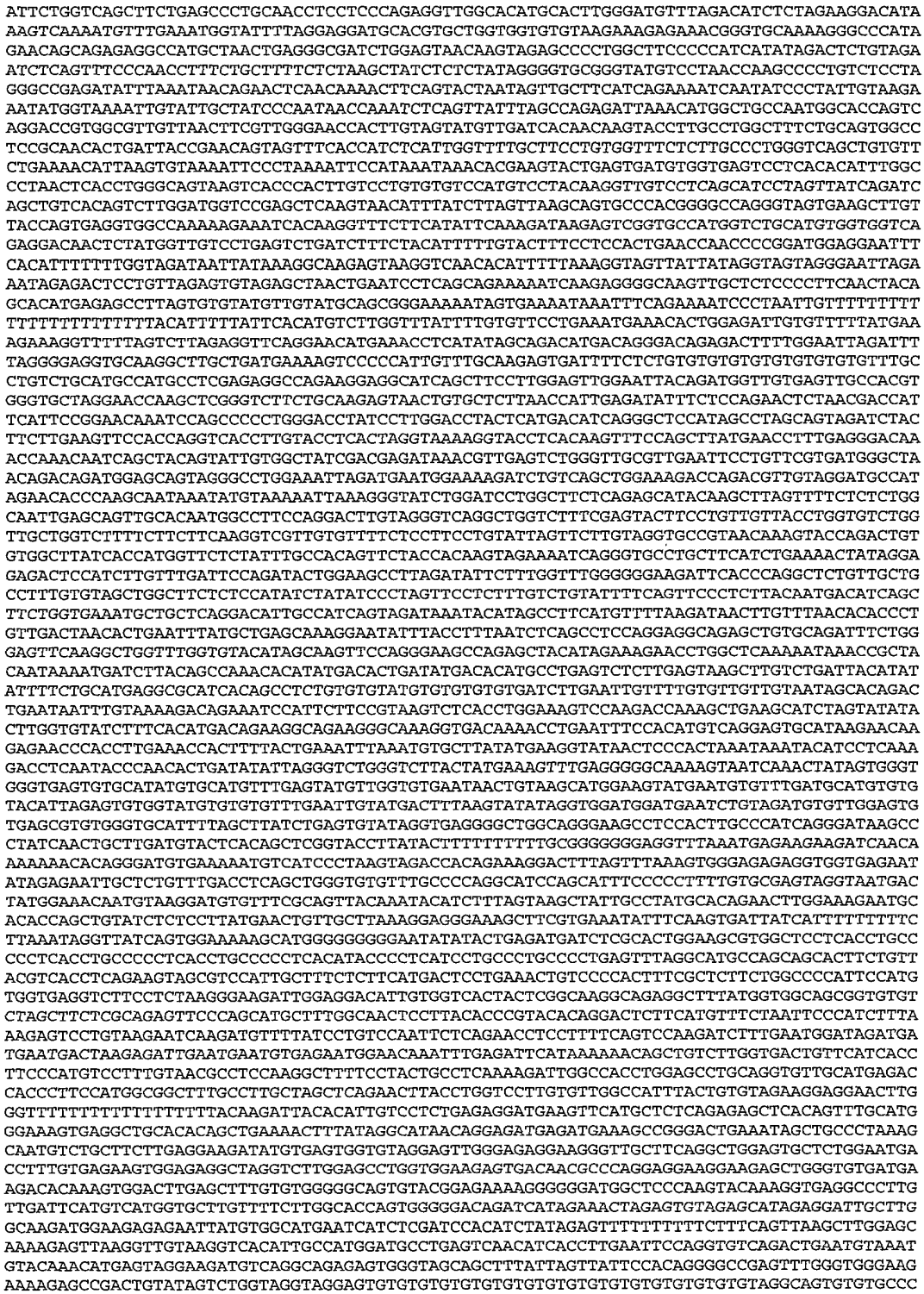


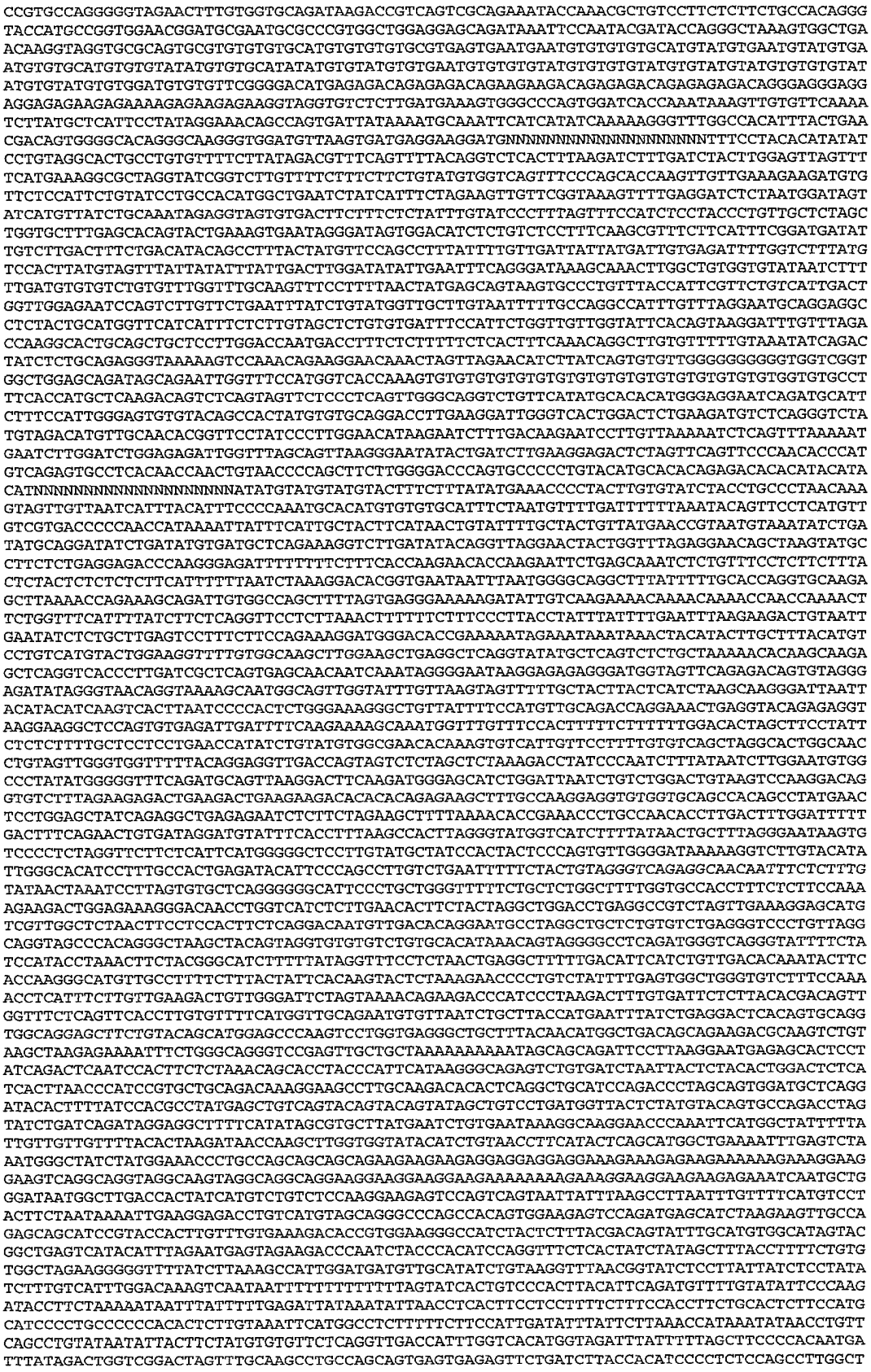


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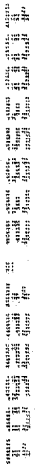
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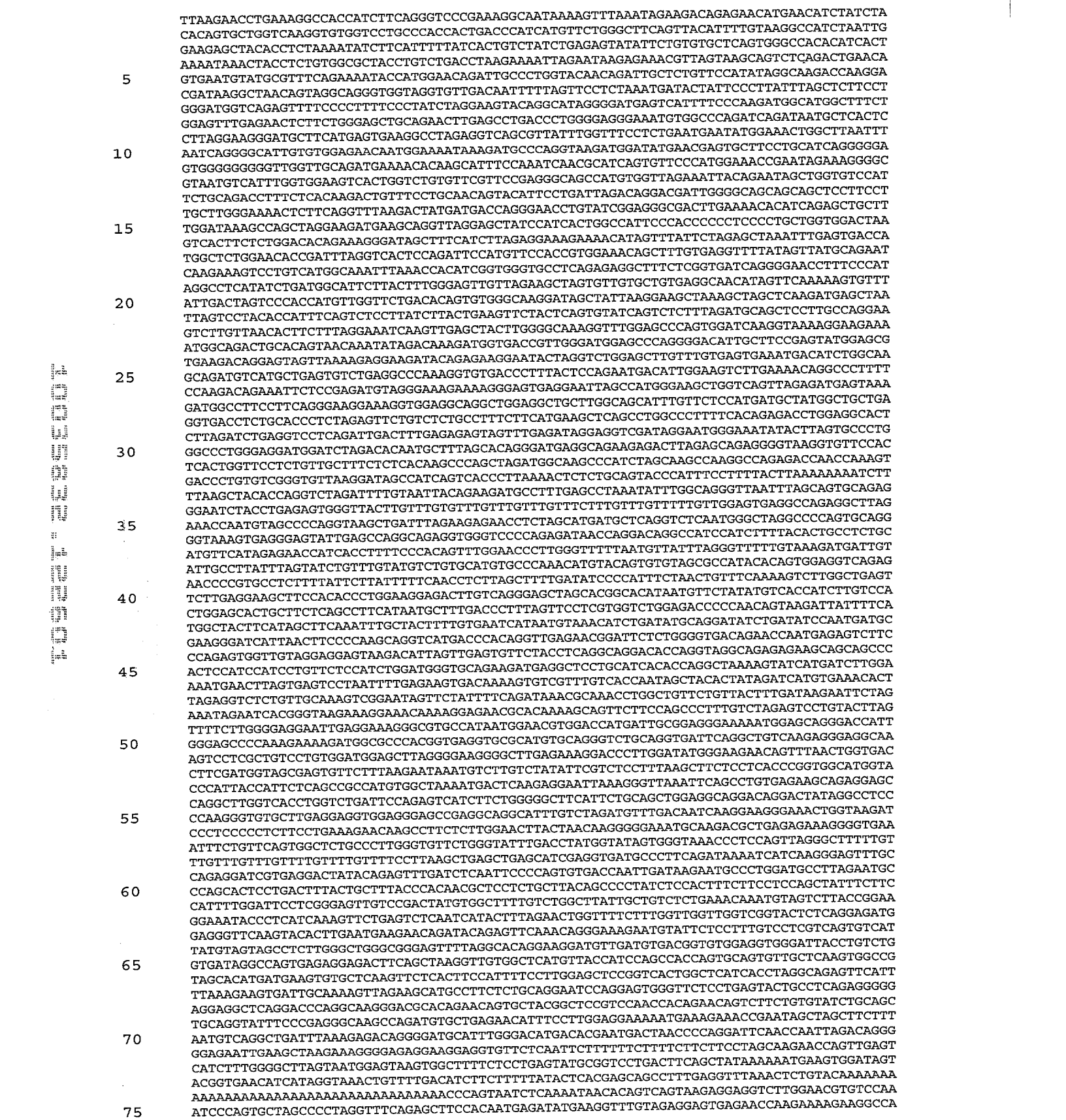




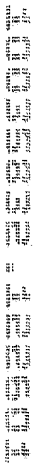
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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

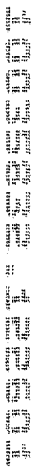
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HUMAN SEQUENCE - GENOMIC

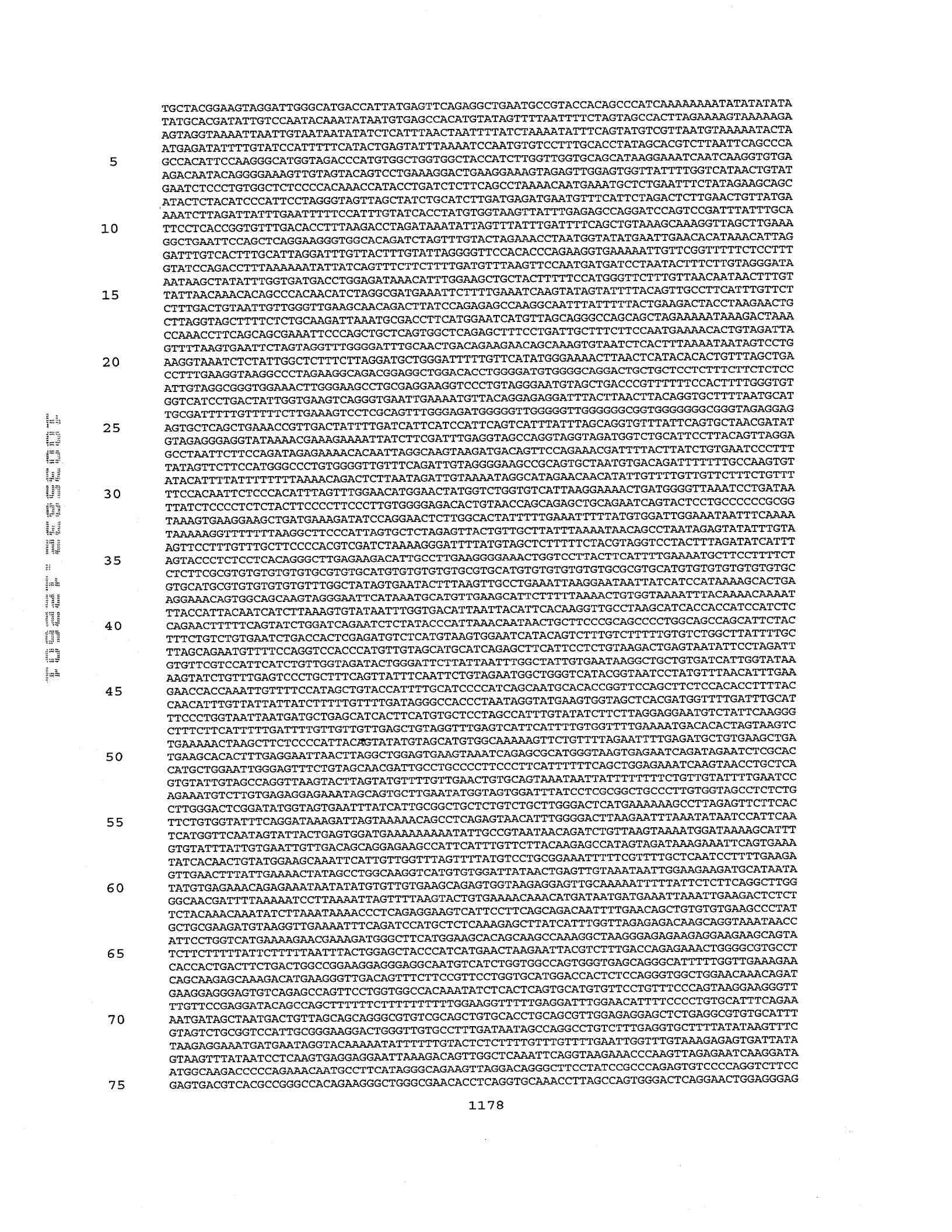
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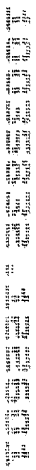
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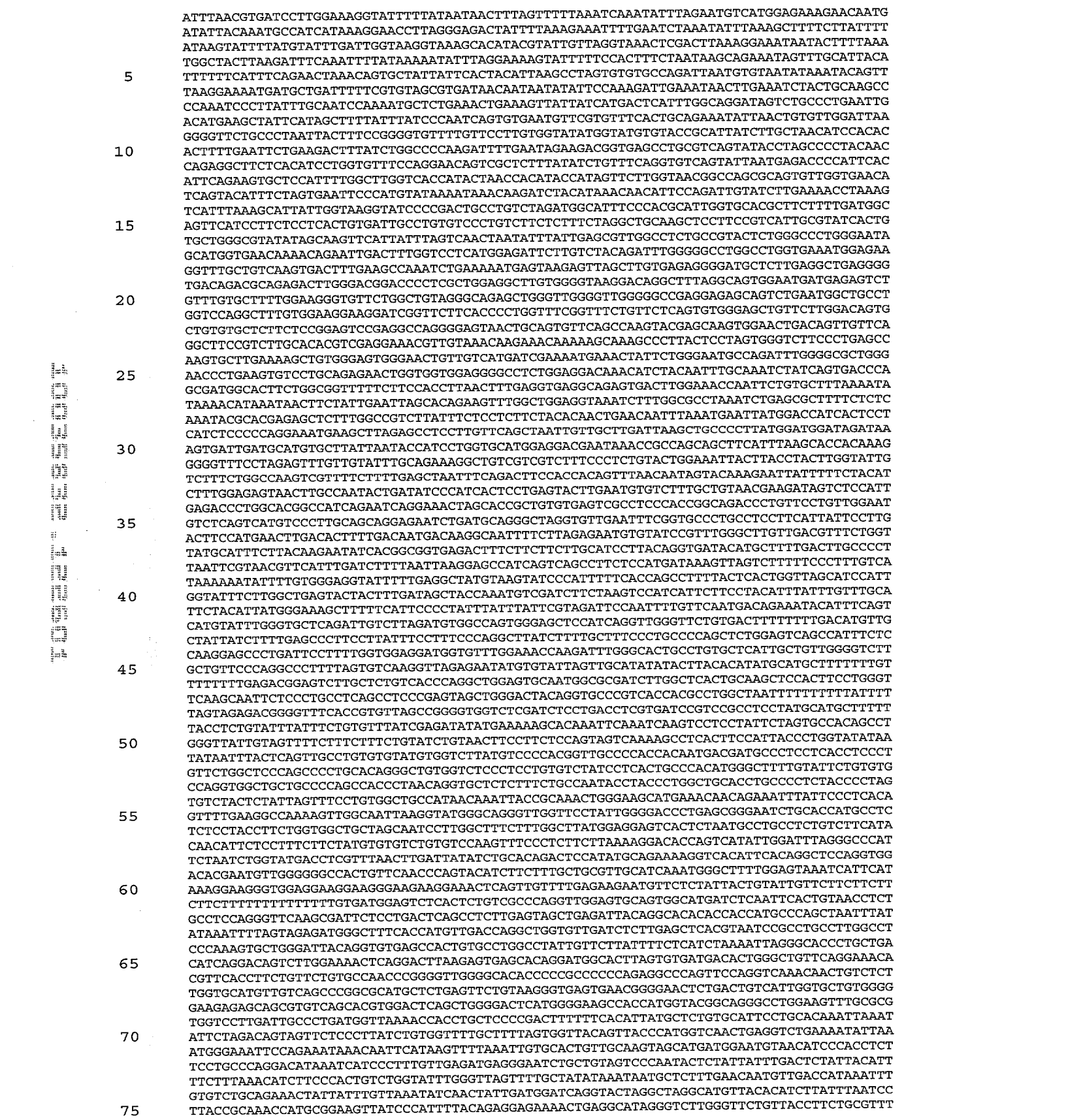
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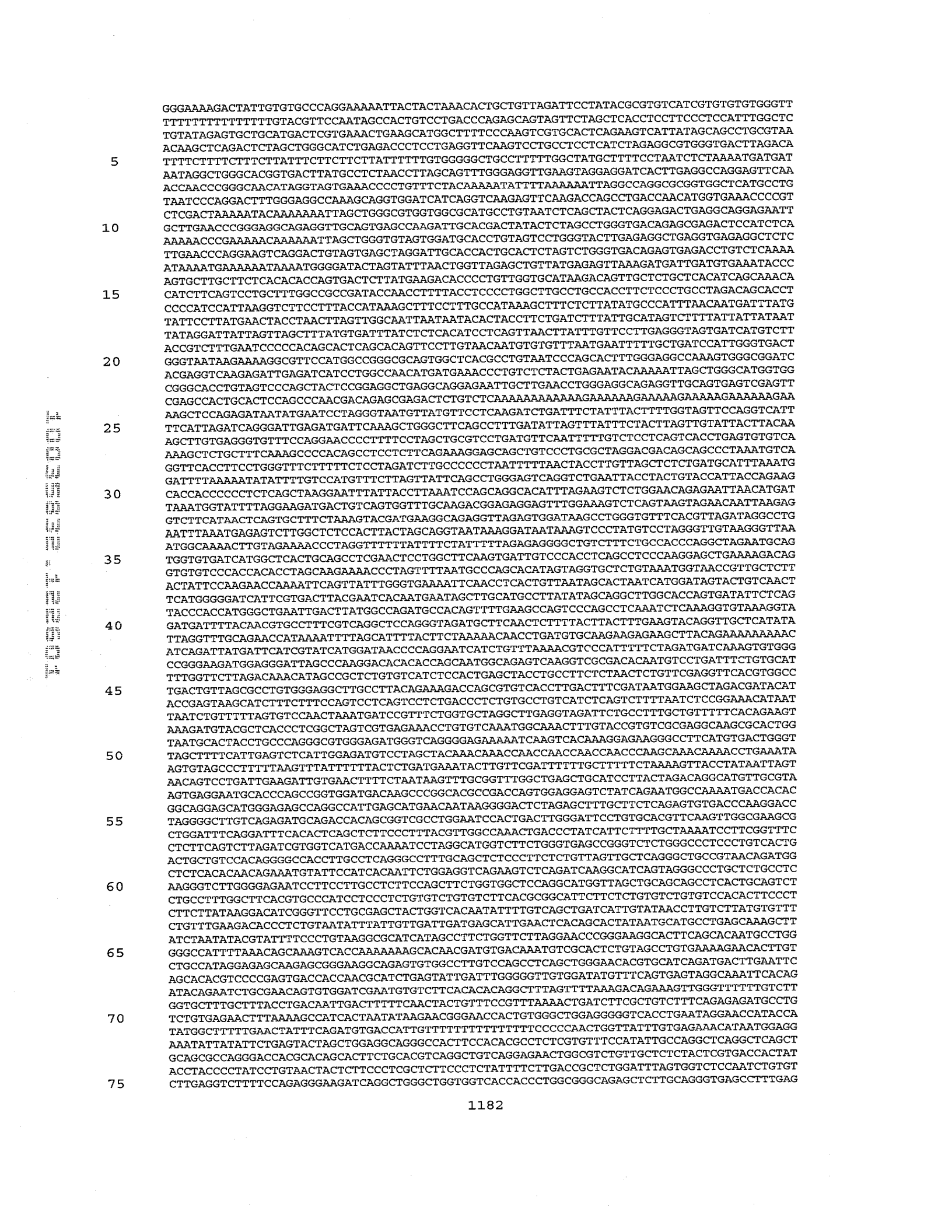


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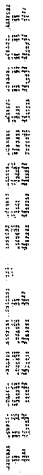
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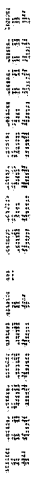
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HUMAN SEQUENCE - mRNA

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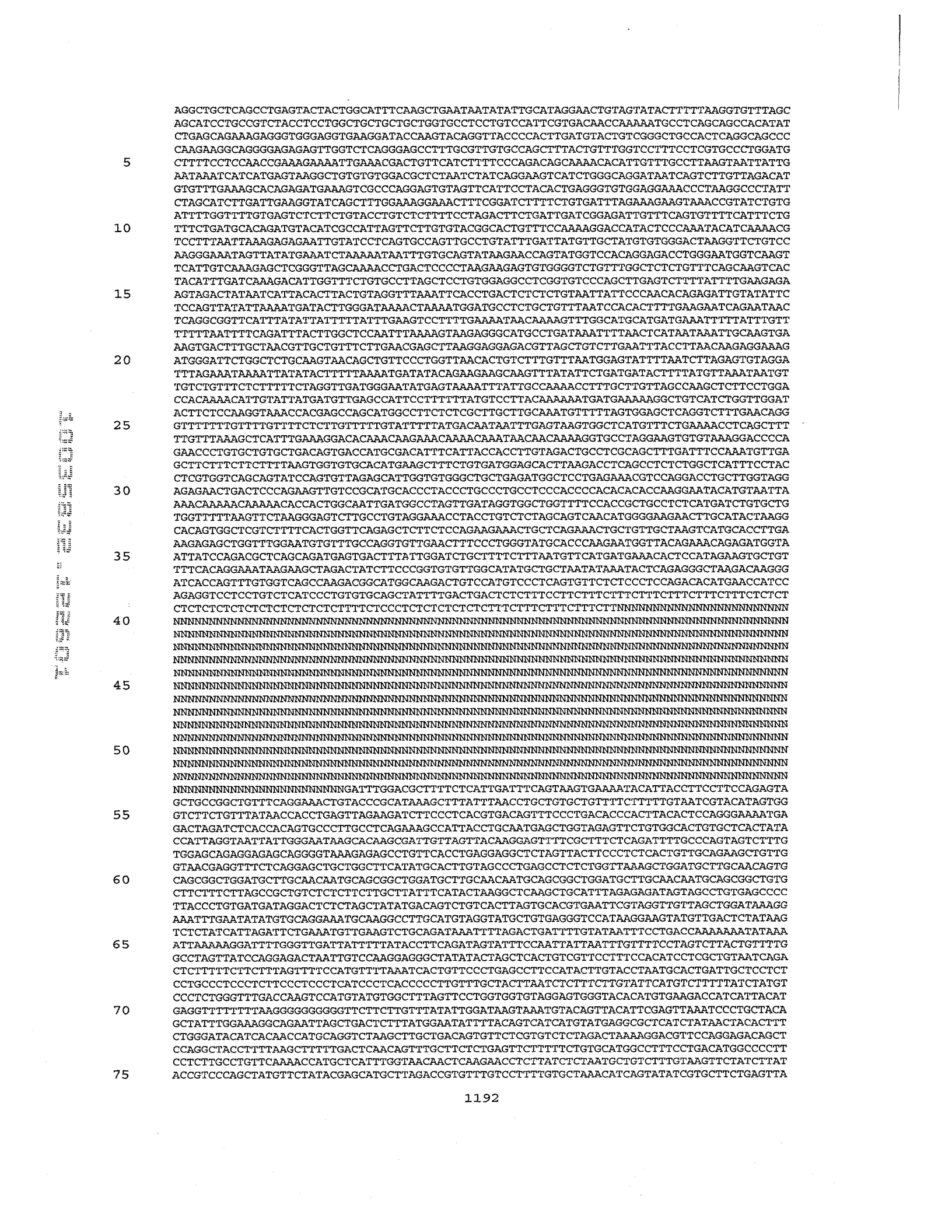
Table 56

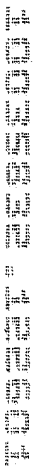
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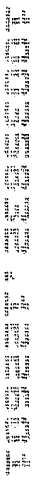
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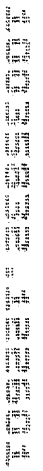


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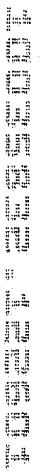
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MOUSE SEQUENCE - mRNA
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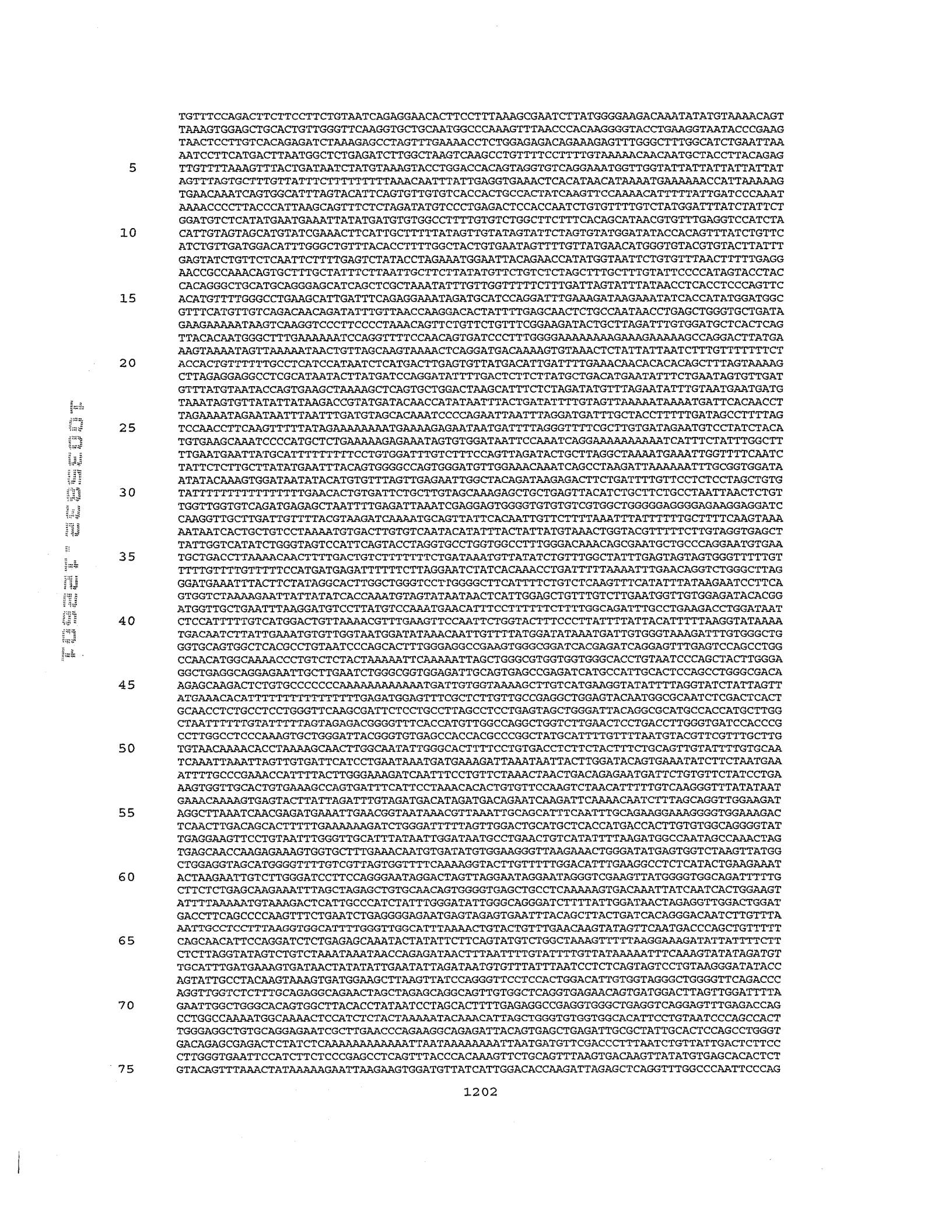
MOUSE SEQUENCE - CODING

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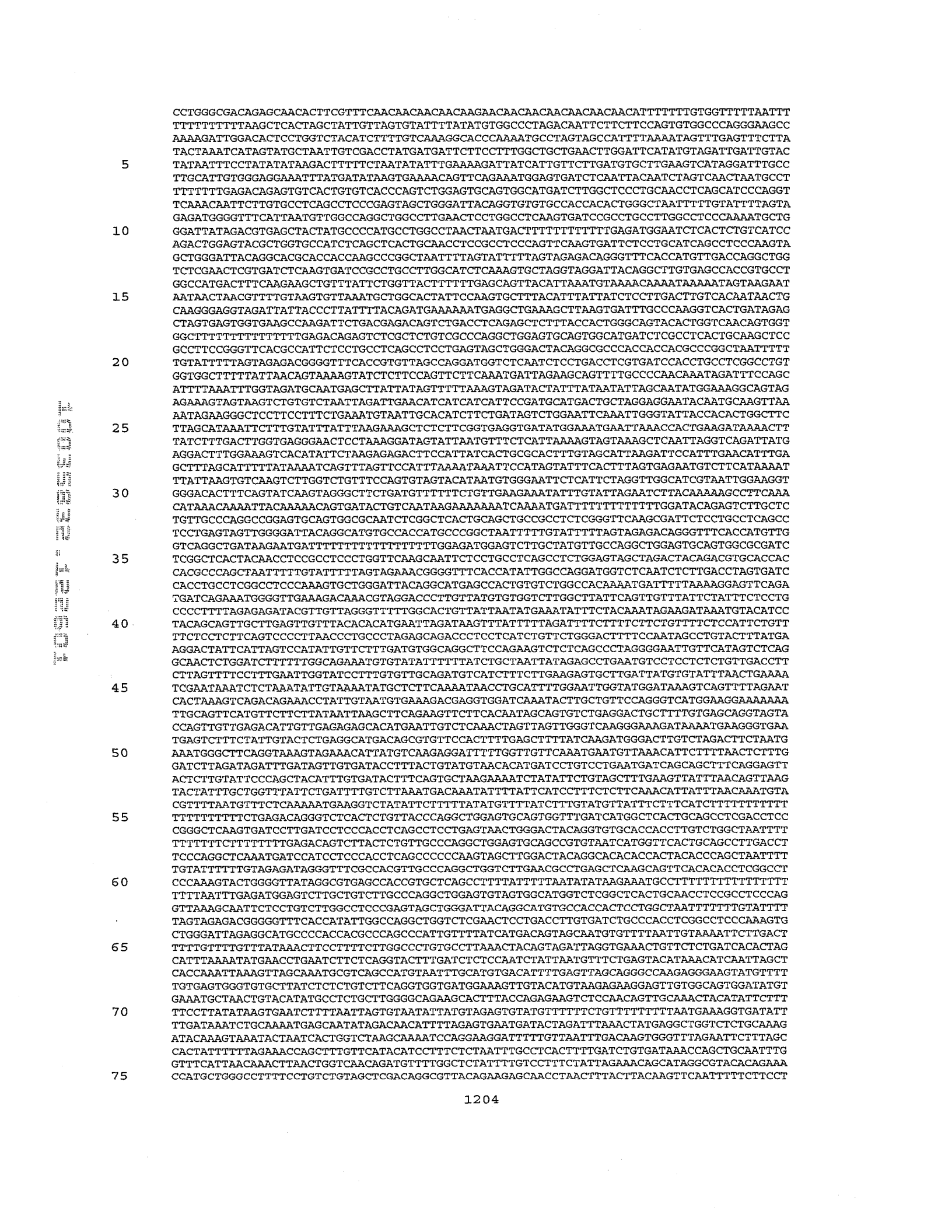
HUMAN SEQUENCE - GENOMIC

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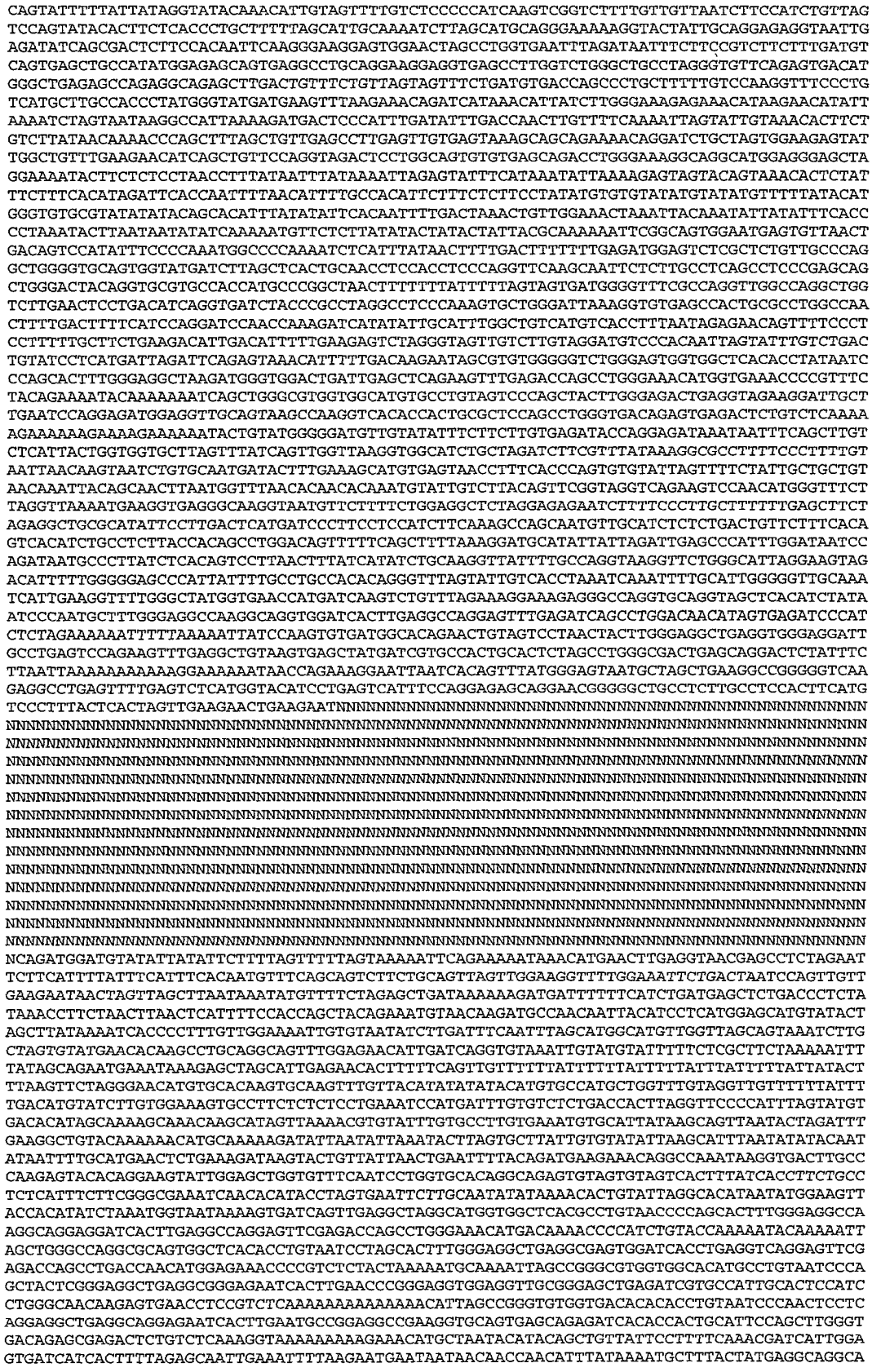


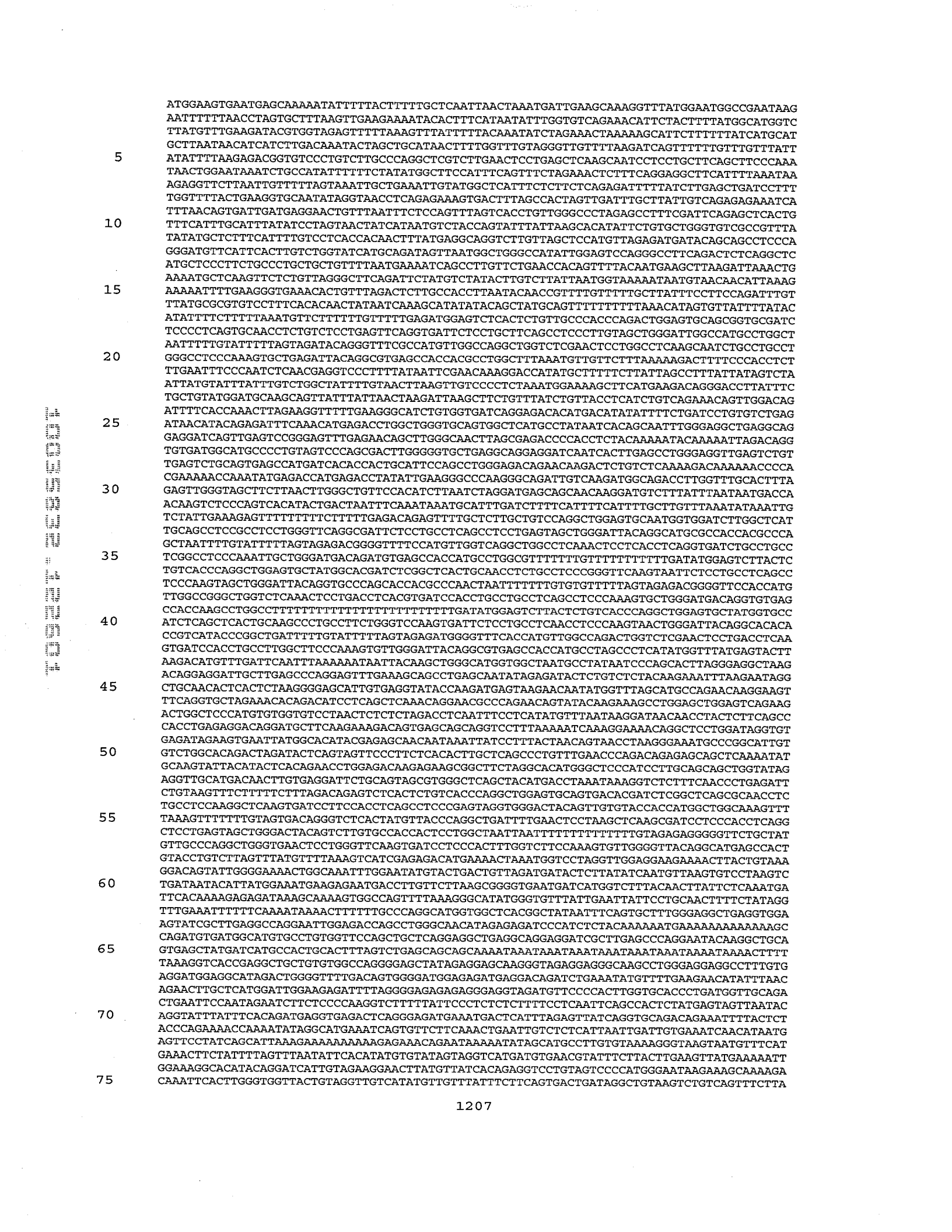
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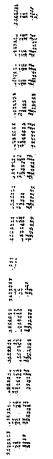




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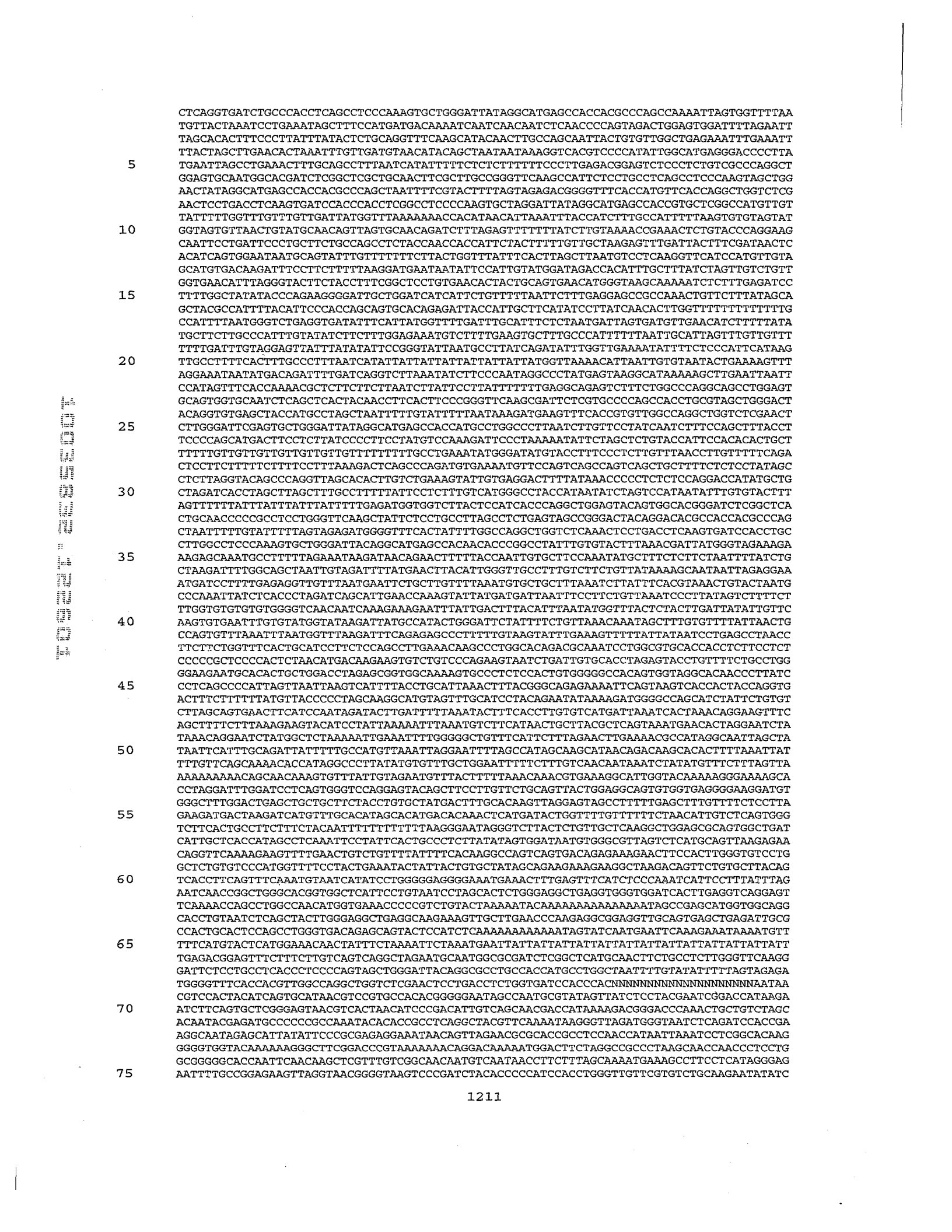
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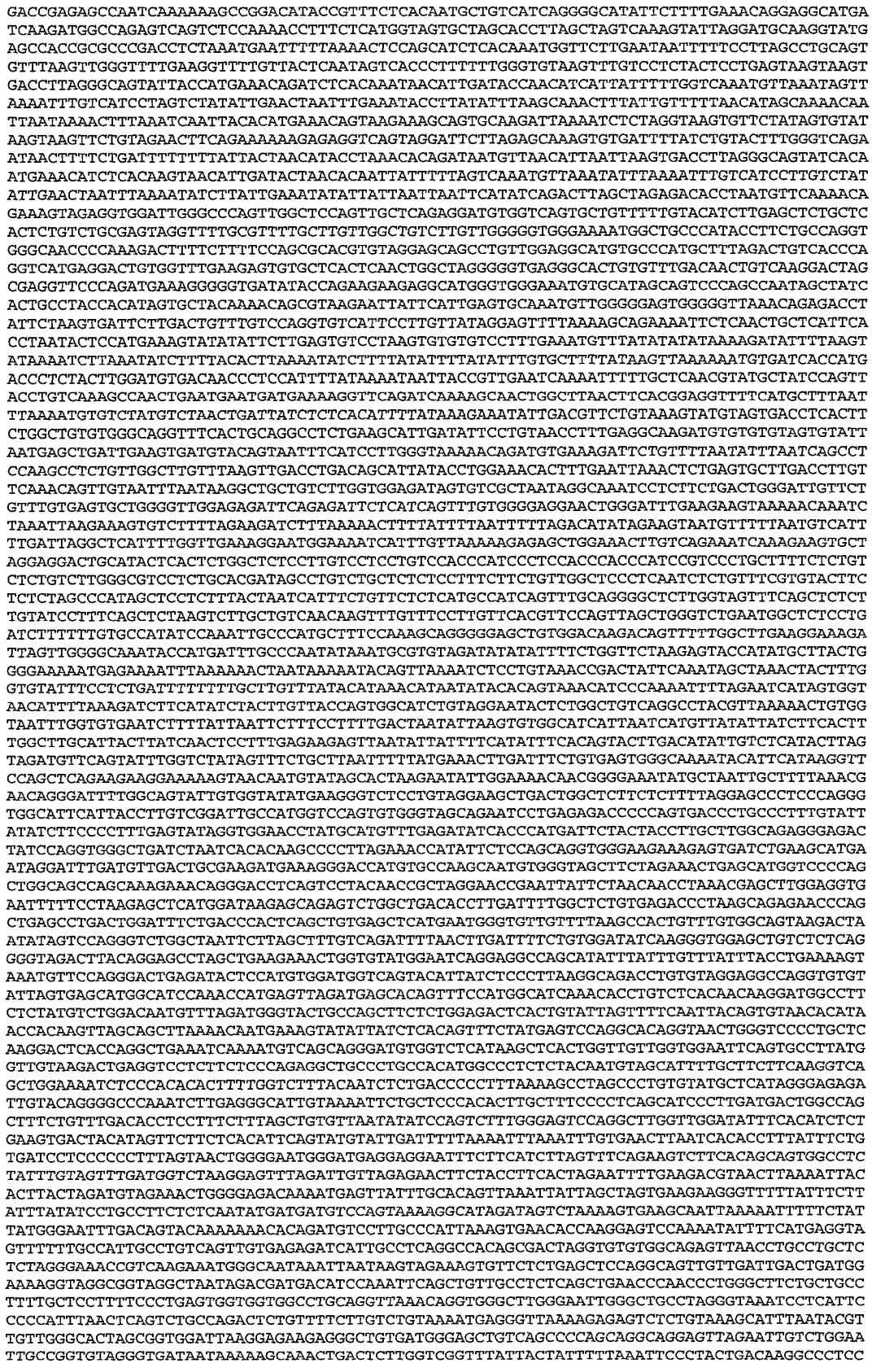
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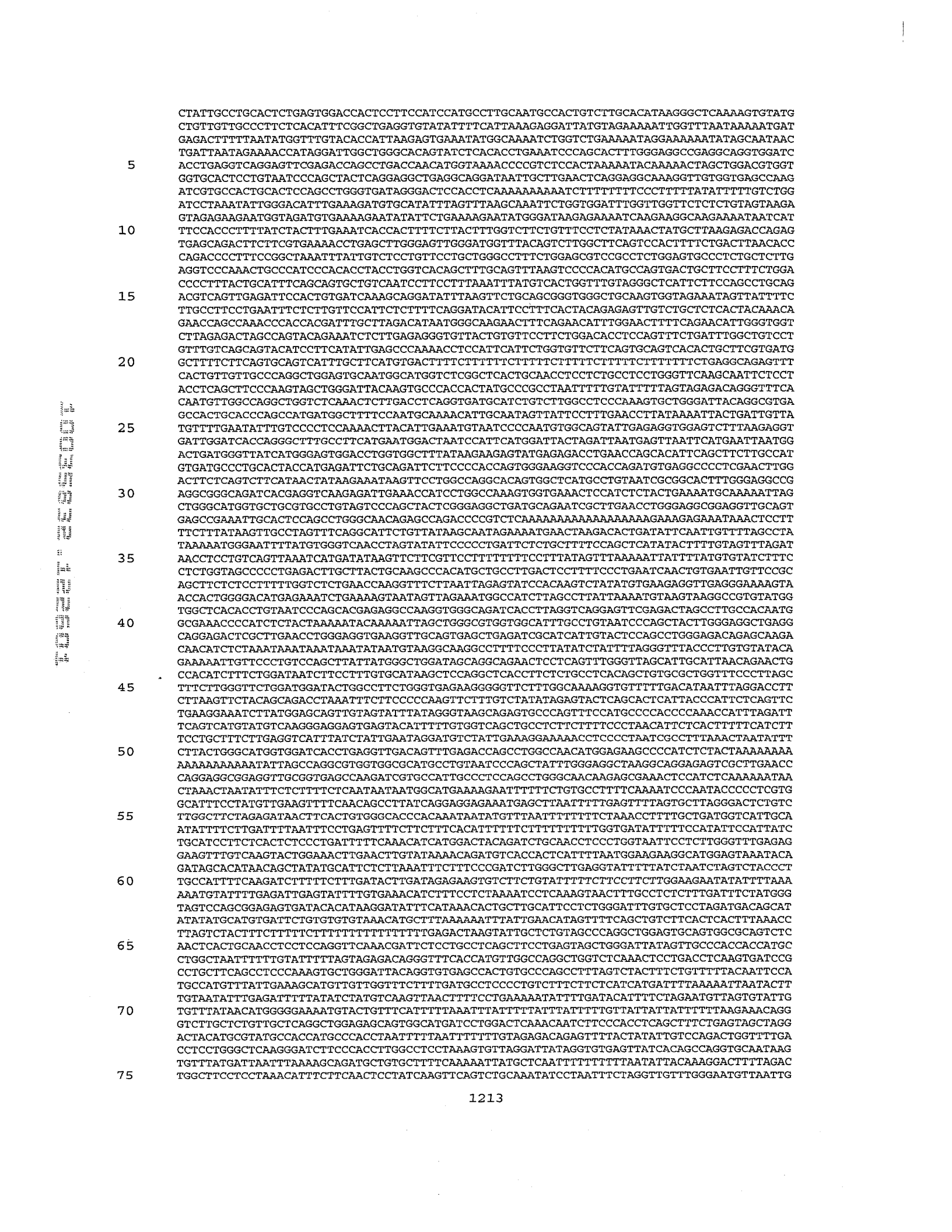
Translated by Tarjomyar

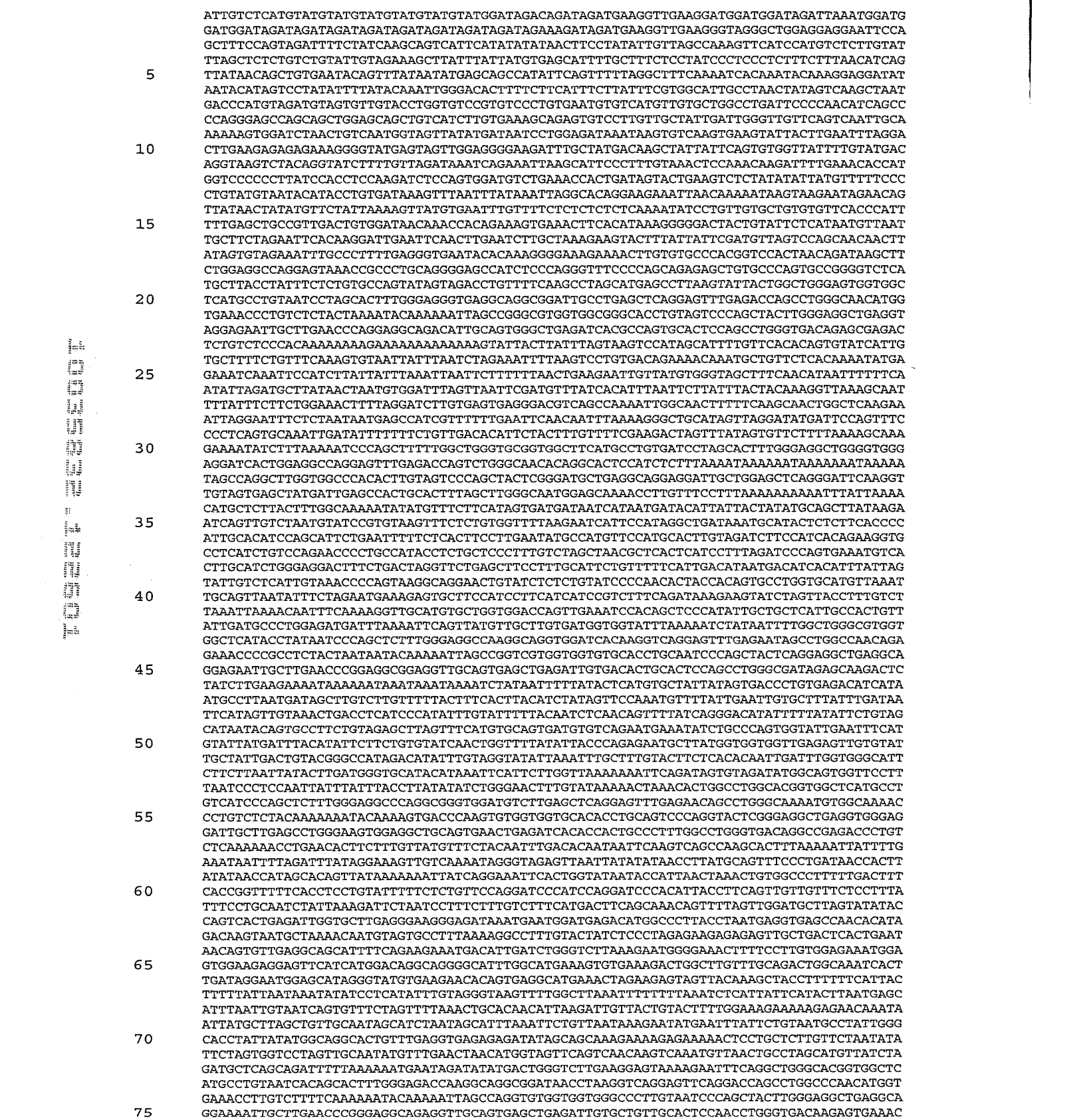
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Replacement Sheet - 2/2/2006







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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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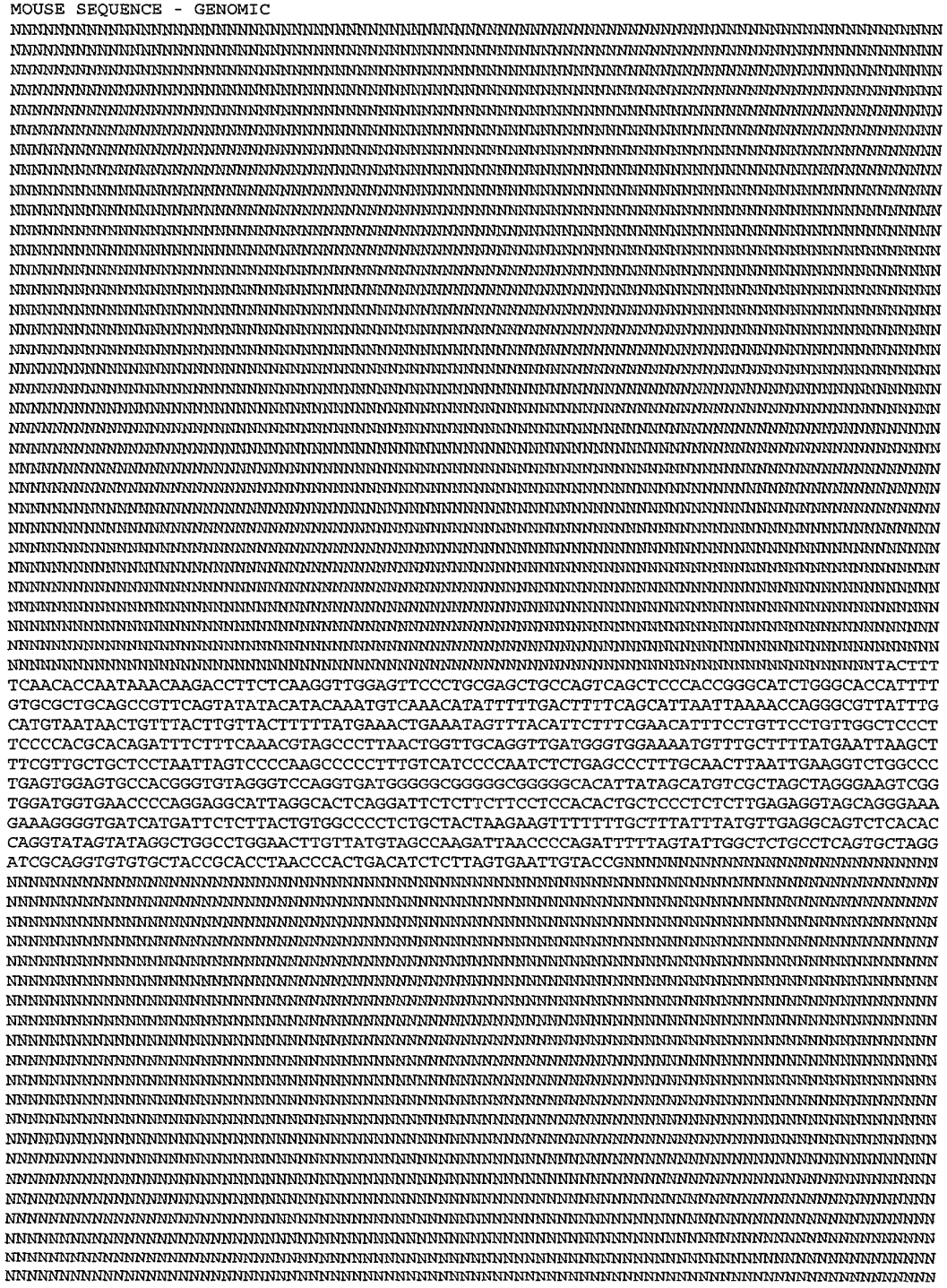
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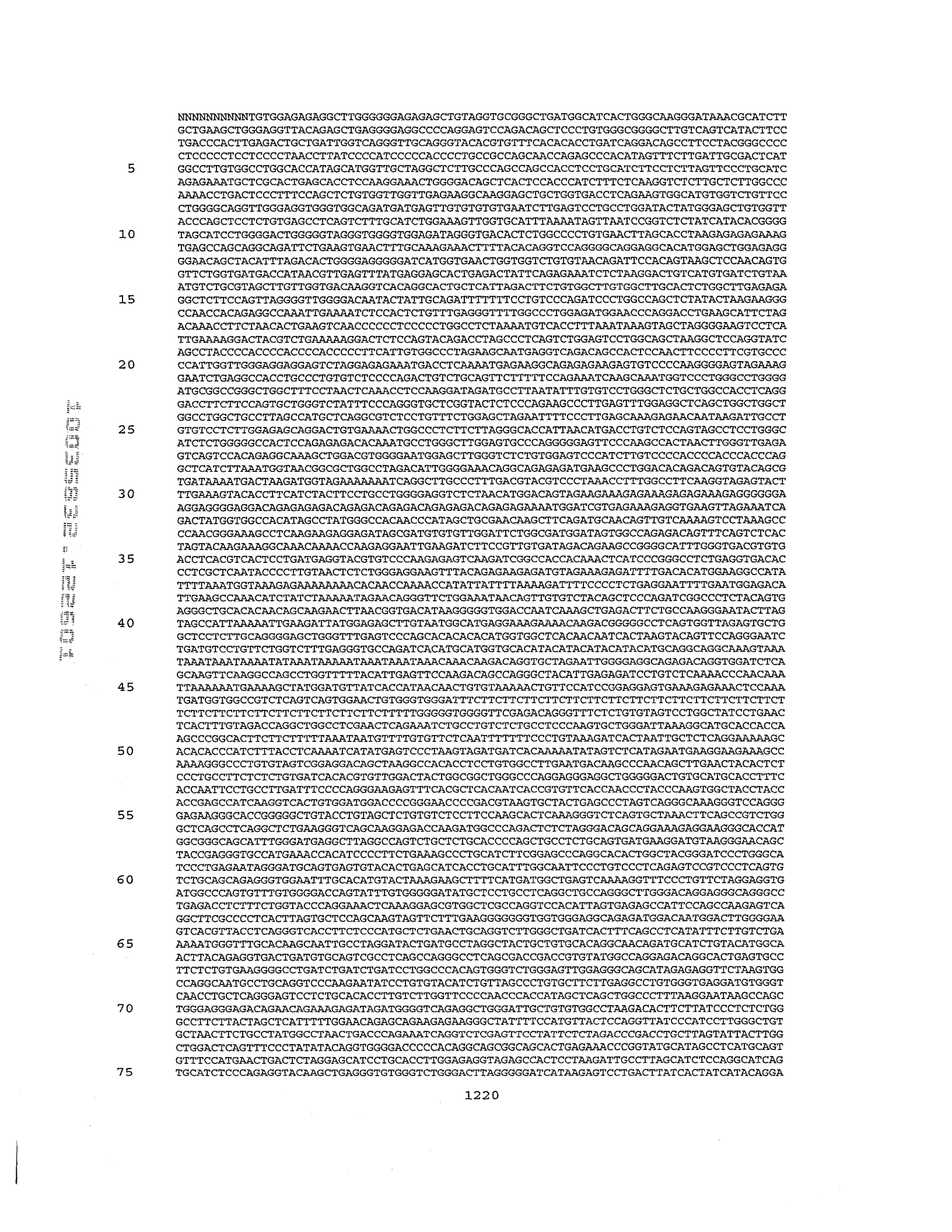
Table 57

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Celera mCG17461

HUMAN NOMENCLATURE
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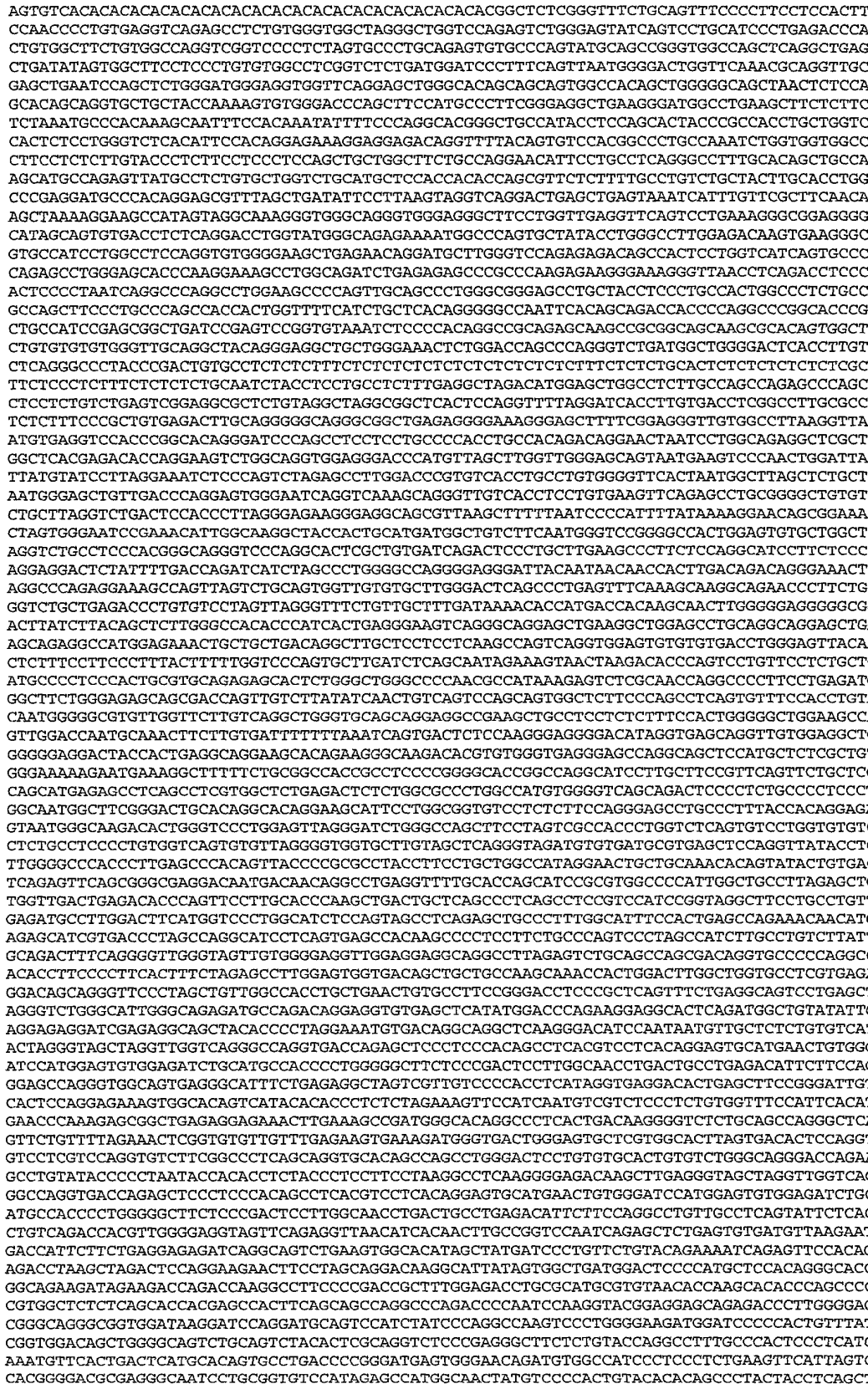
MOUSE SEQUENCE - GENOMIC





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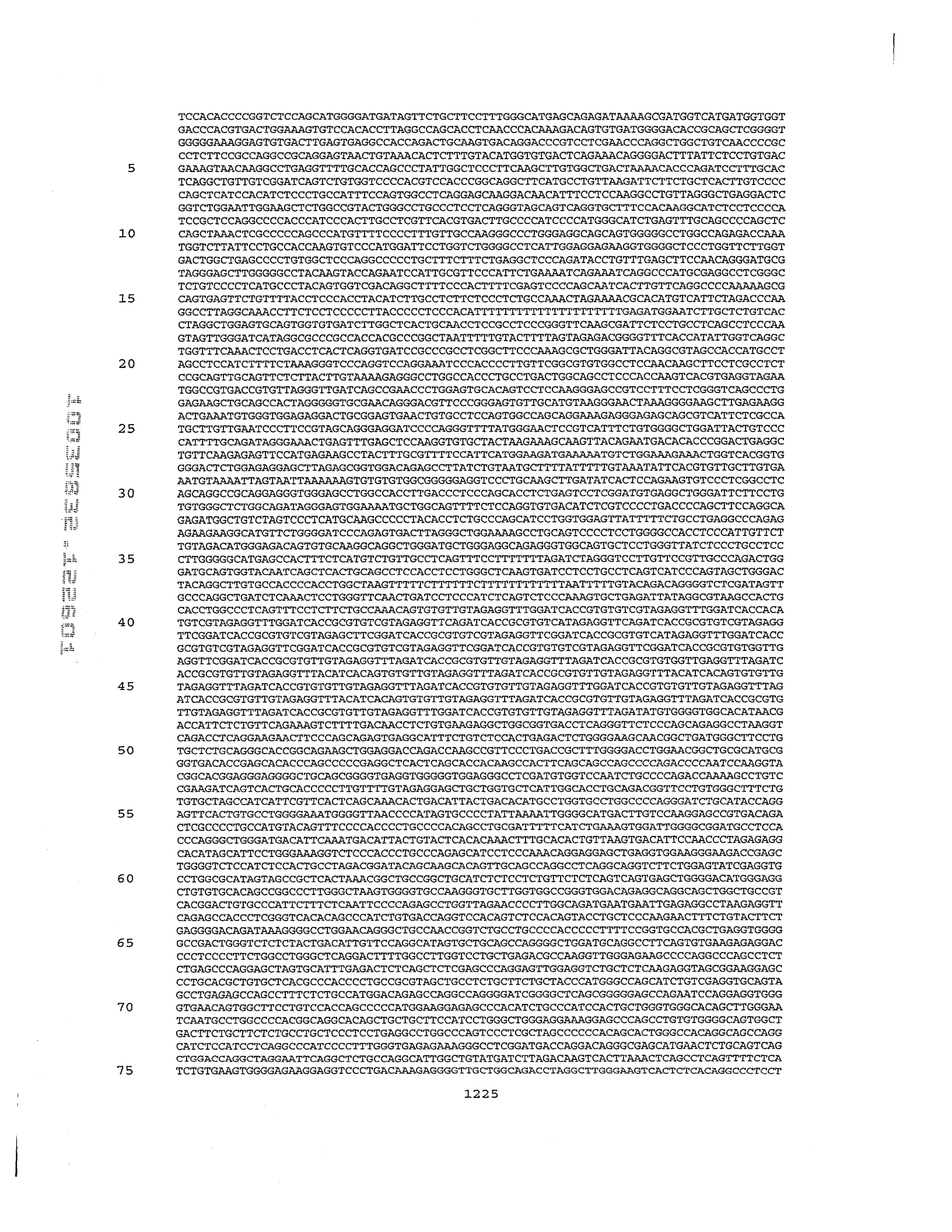
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MOUSE SEQUENCE - mRNA
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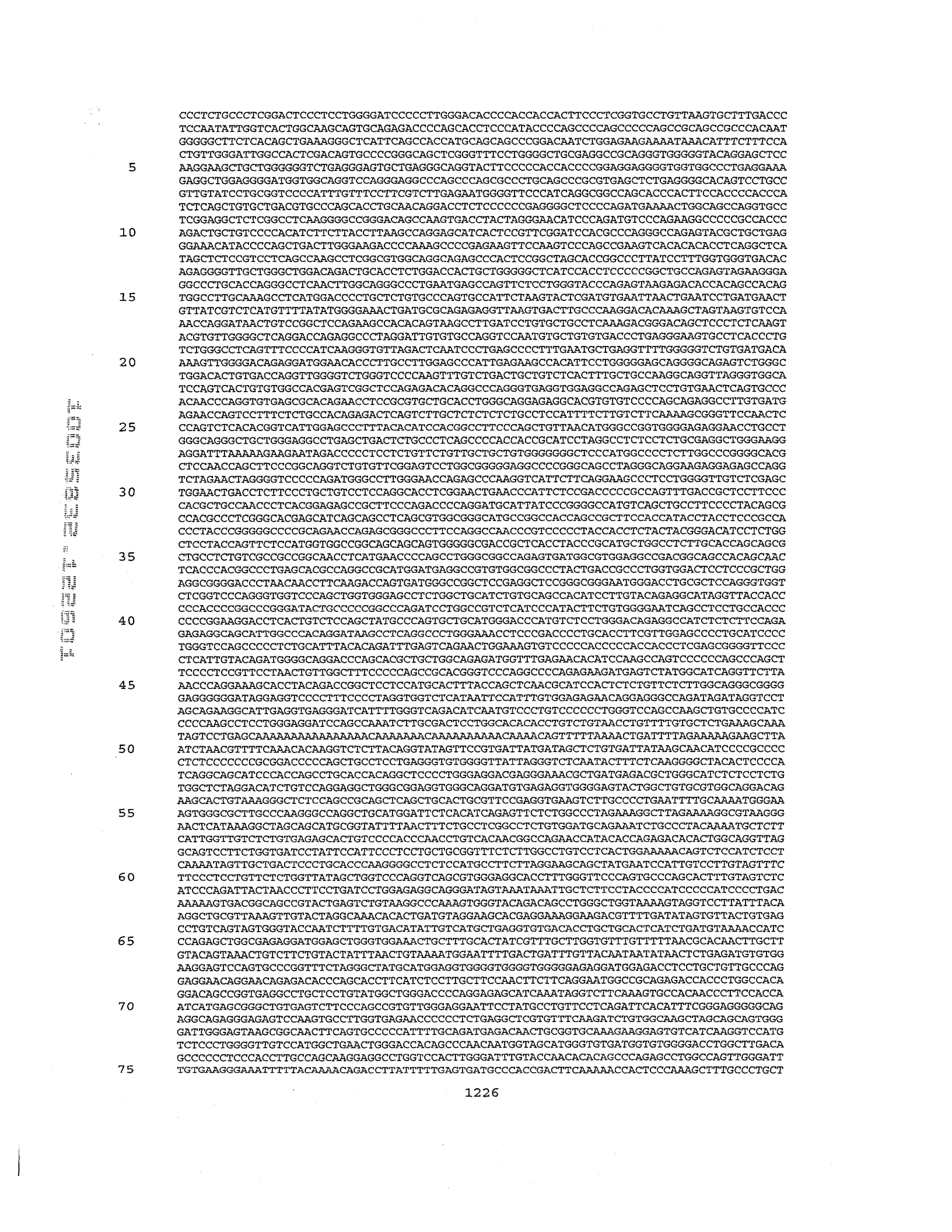
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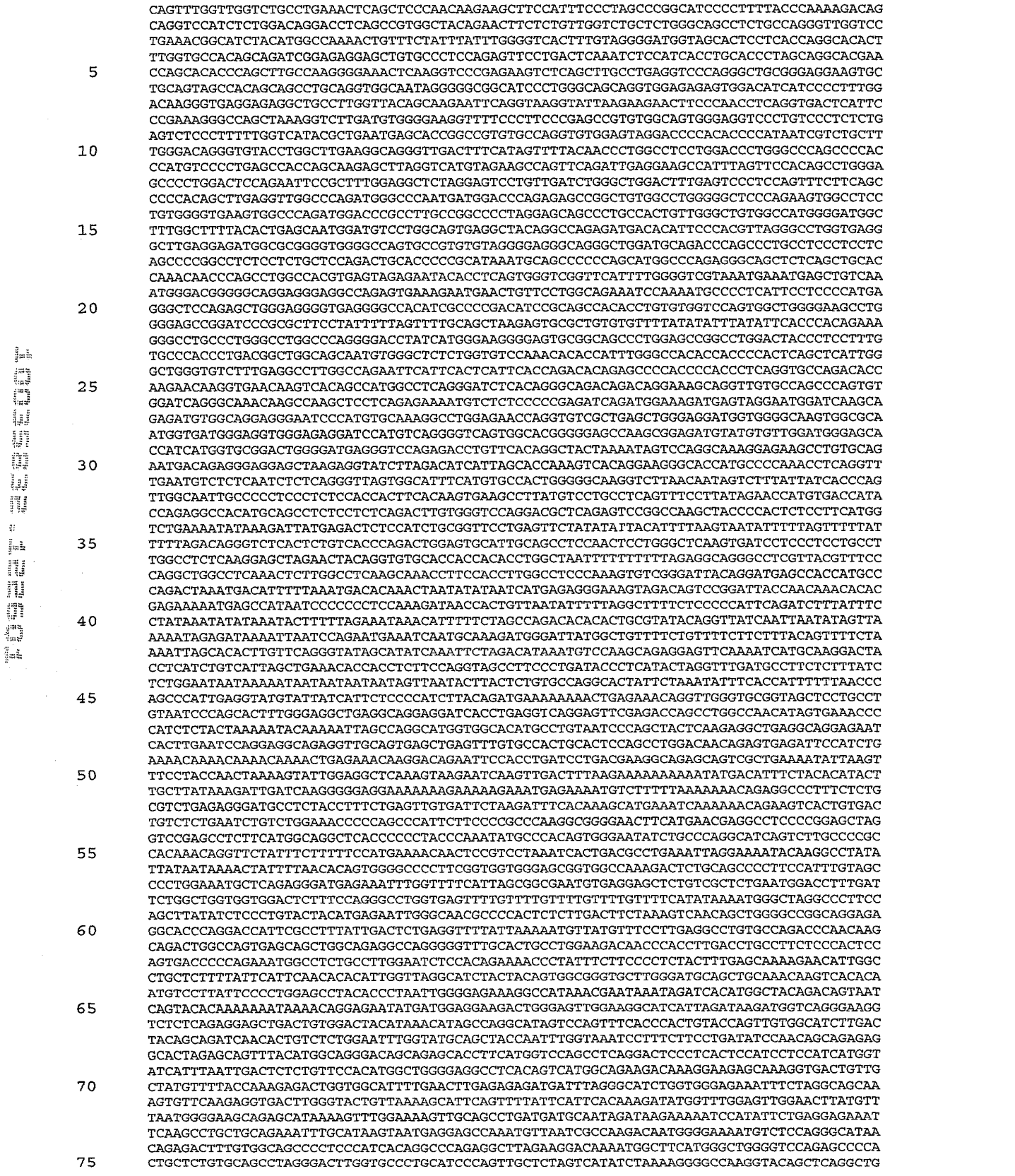
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 58

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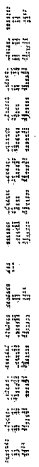
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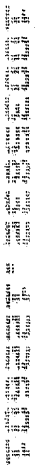
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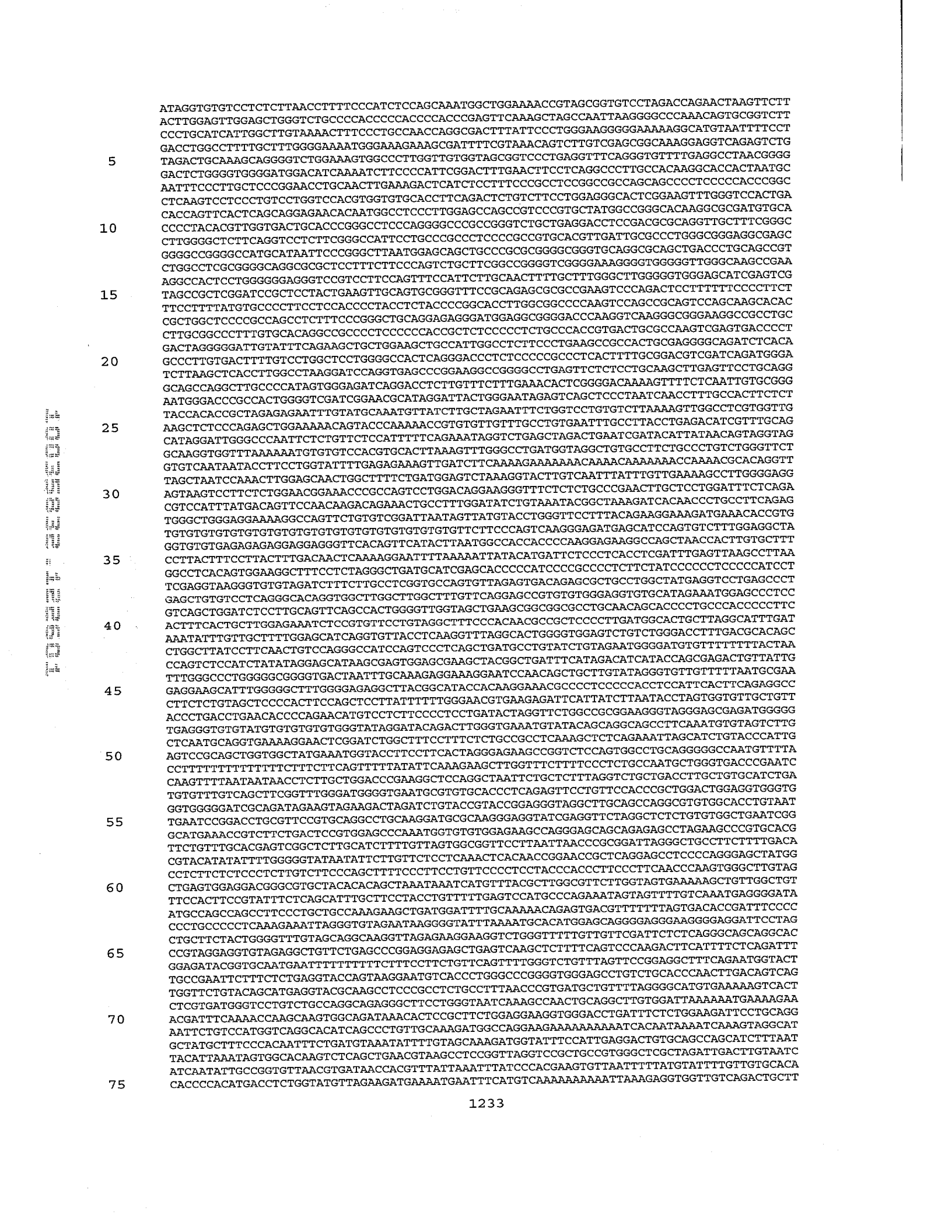
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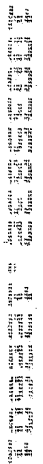
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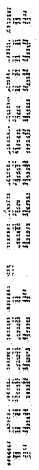


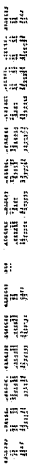
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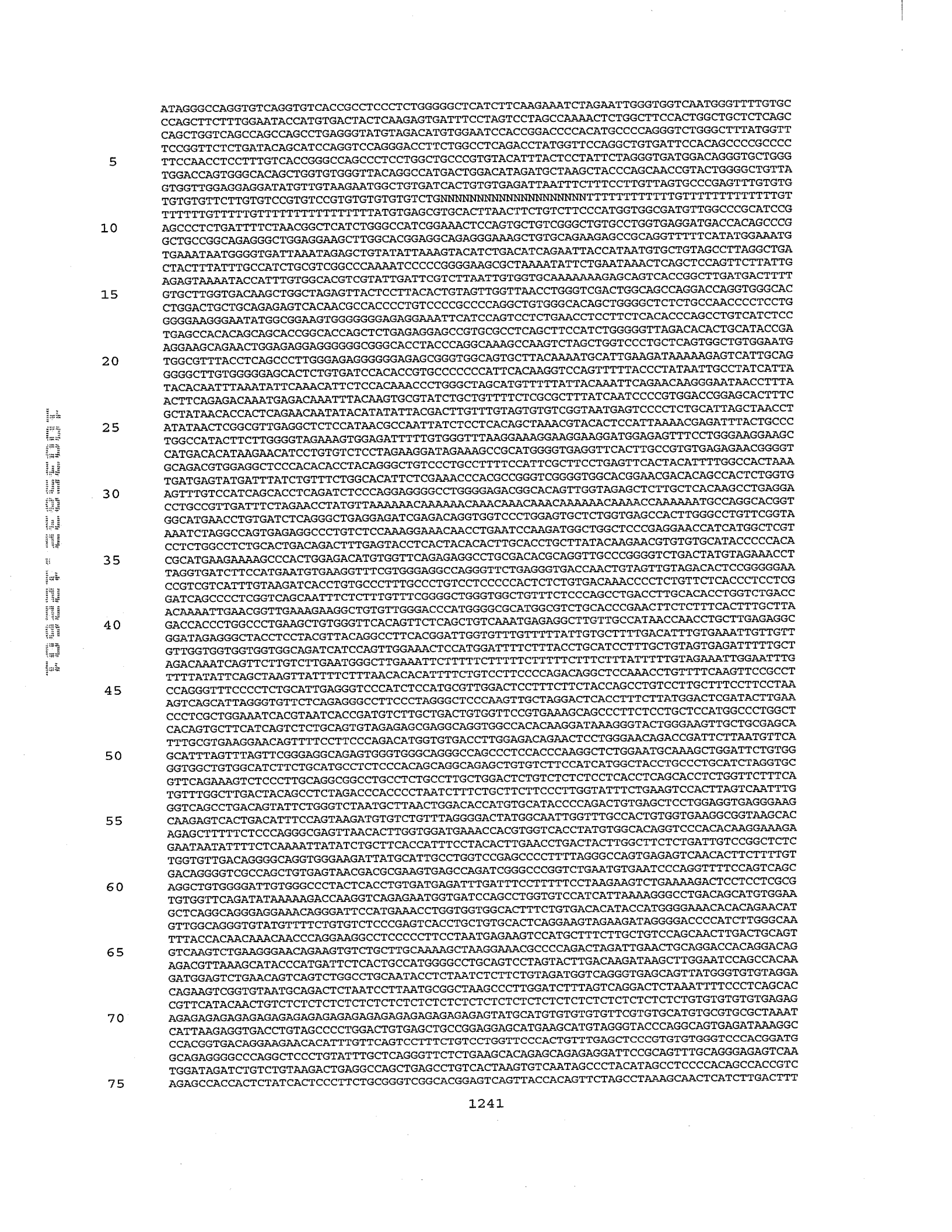




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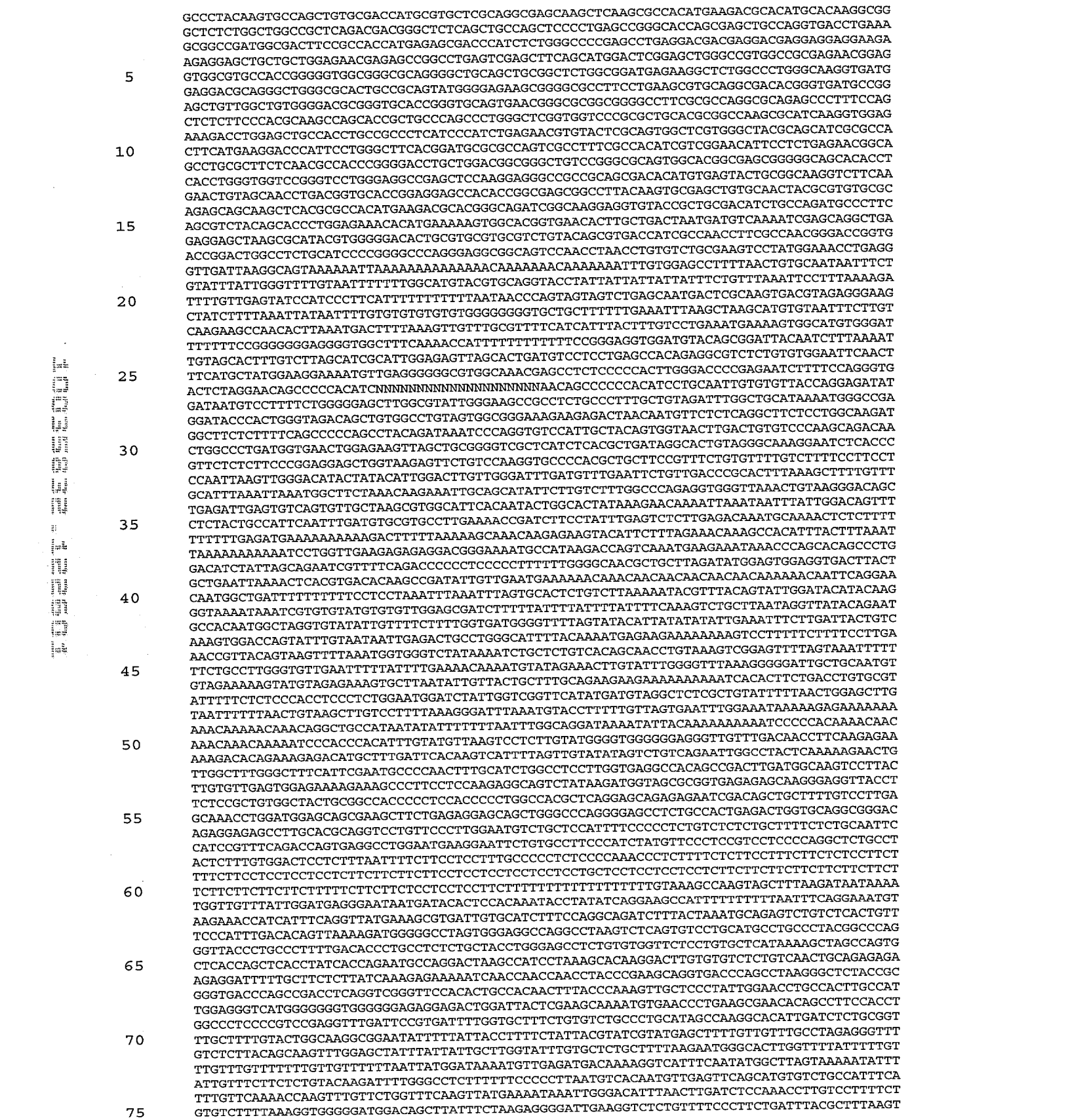
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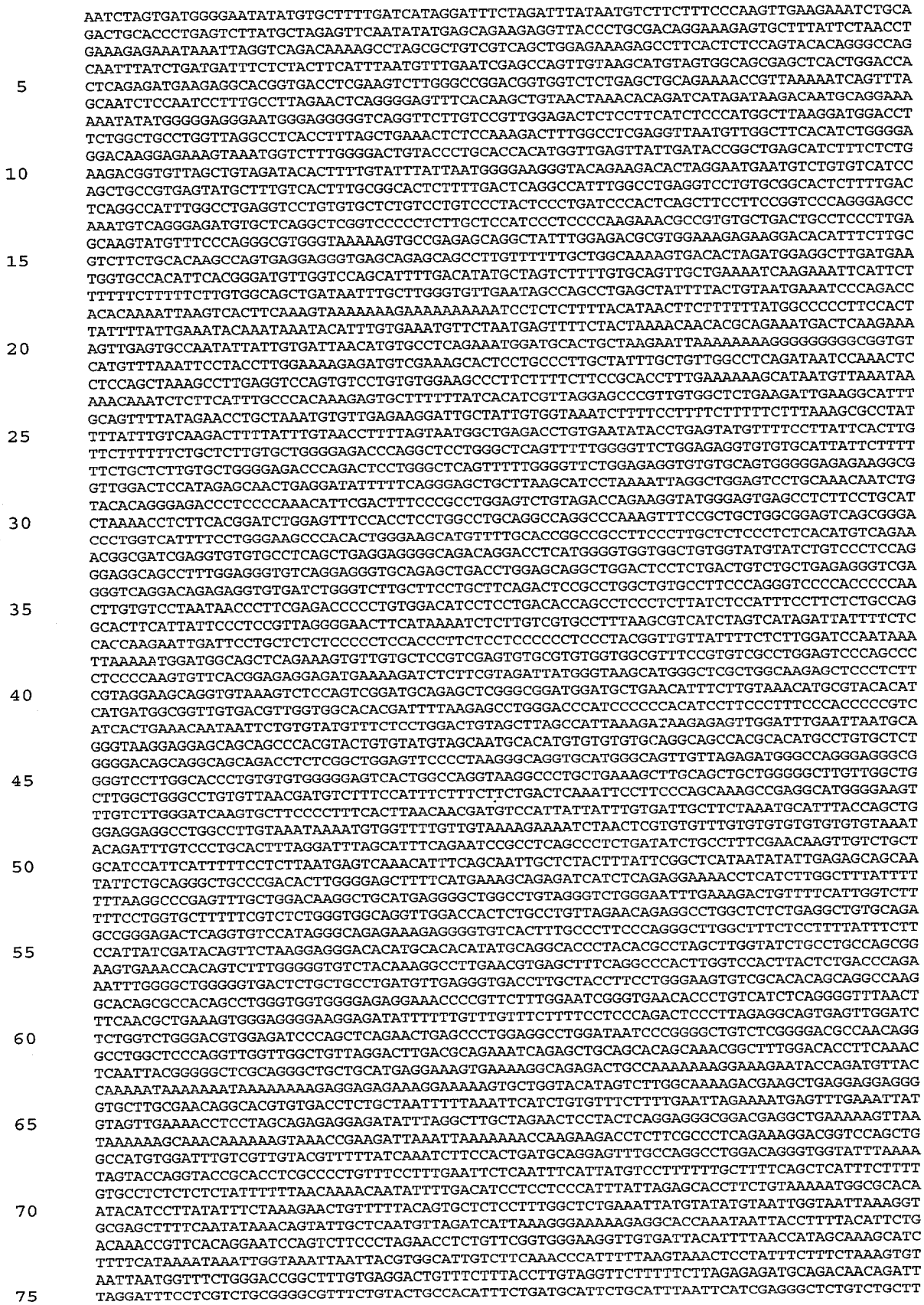
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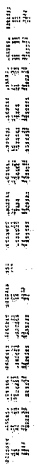
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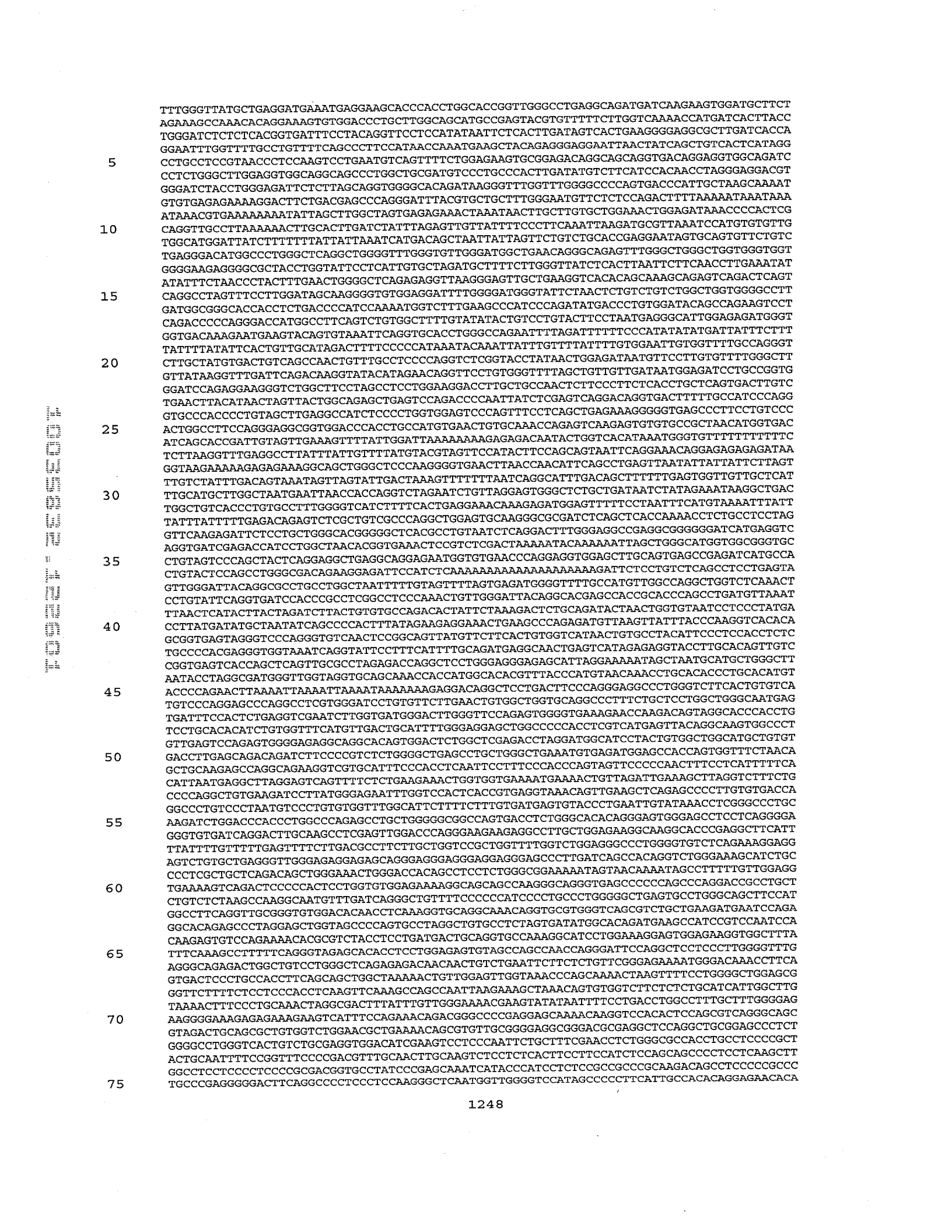
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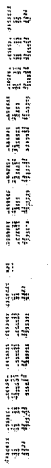




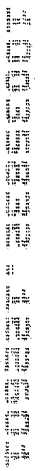
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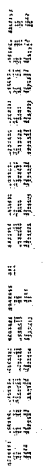
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HUMAN SEQUENCE - mRNA

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Date Recue/Date Received 2020-12-22

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HUMAN SEQUENCE - CODING
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Table 59

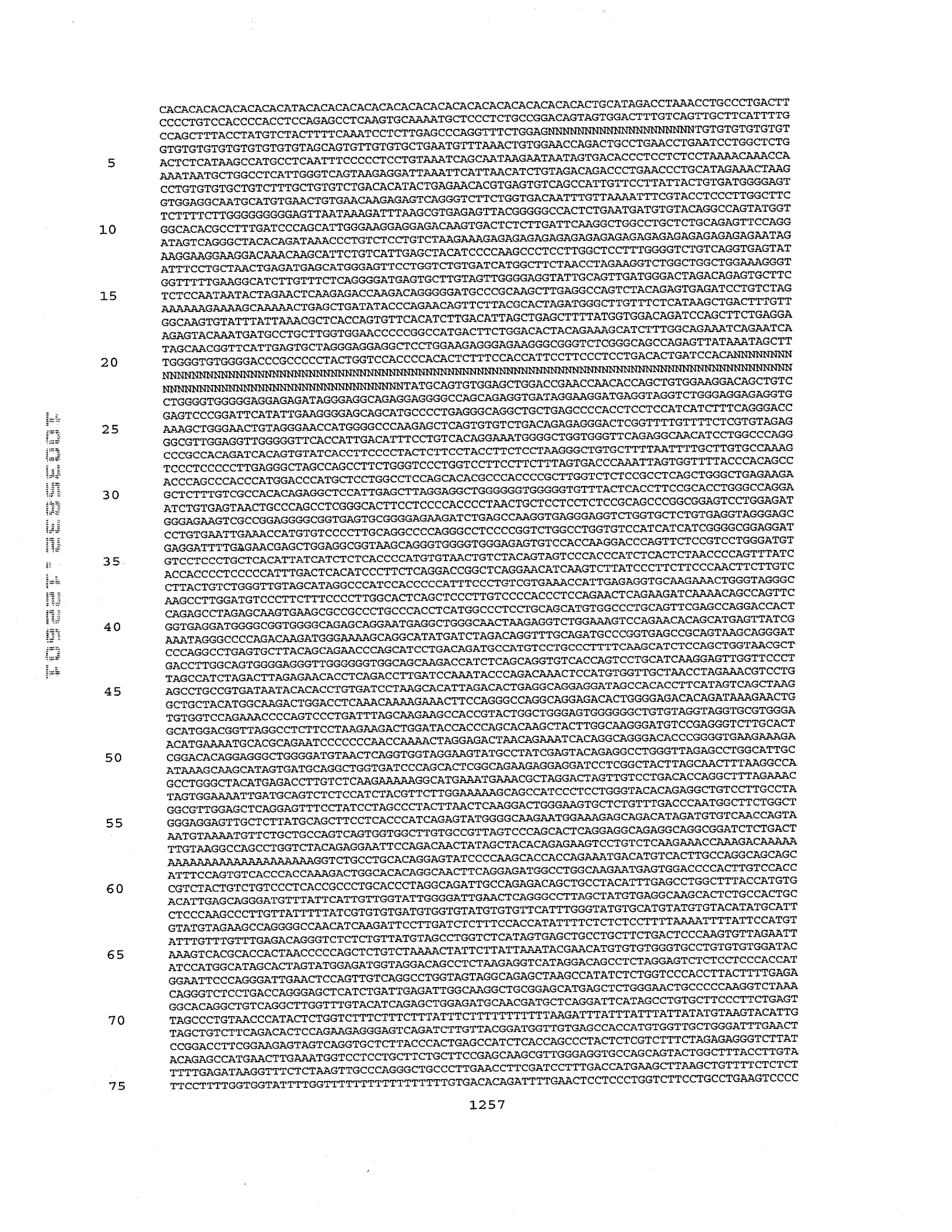
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MOUSE SEQUENCE - GENOMIC
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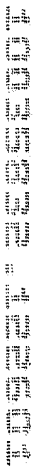


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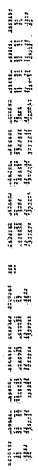
MOUSE SEQUENCE - mRNA

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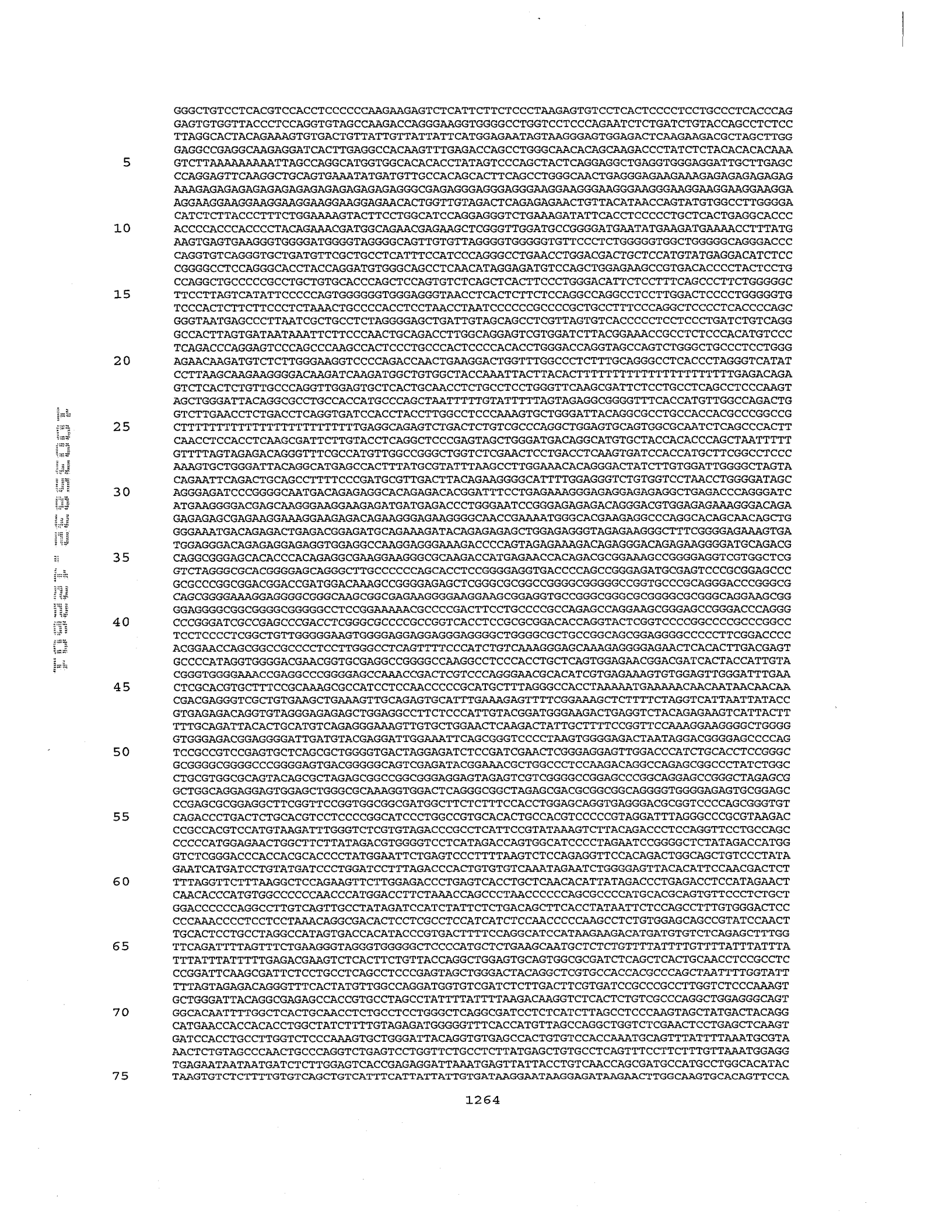
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MOUSE SEQUENCE - CODING
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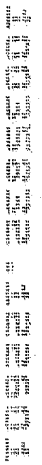
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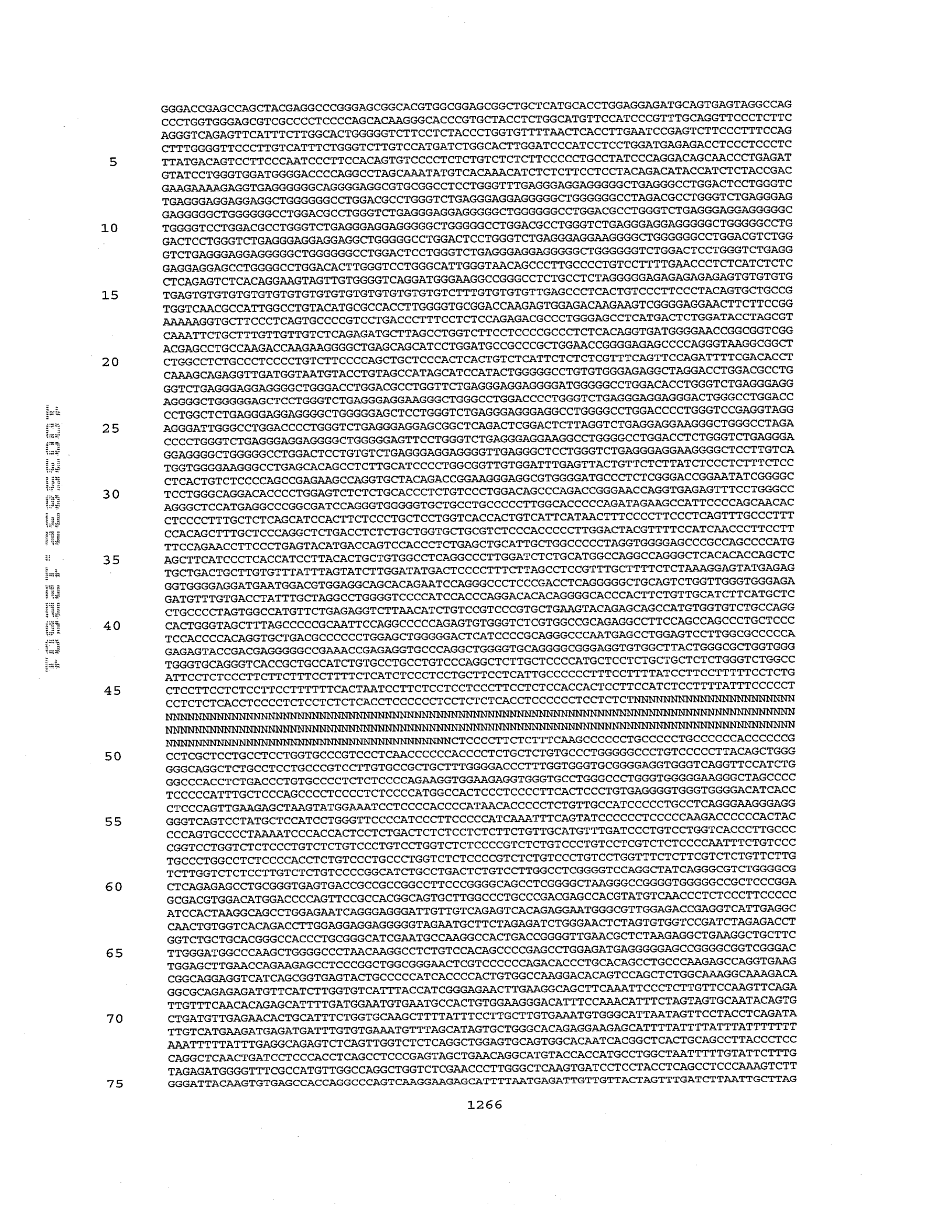
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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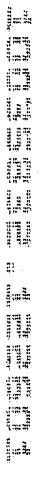
Table 60

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Celera mCG8923

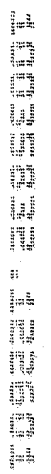
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MOUSE SEQUENCE - GENOMIC

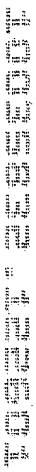
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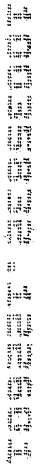
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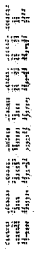
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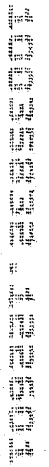
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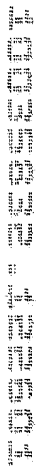
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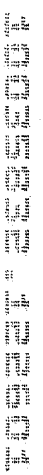
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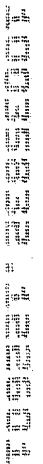
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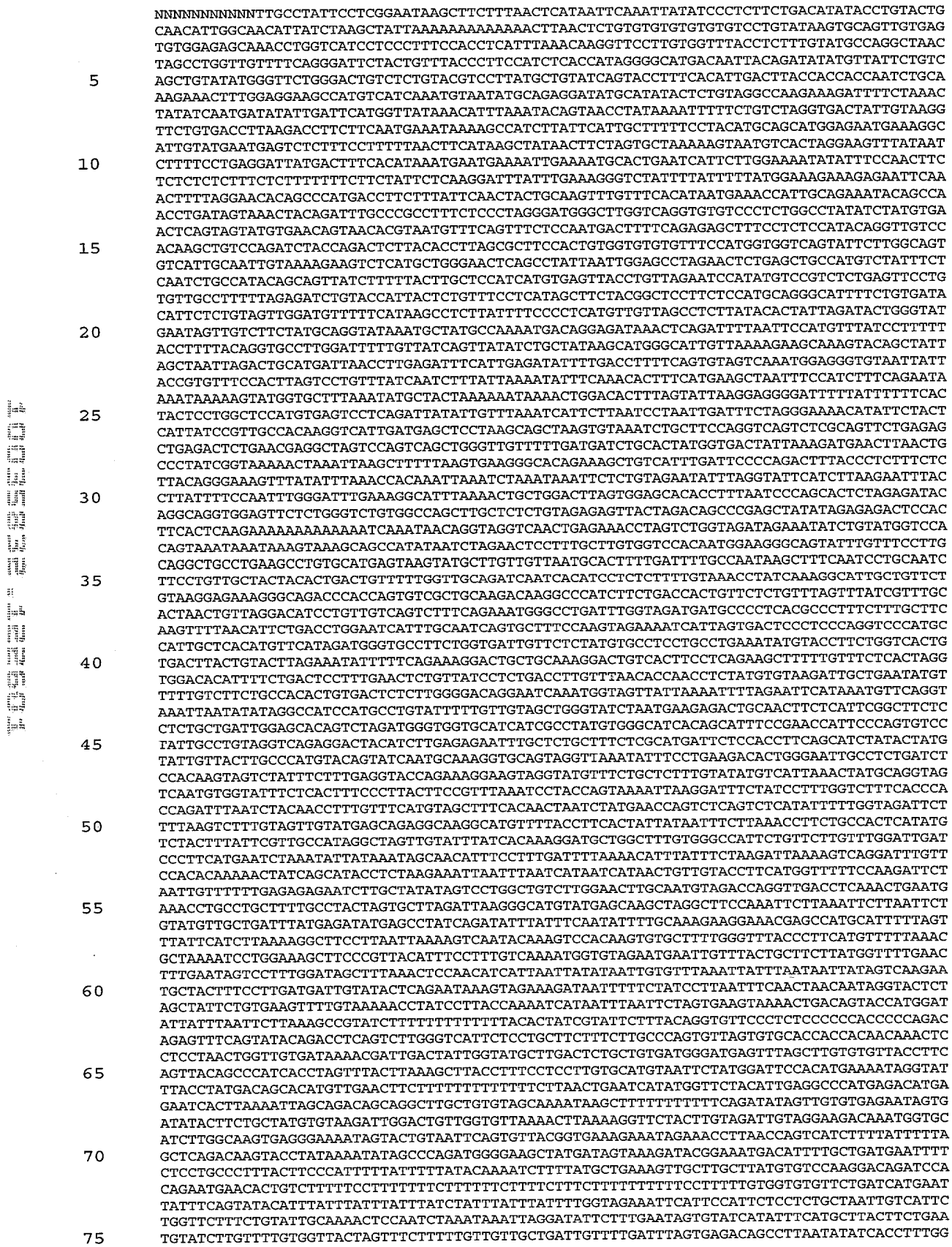
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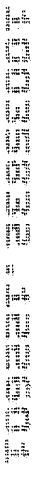


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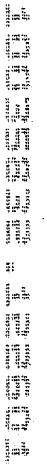


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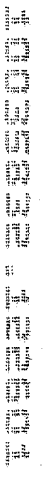




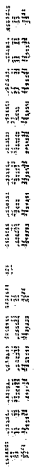
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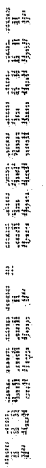
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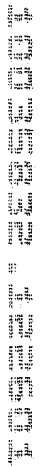
MOUSE SEQUENCE - CODING
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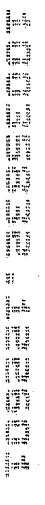


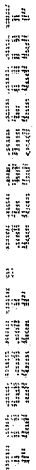
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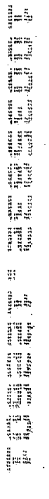
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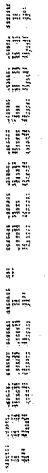




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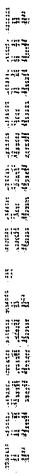
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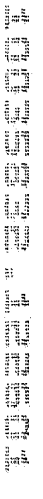
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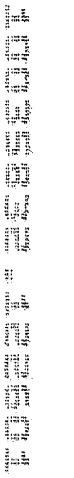
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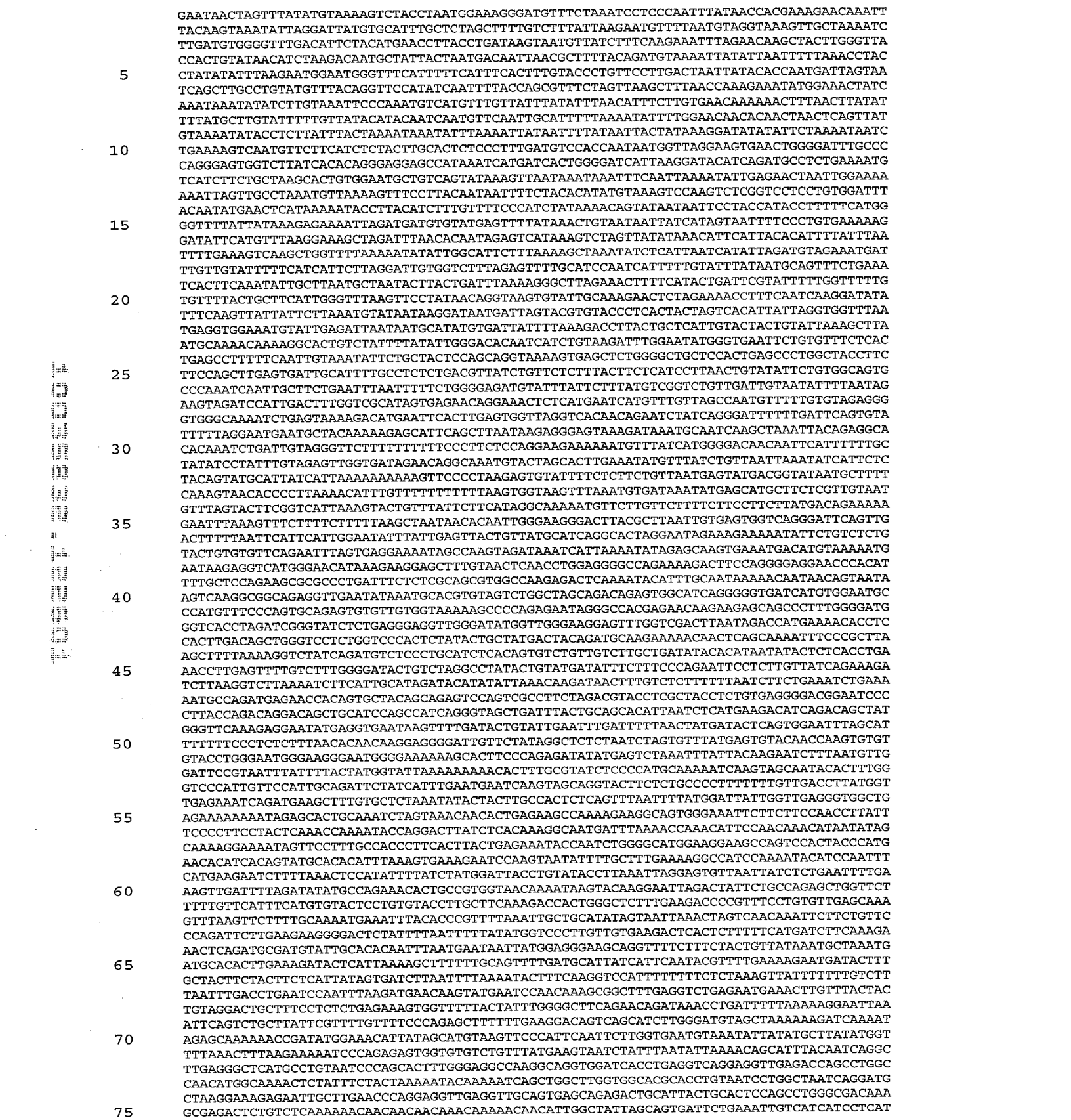
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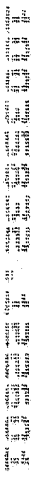
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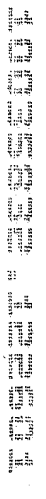
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1300



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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 61

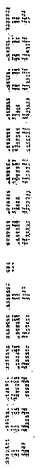
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ICSGNM Mcmd5
Celera mCG14998

HUMAN NOMENCLATURE
HGNC MCM5
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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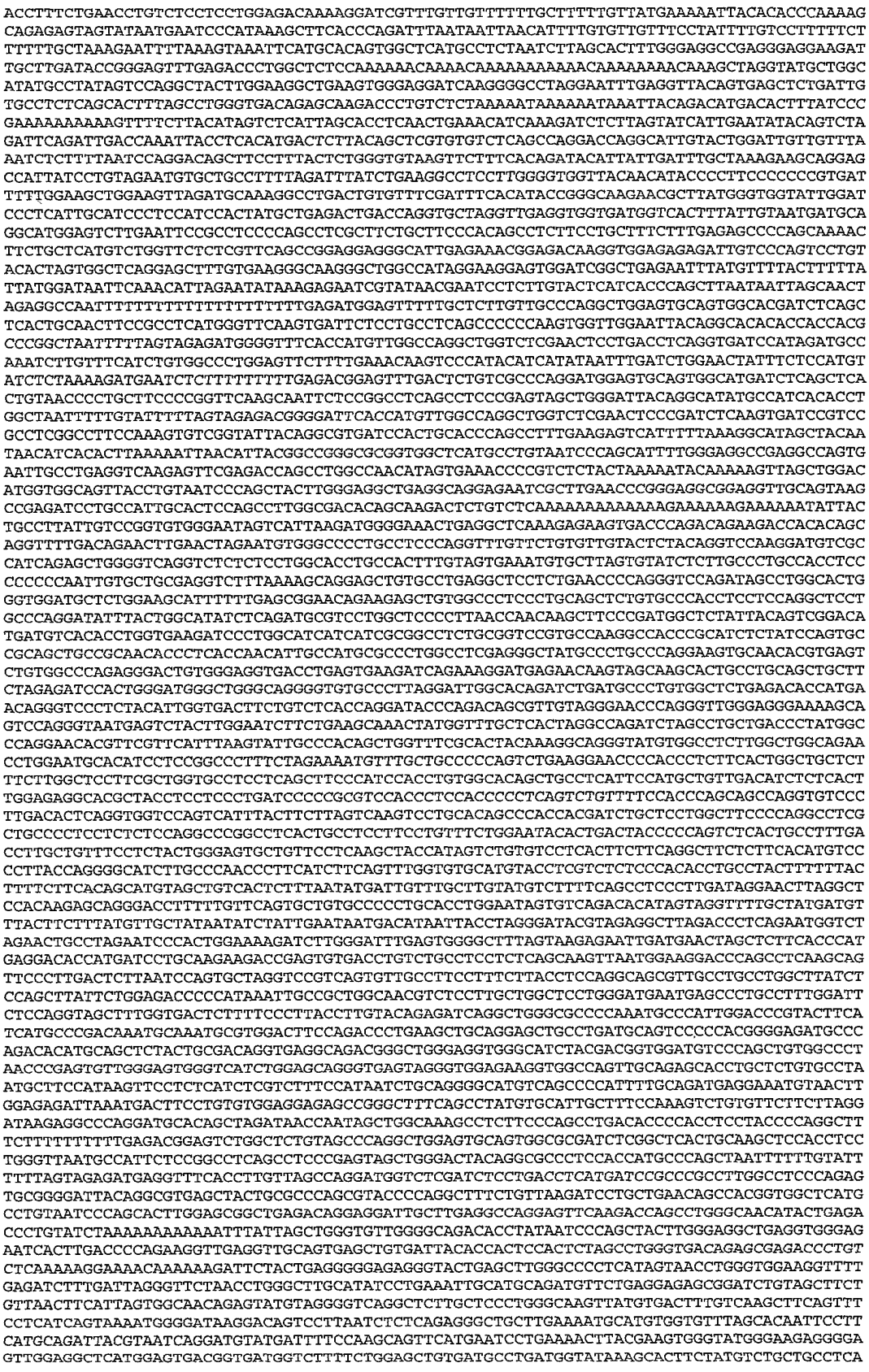
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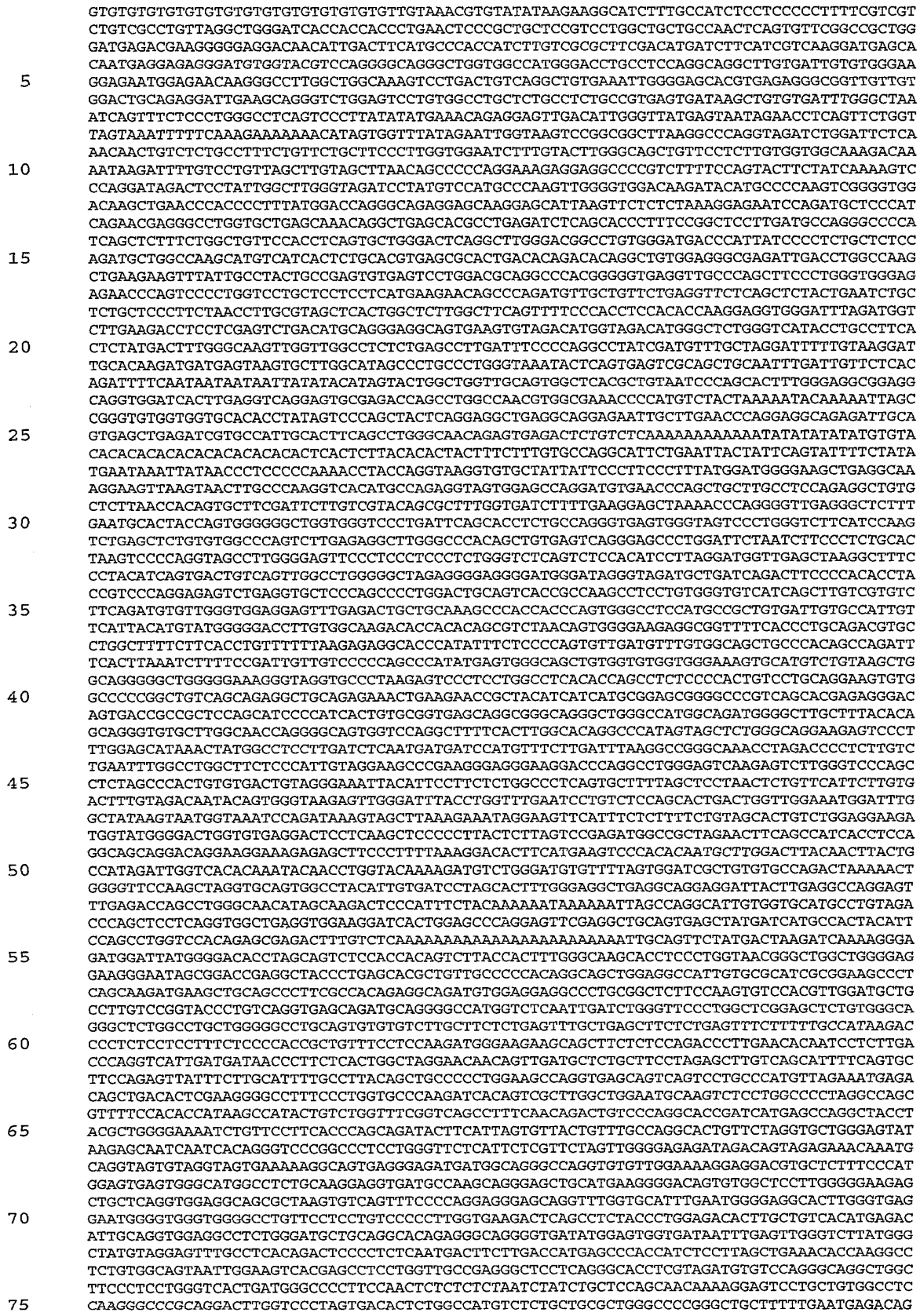
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Application/Control Number: 10/552,000
Art Unit: 1635

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CATCCATTTTGCTGTGTGGATGGTGGTAGAGTGCAGGCCTAATGCTGGAGCTGGCAGTTGTAATGGTGGCTTCTGAATTCCACAGC
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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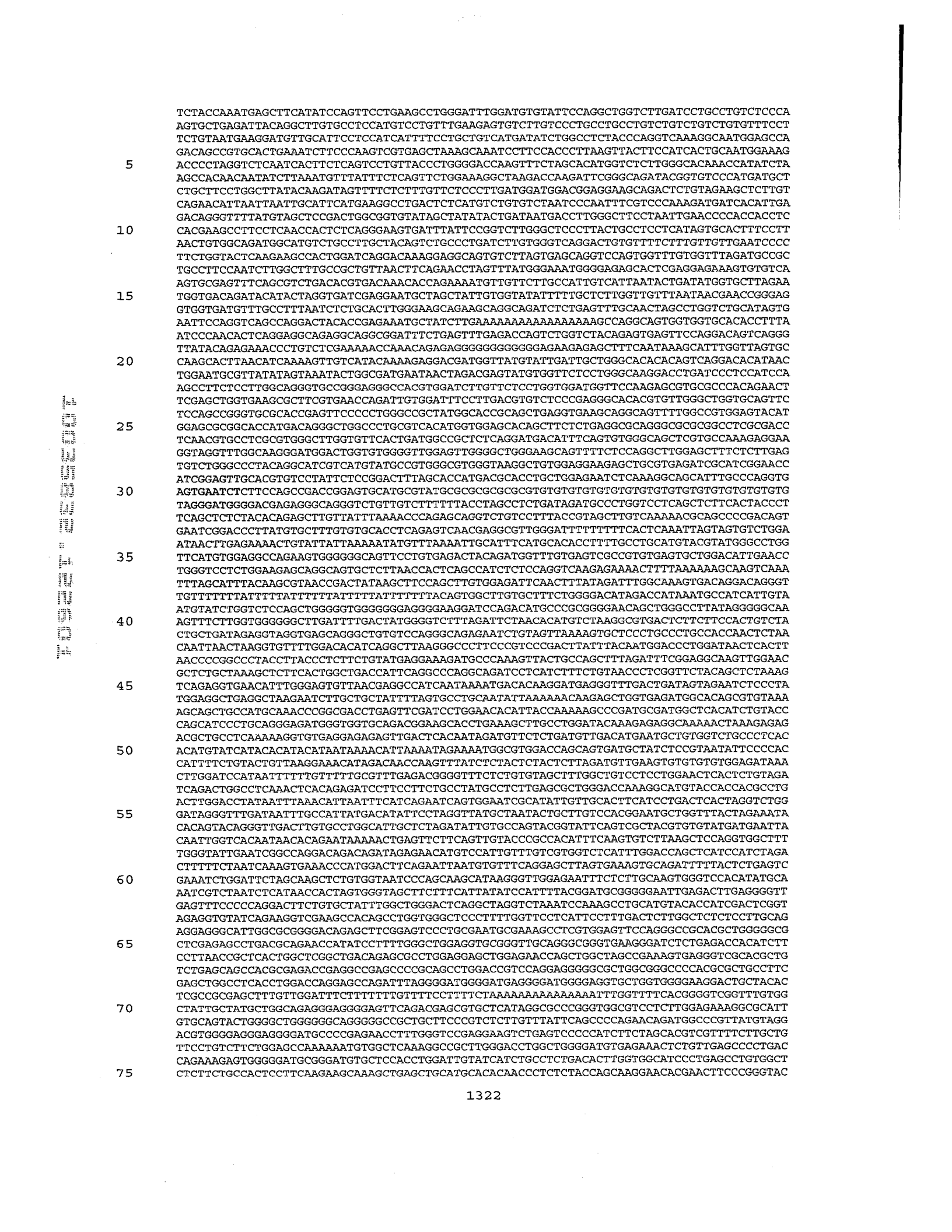
Table 62

MOUSE NOMENCLATURE
ICSGNM Matn4
Celera mCG5439

HUMAN NOMENCLATURE
HGNC MATN4
Celera hCG38364

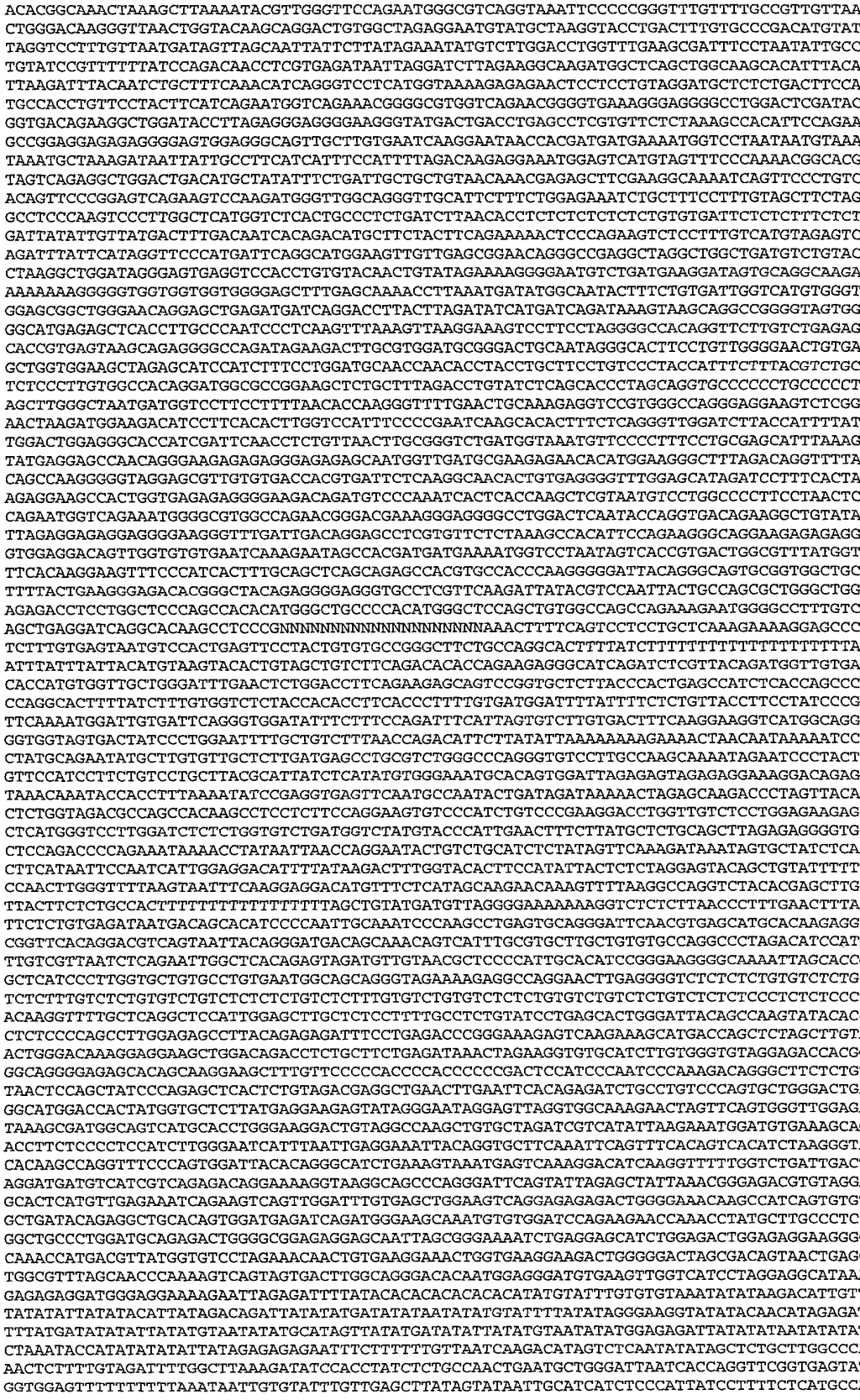
MOUSE SEQUENCE - GENOMIC
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MOUSE SEQUENCE - mRNA

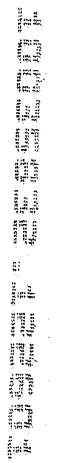
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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC
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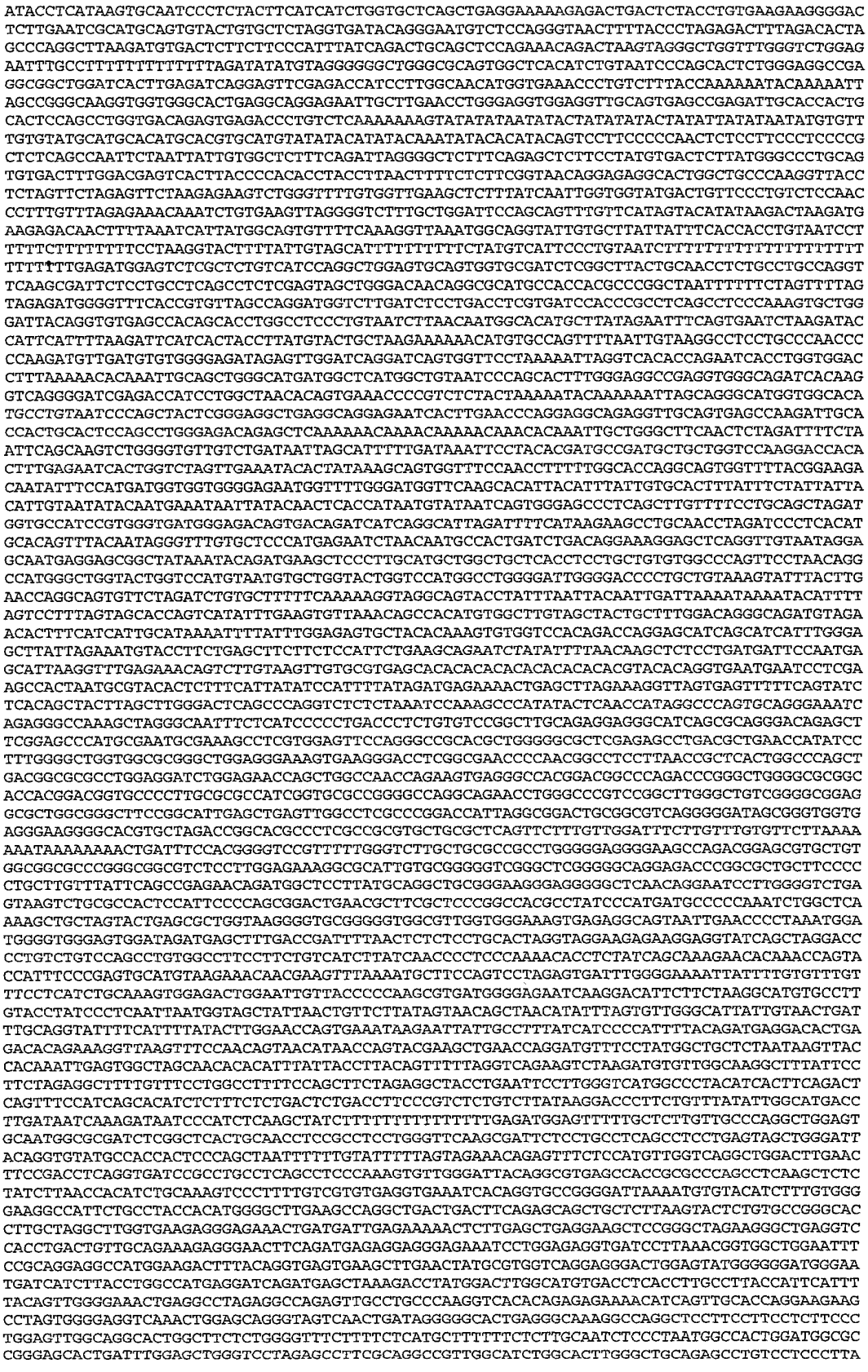


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HUMAN SEQUENCE - mRNA
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GATTTCCACGGAAAAAAAAAAAAAAAA

HUMAN SEQUENCE - CODING
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Table 63

MOUSE NOMENCLATURE
ICSGNM Tnfsf11
Celera mCG1914

HUMAN NOMENCLATURE
HGNC TNFSF11
Celera hCG32838

MOUSE SEQUENCE - GENOMIC

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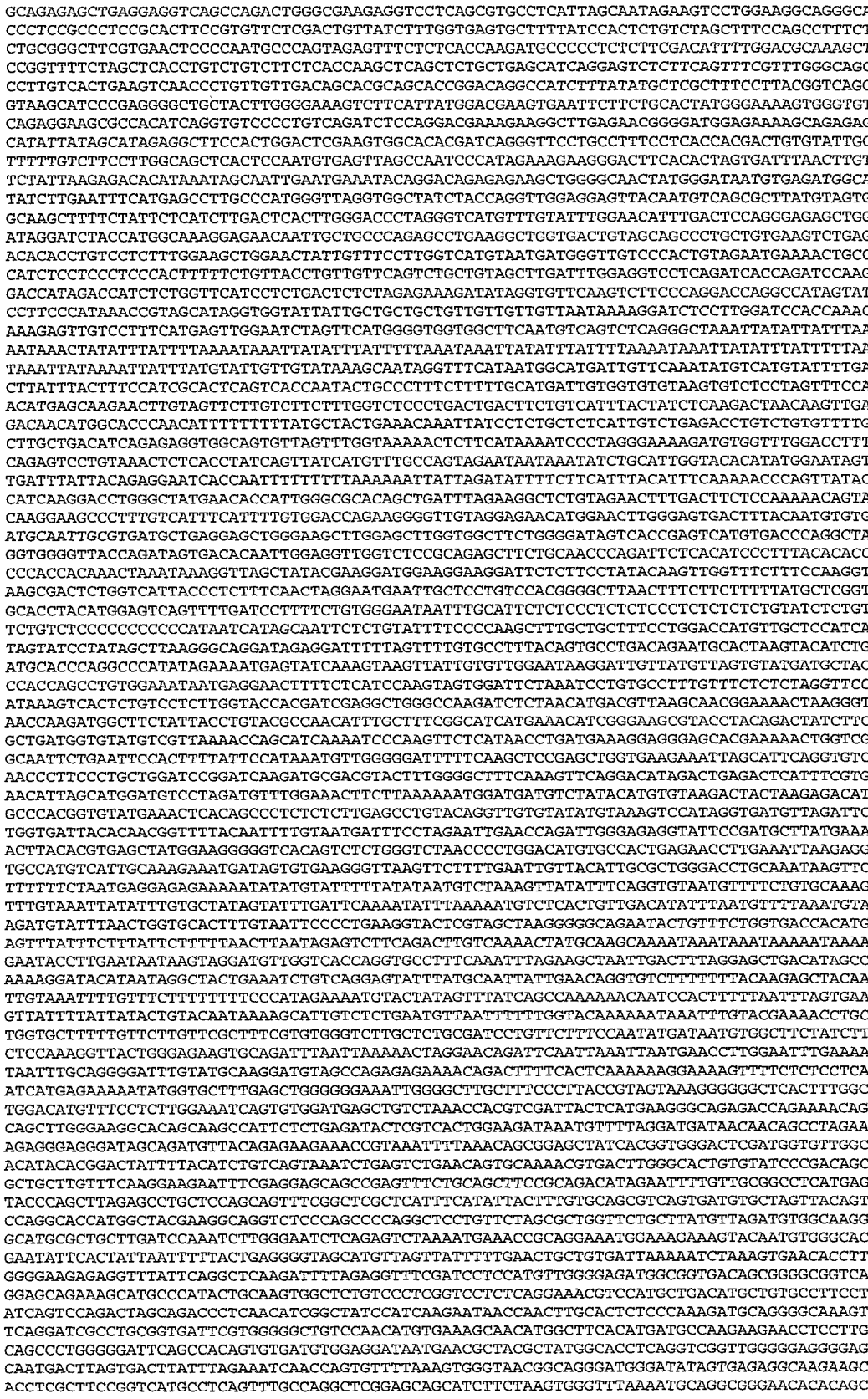
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Replacement Sheet



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MOUSE SEQUENCE - mRNA

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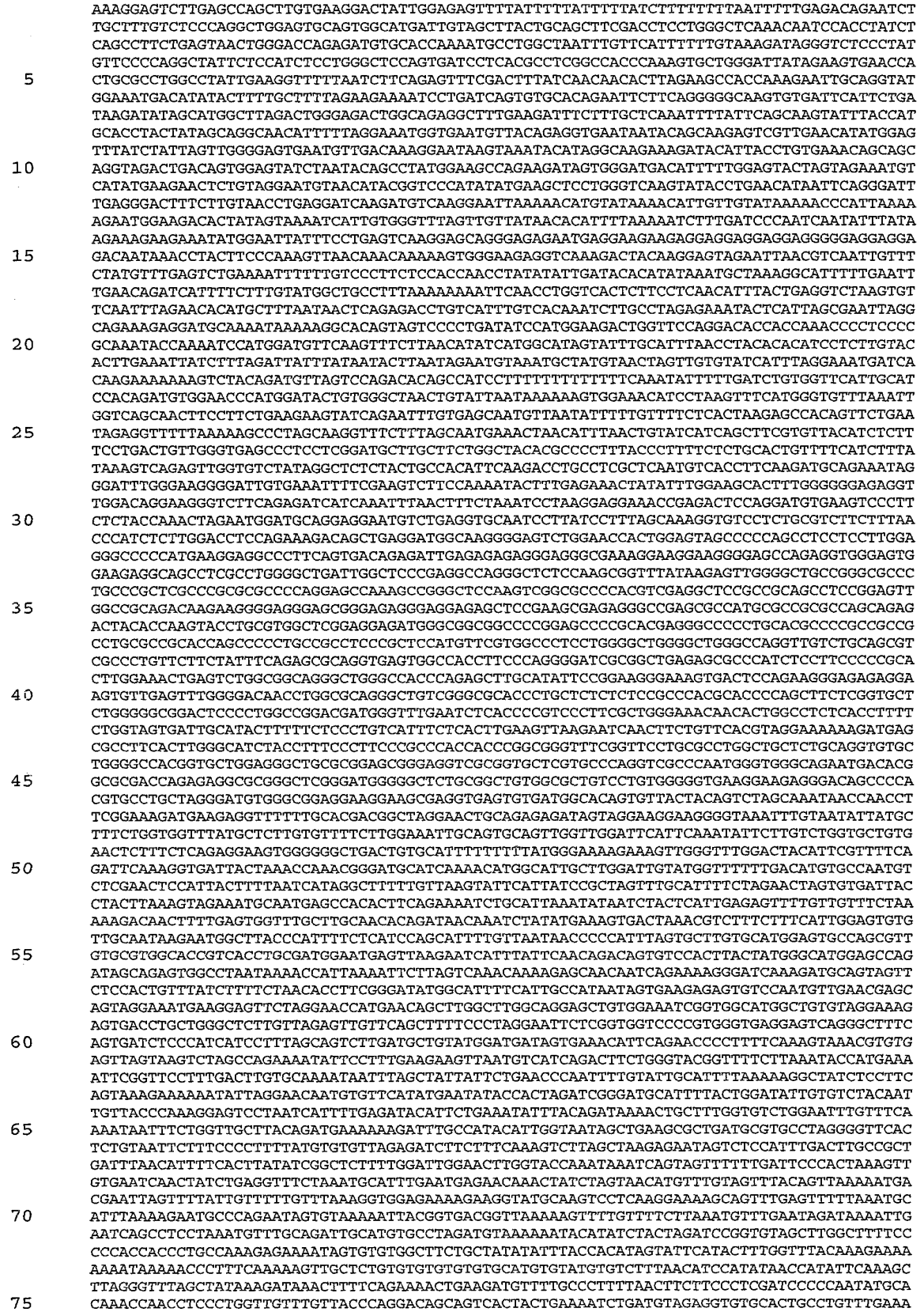
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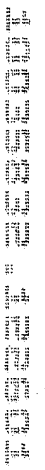
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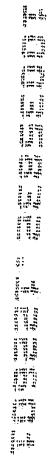
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Sequence Listing

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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 64

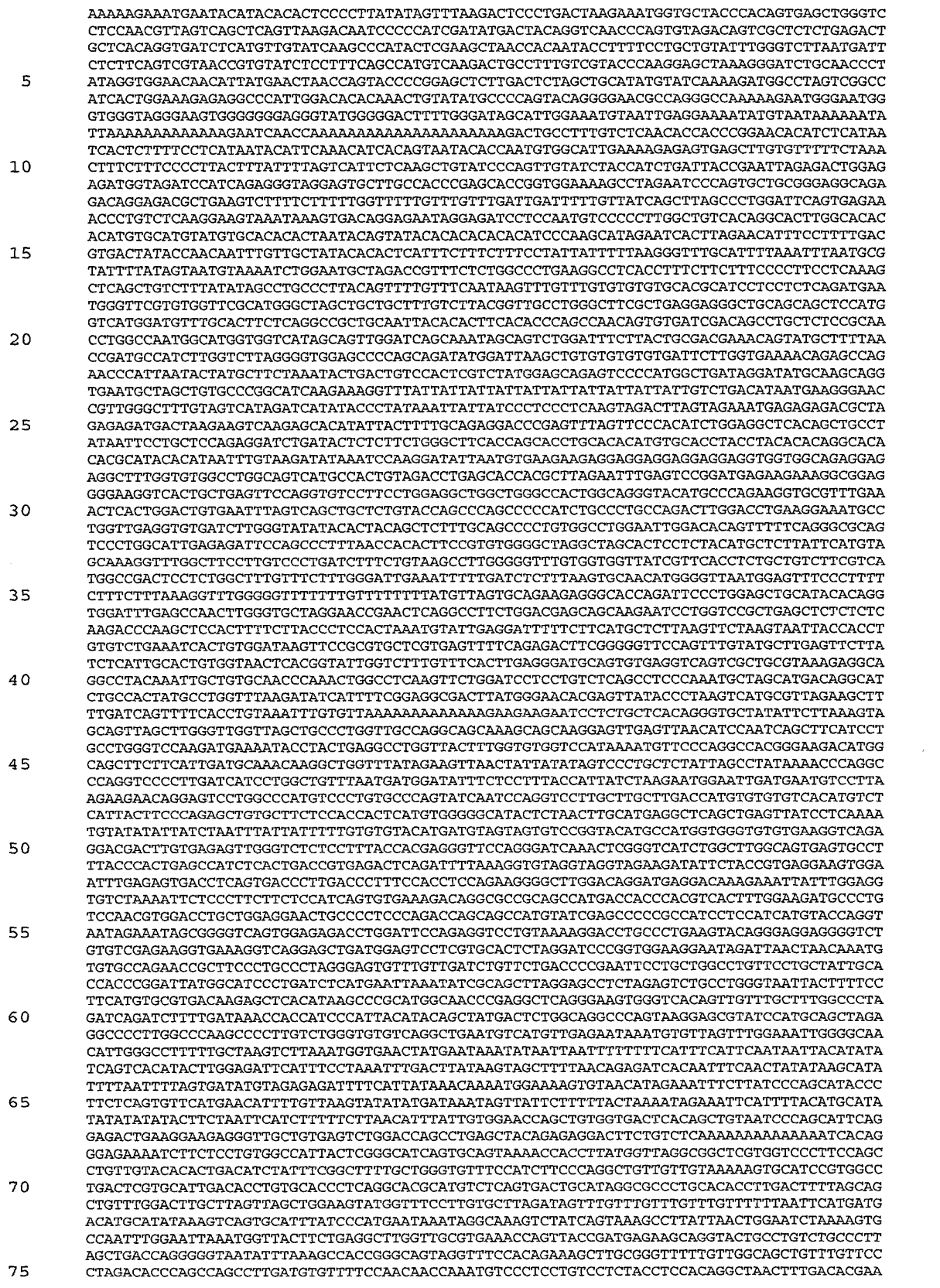
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HUMAN NOMENCLATURE
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MOUSE SEQUENCE - GENOMIC

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Replacement Sheet



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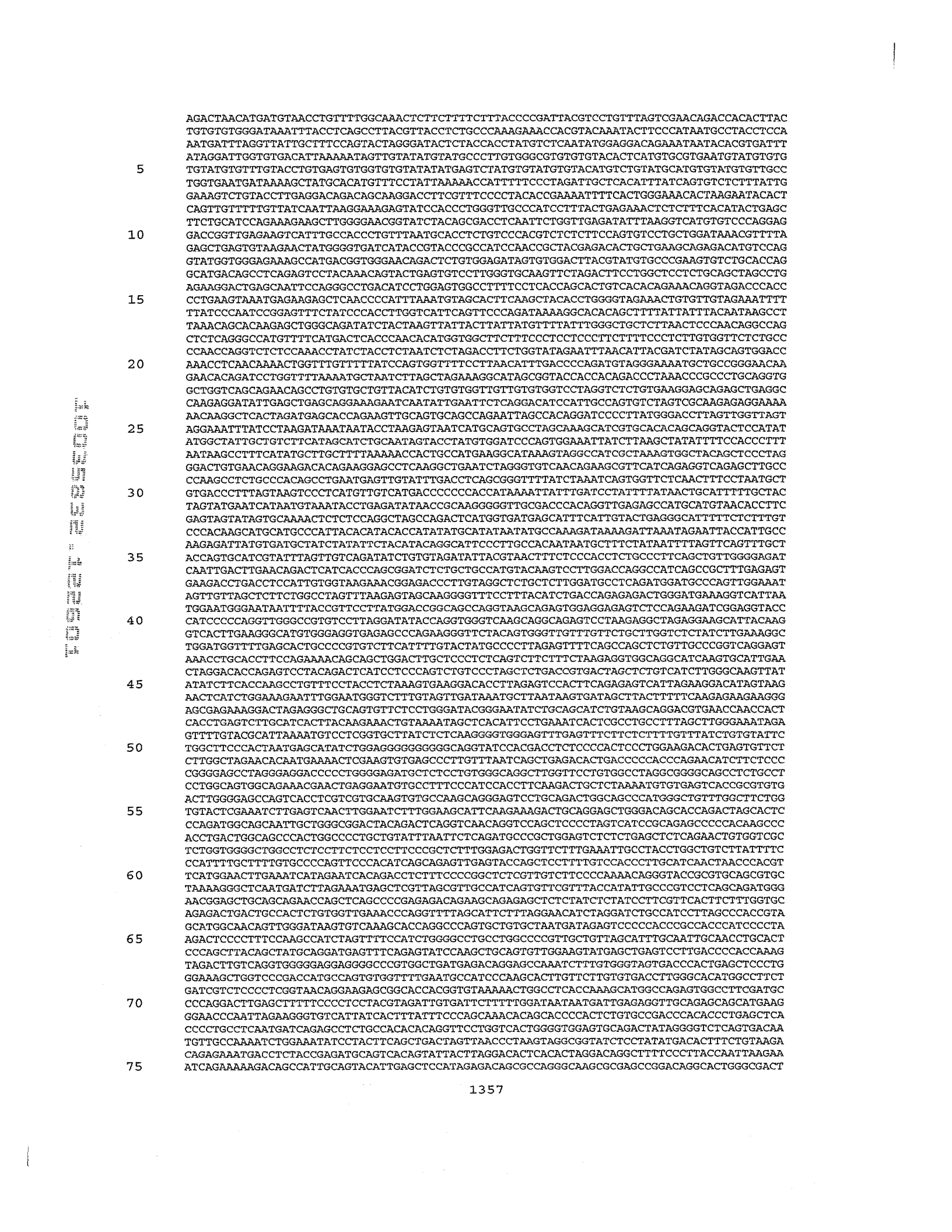
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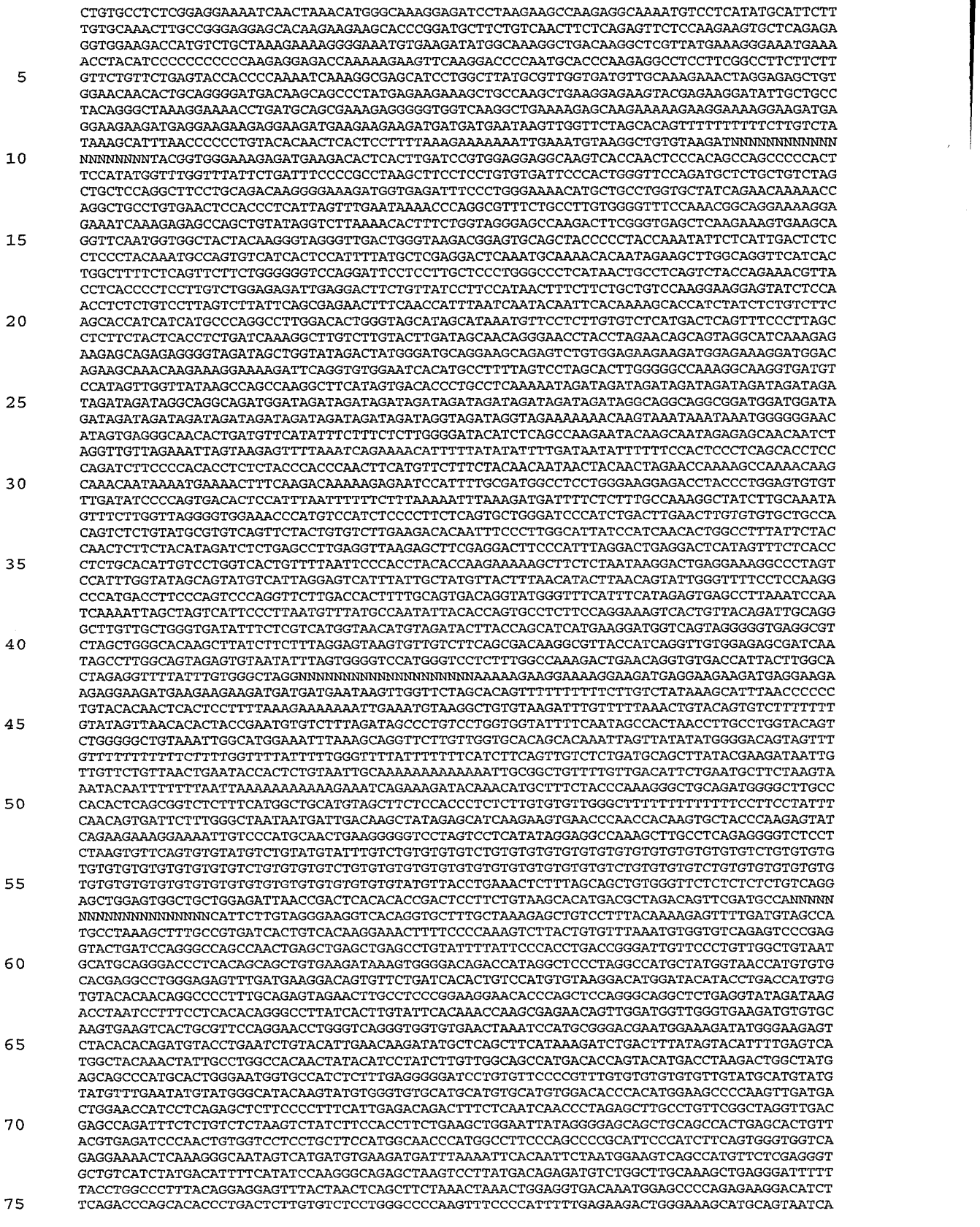
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Replacement Sheet - 30 Jan 2004



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MOUSE SEQUENCE - mRNA

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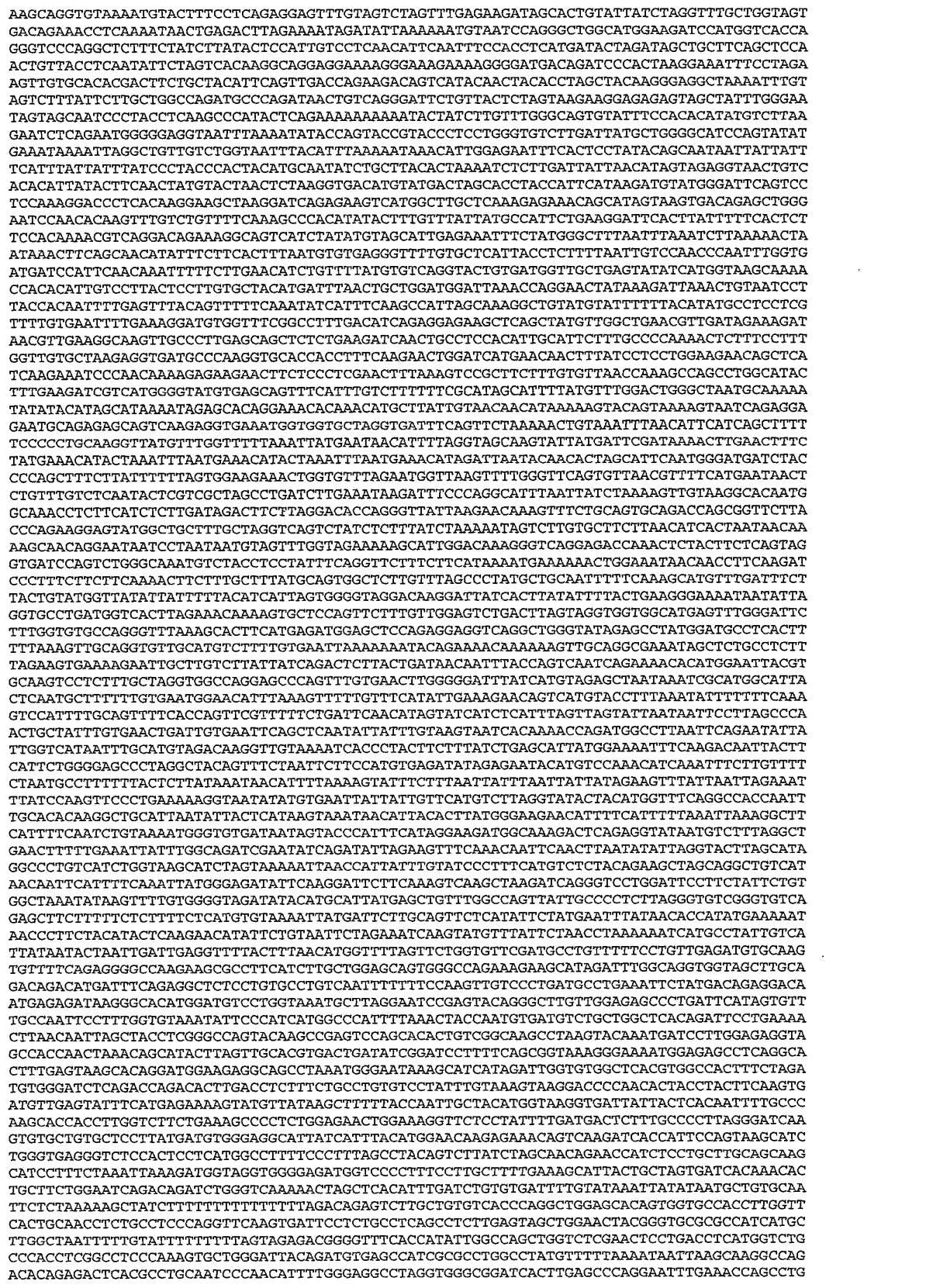
MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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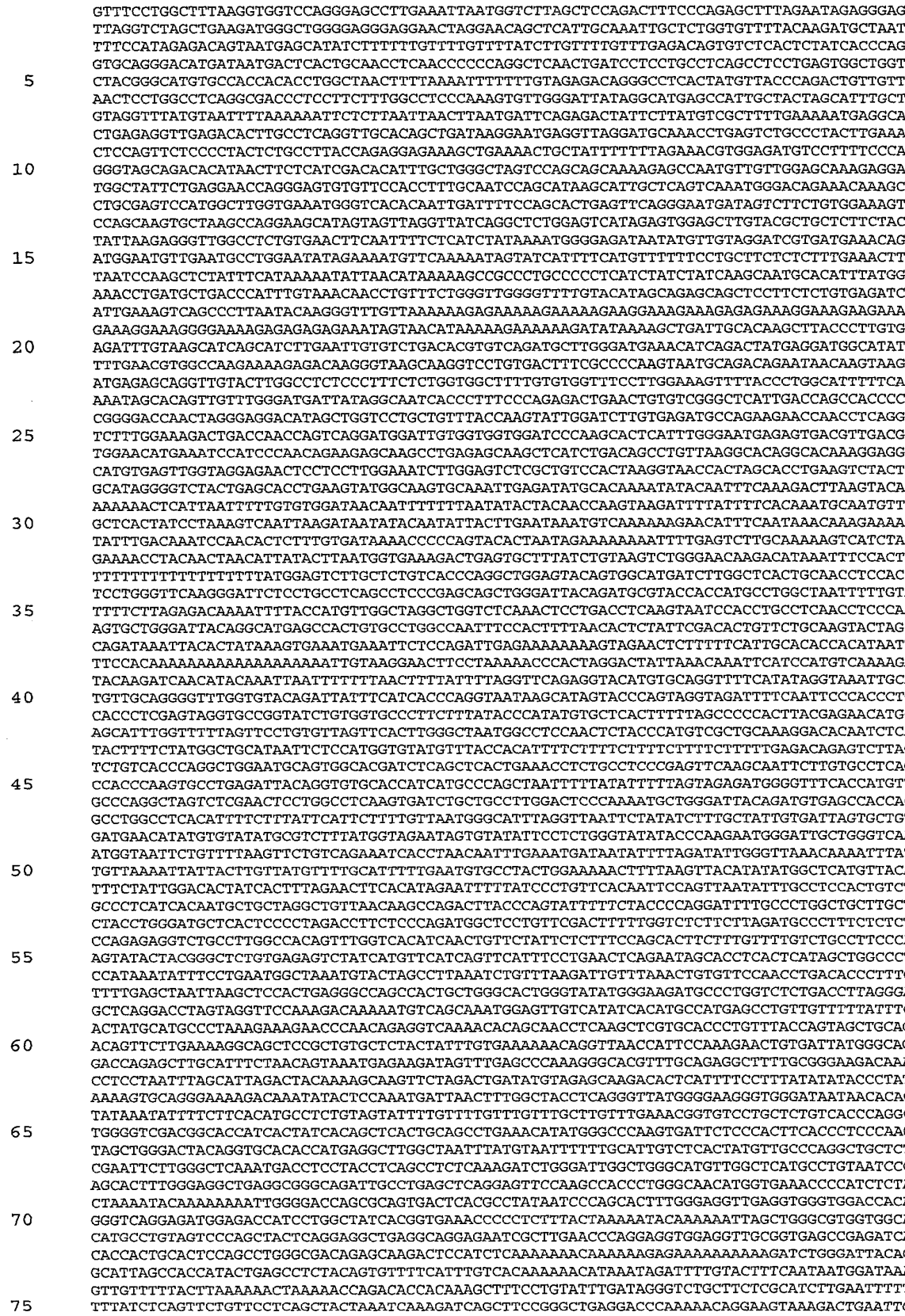


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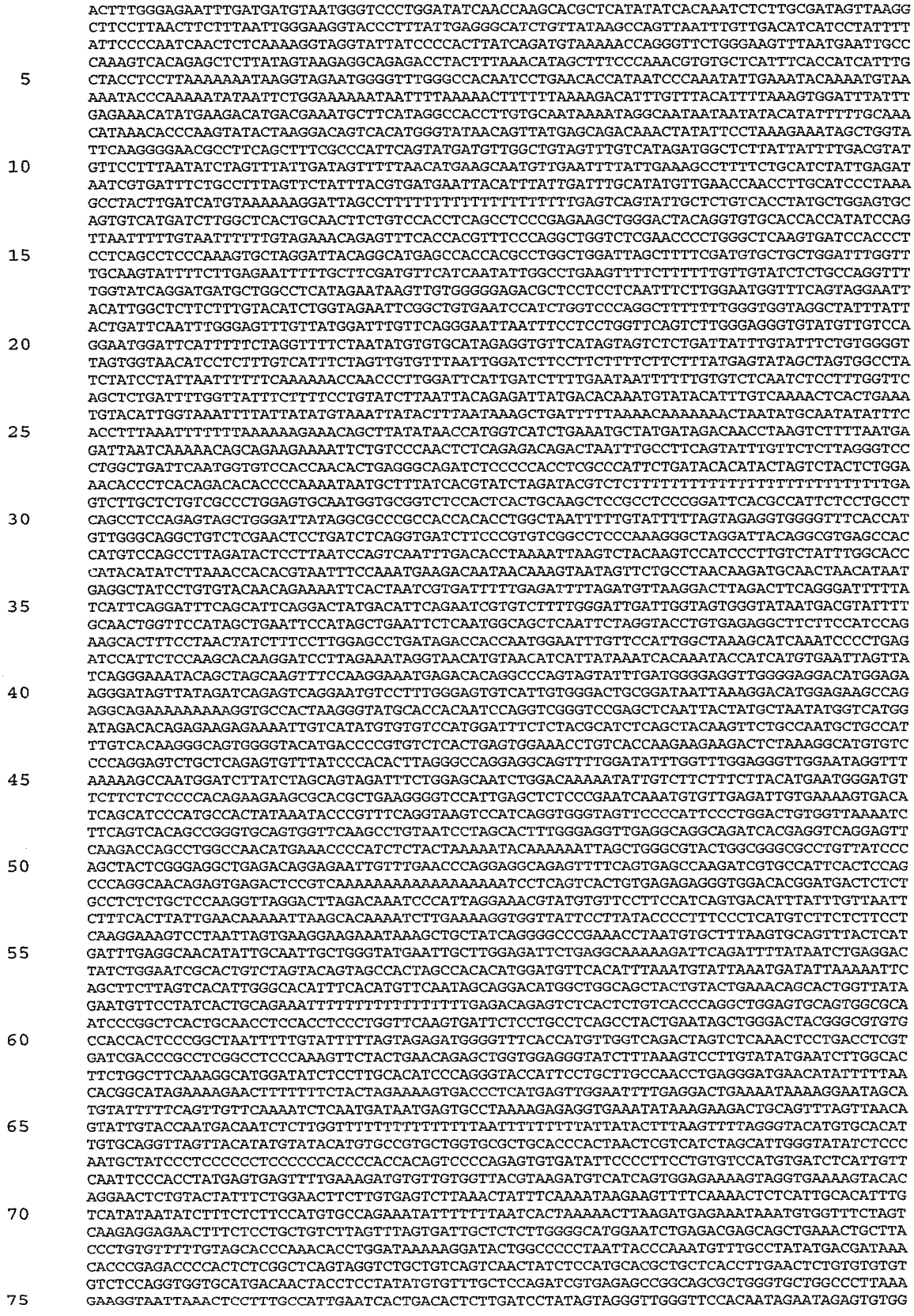
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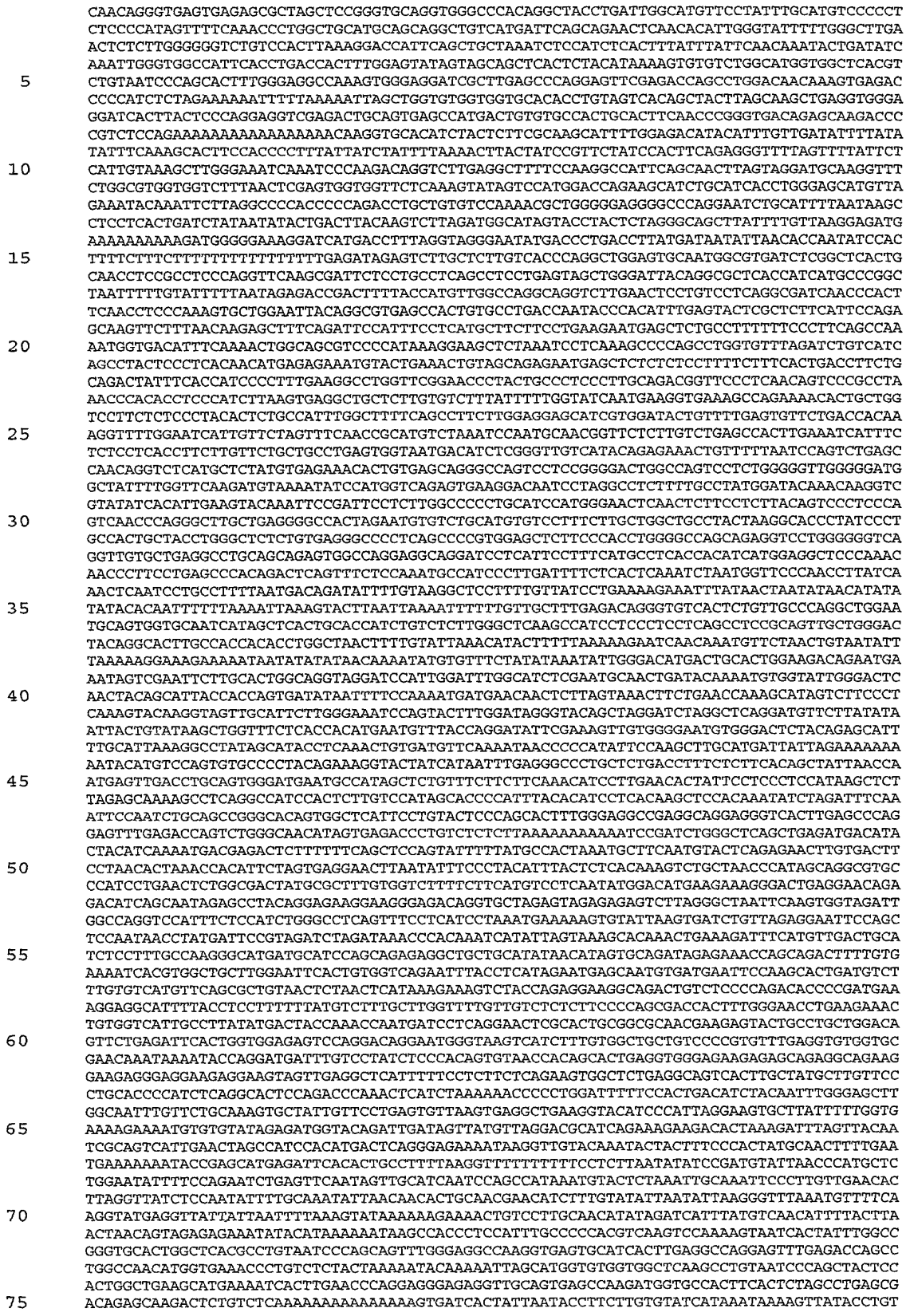


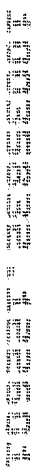
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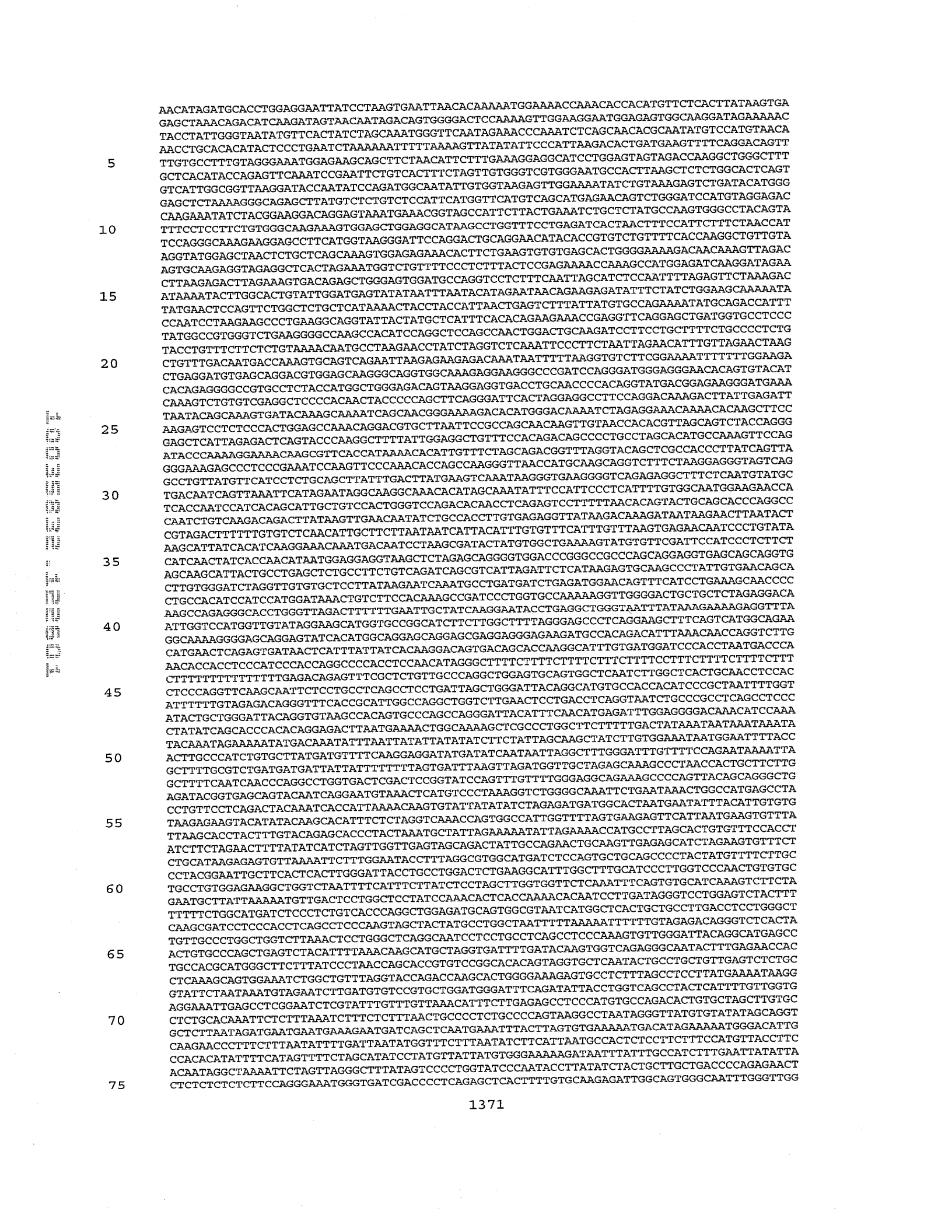
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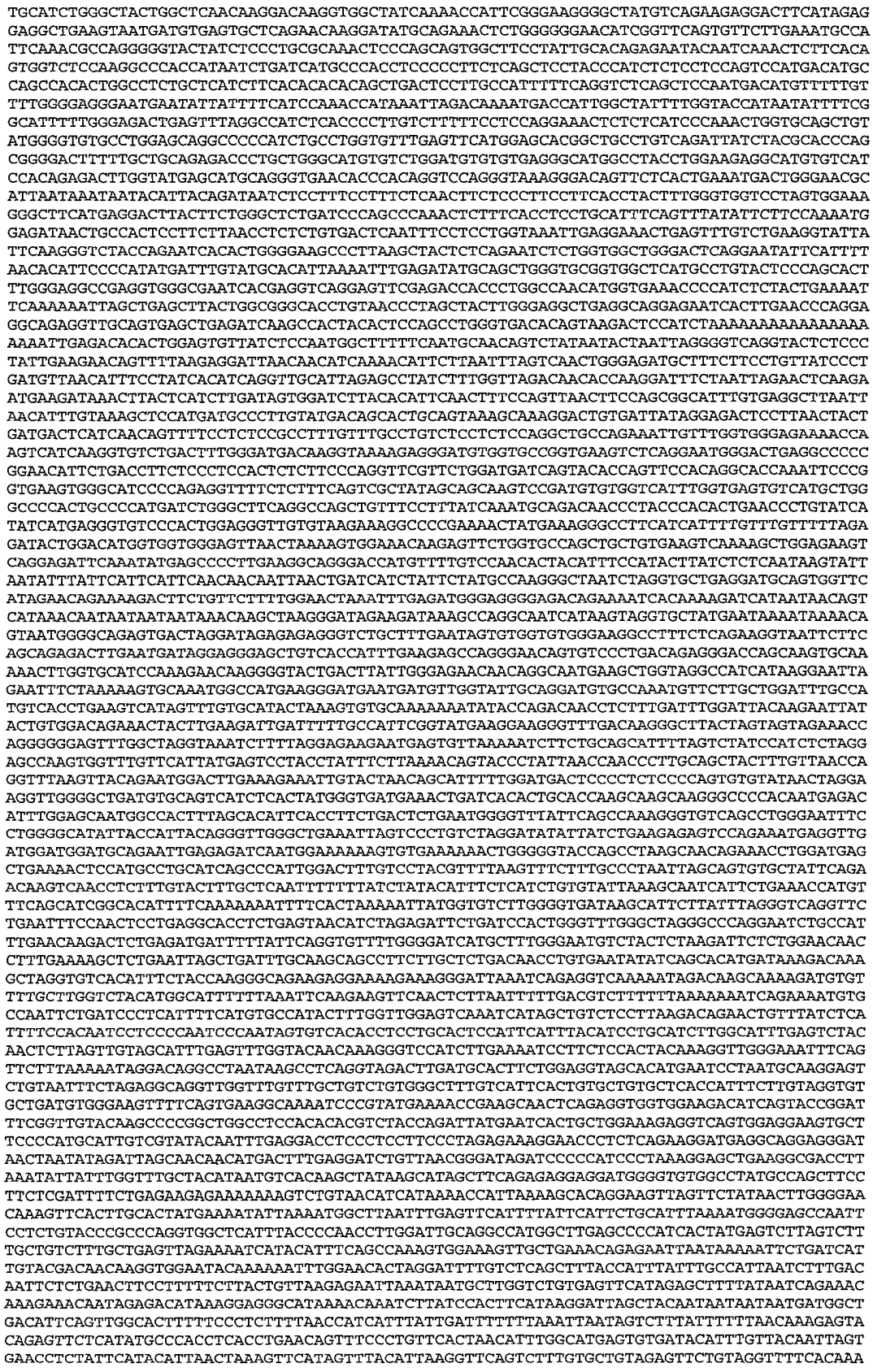




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Feature Sequence = 20050228.ST25

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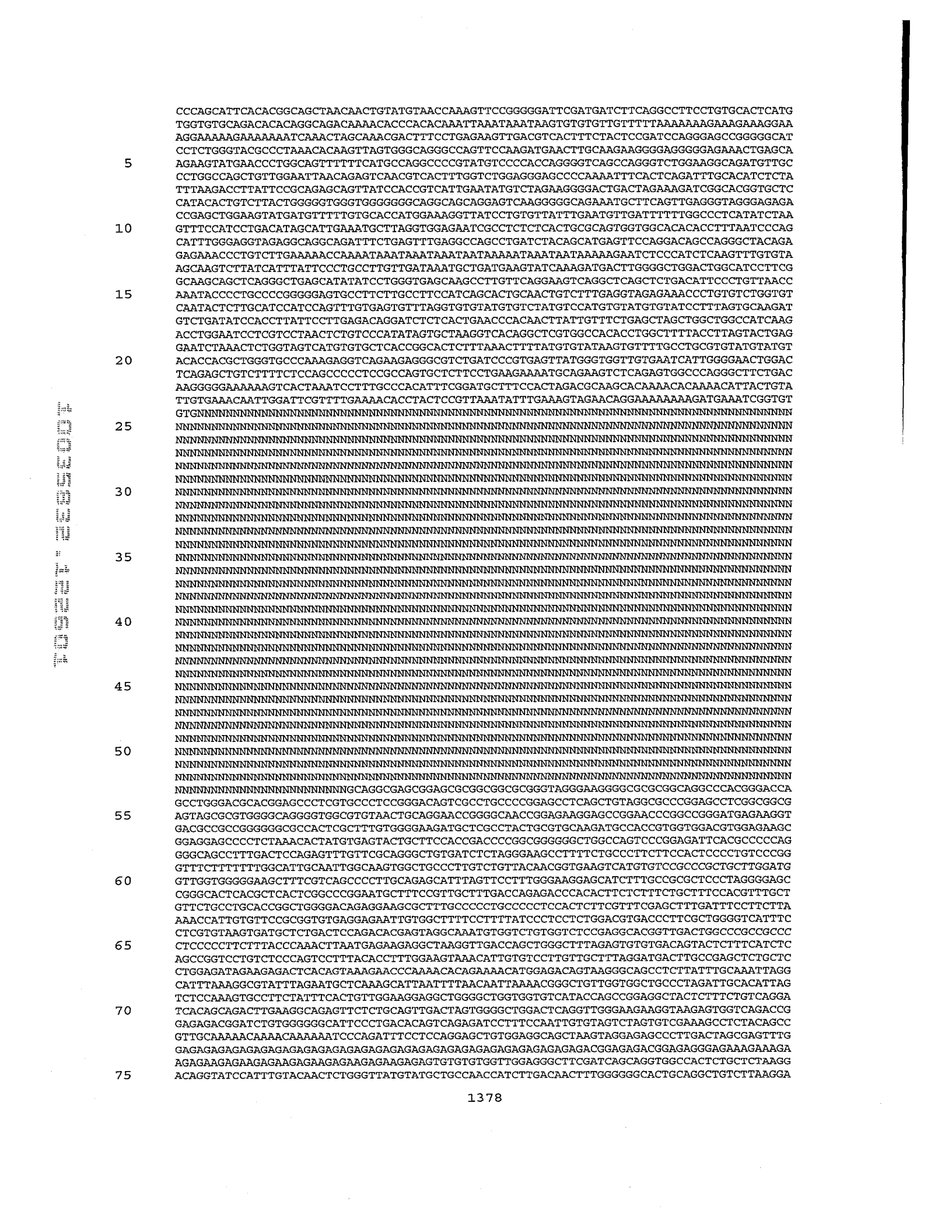
Table 65

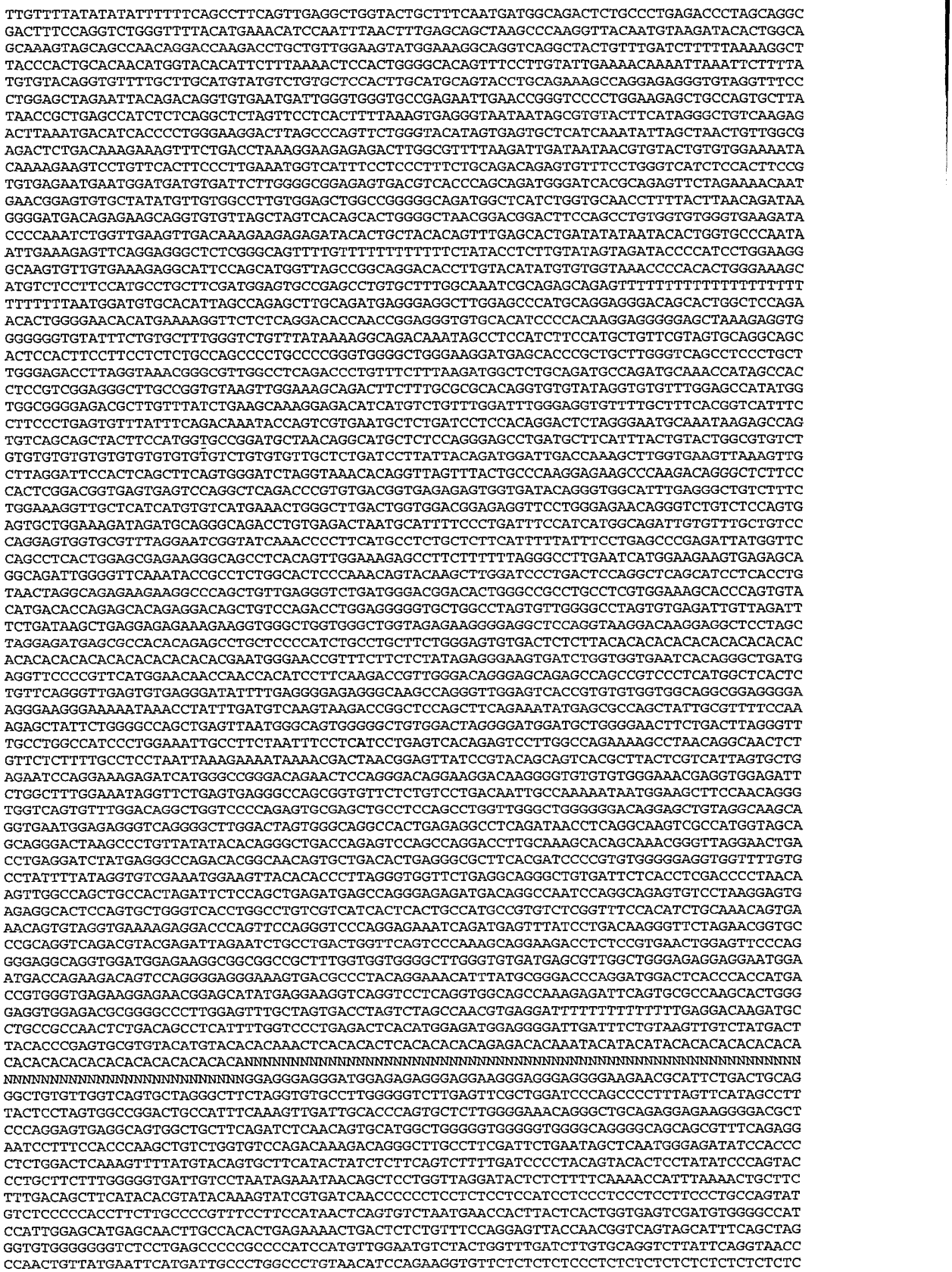
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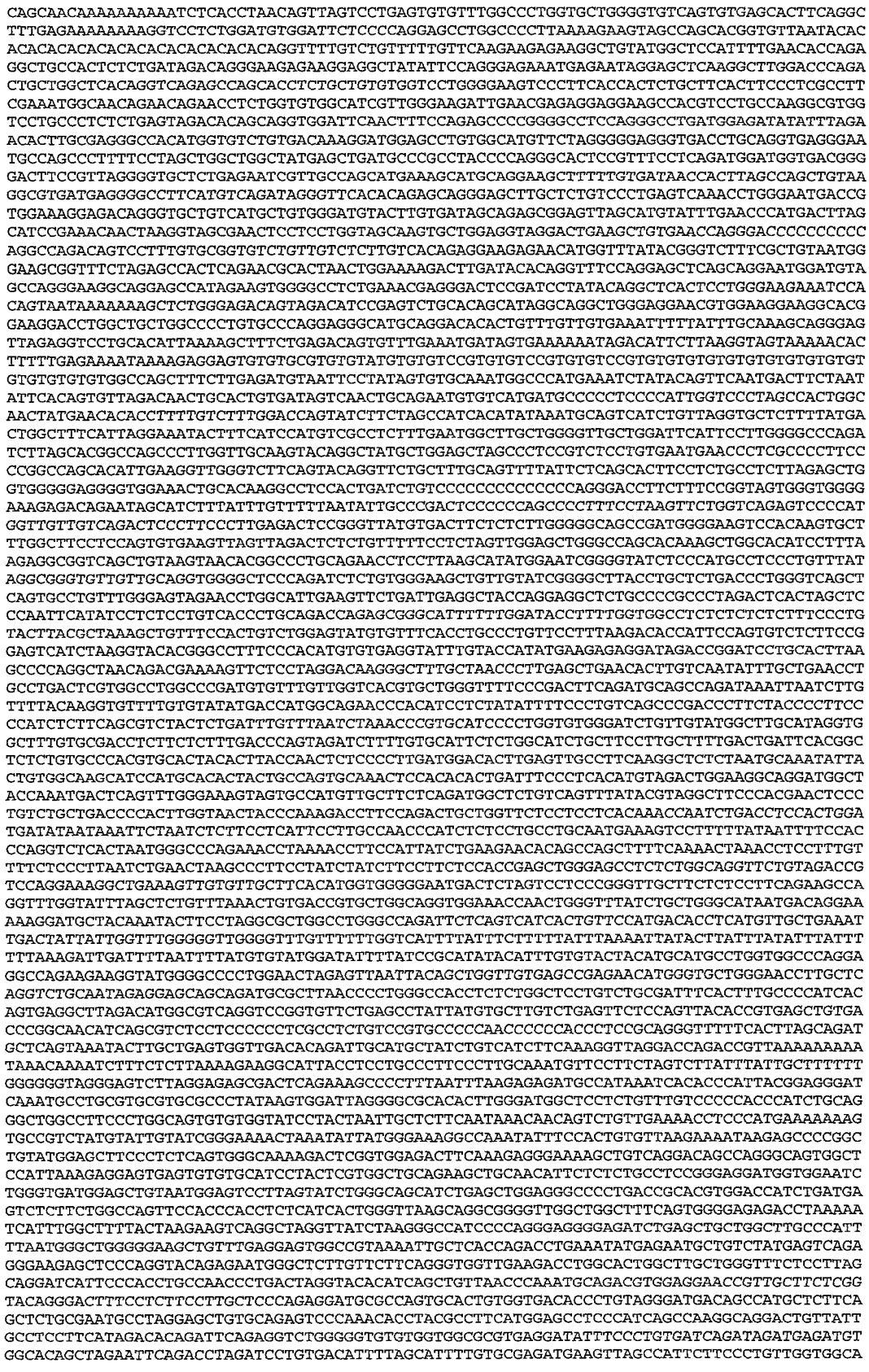


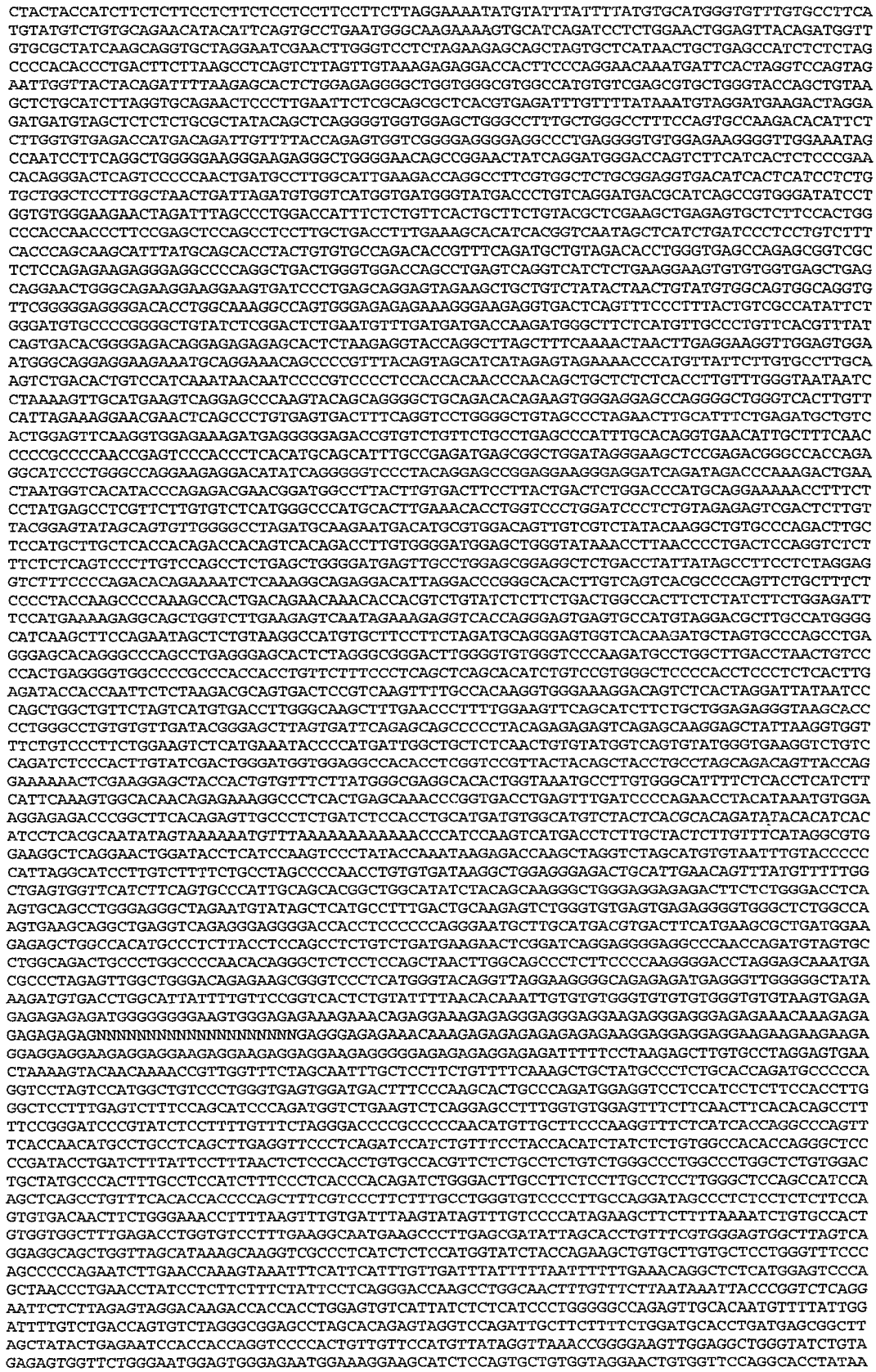


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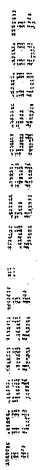
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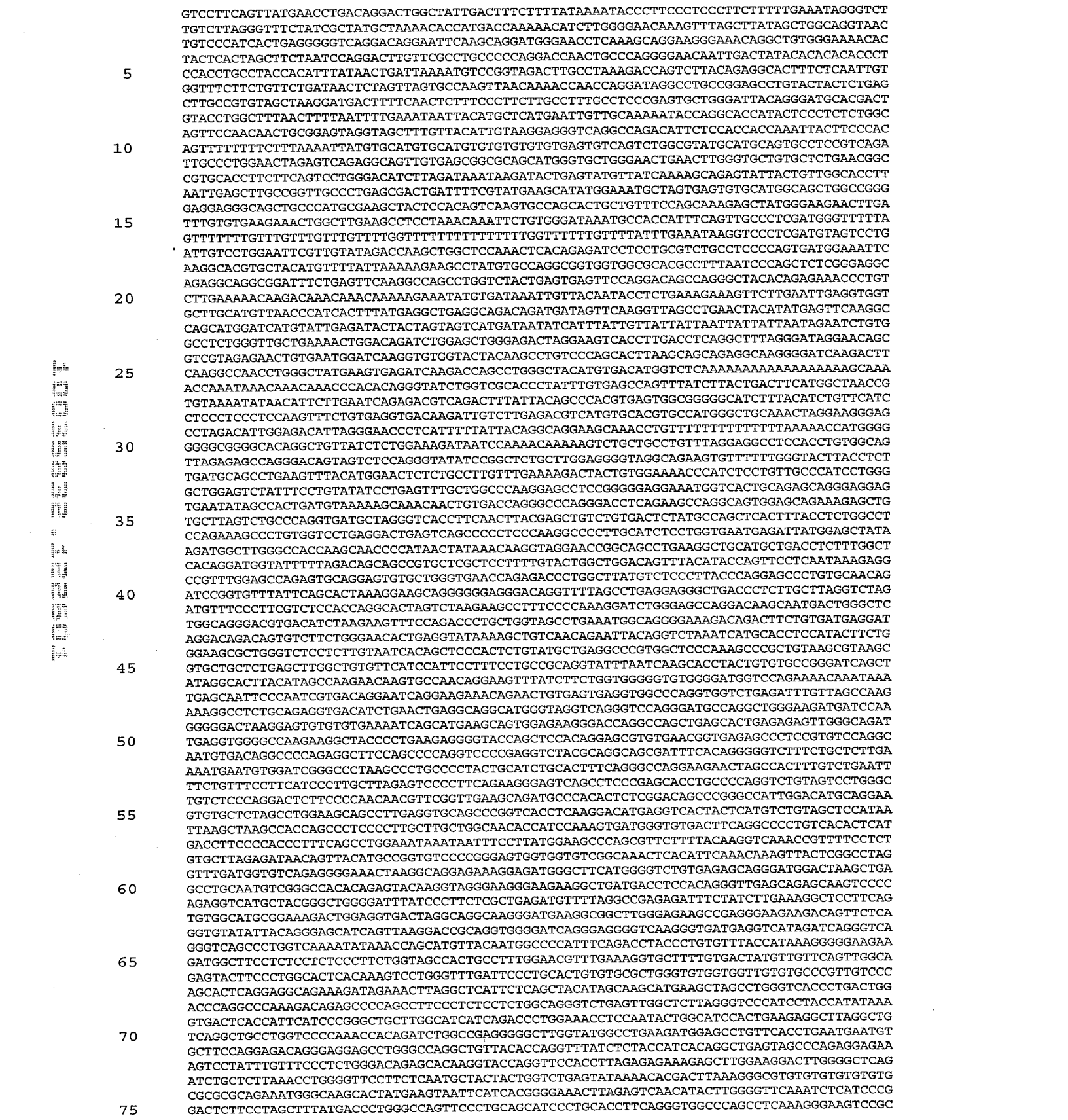


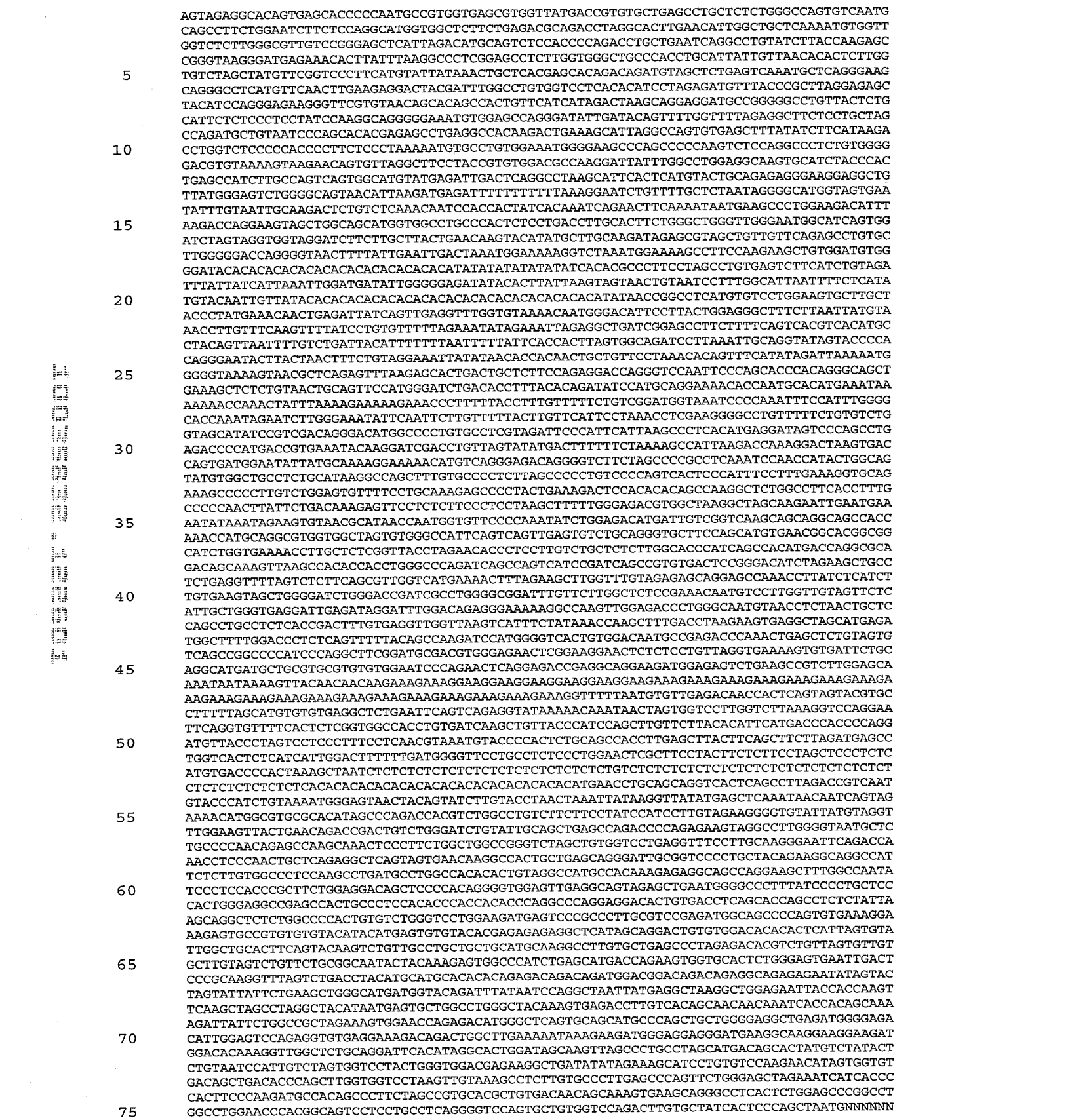
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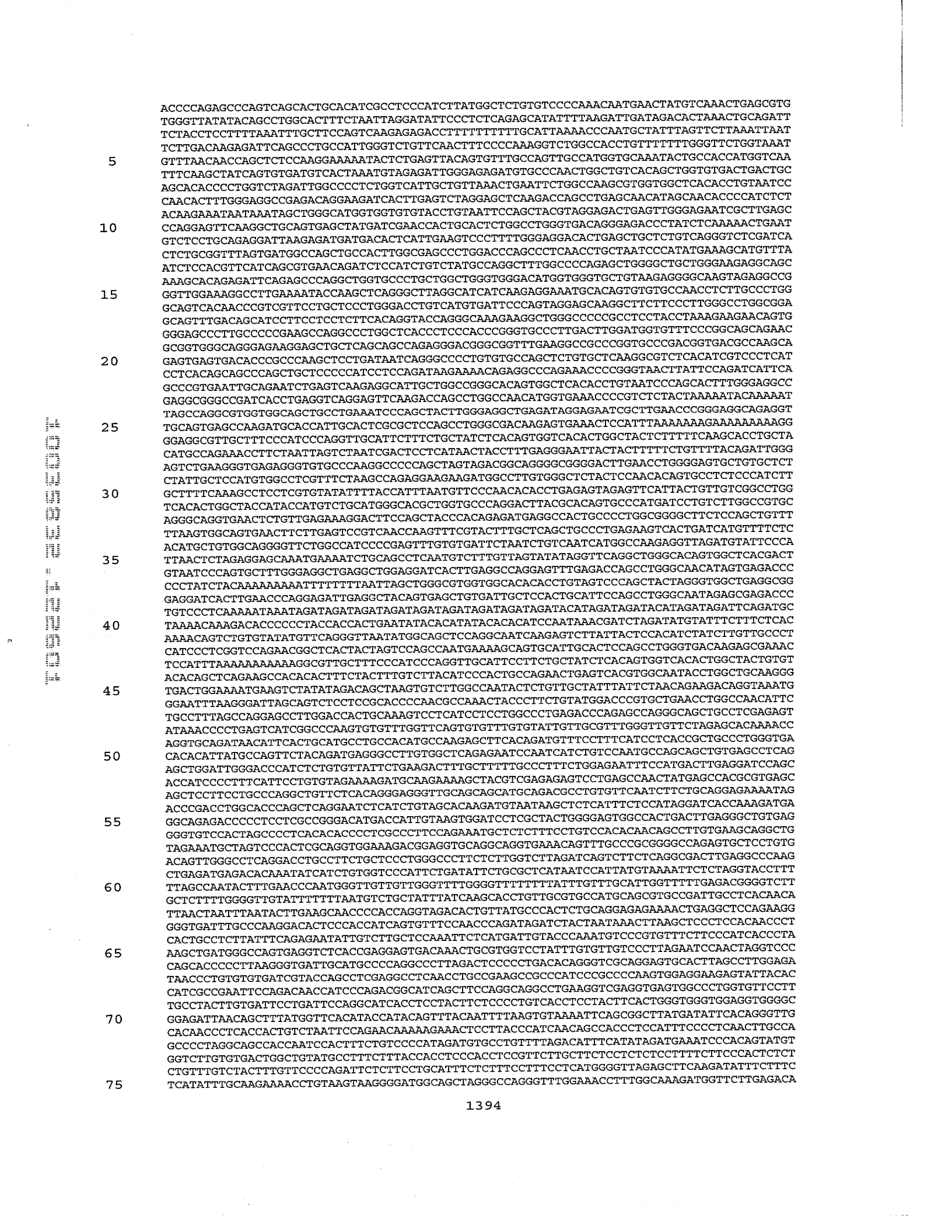
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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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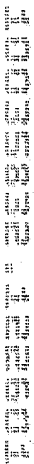
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HUMAN SEQUENCE - CODING
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Table 66

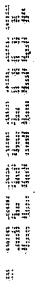
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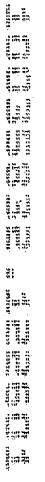
MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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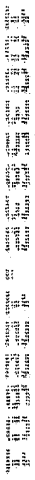
HUMAN SEQUENCE - GENOMIC

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Application/Control Number: 09/944,044
Filing Date: 08/31/2001

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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 67

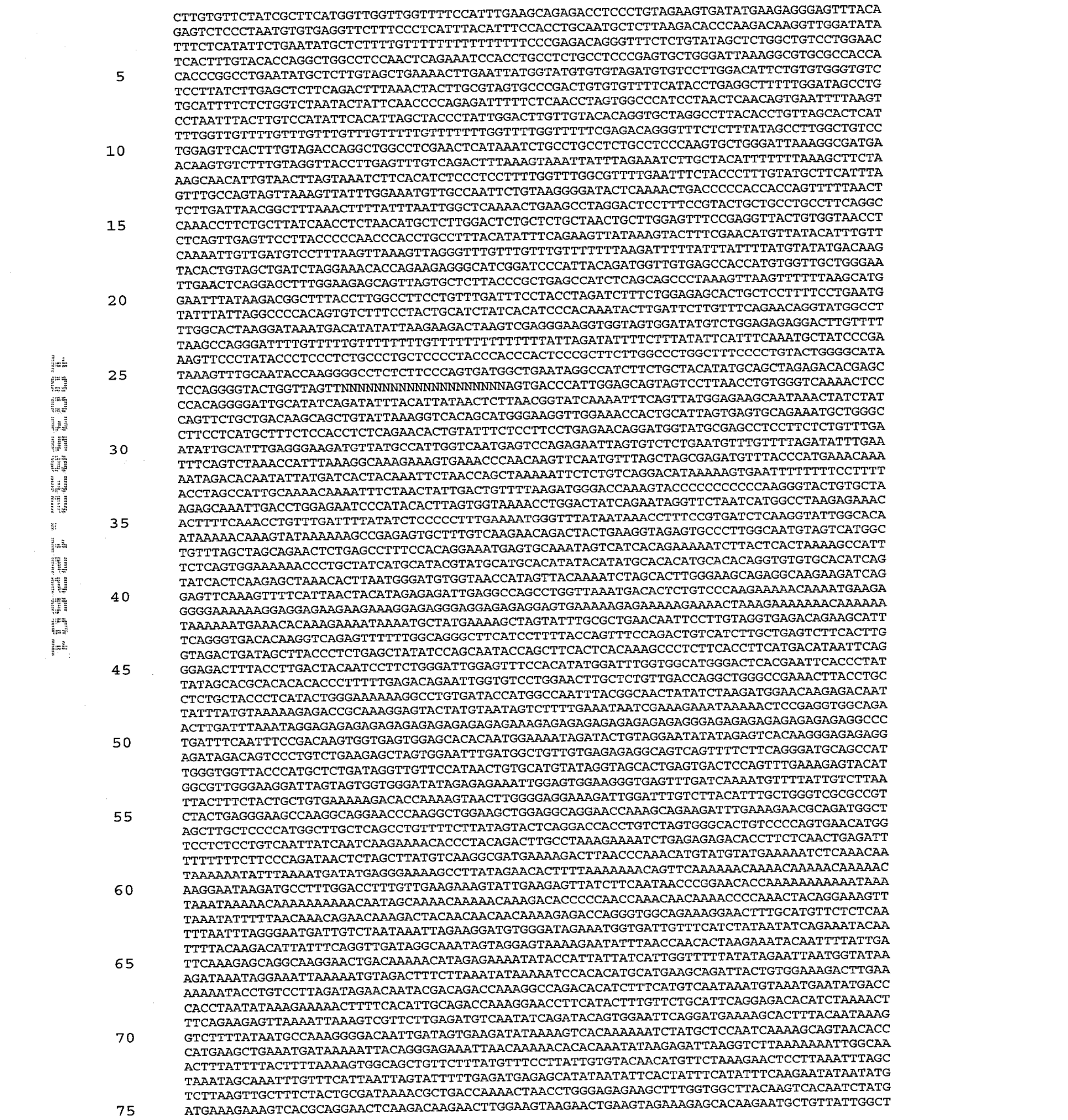
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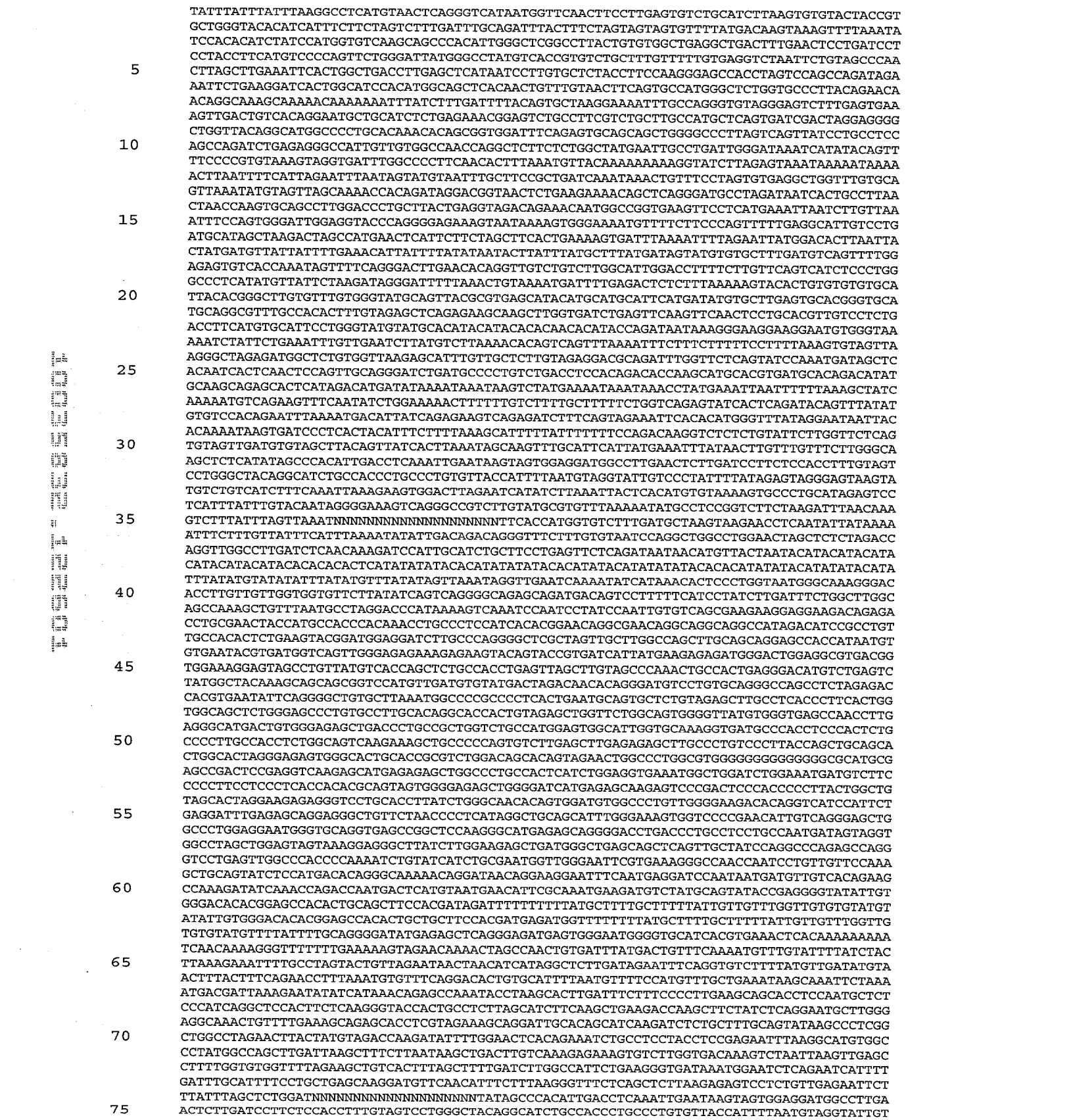
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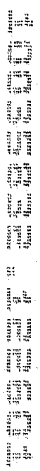
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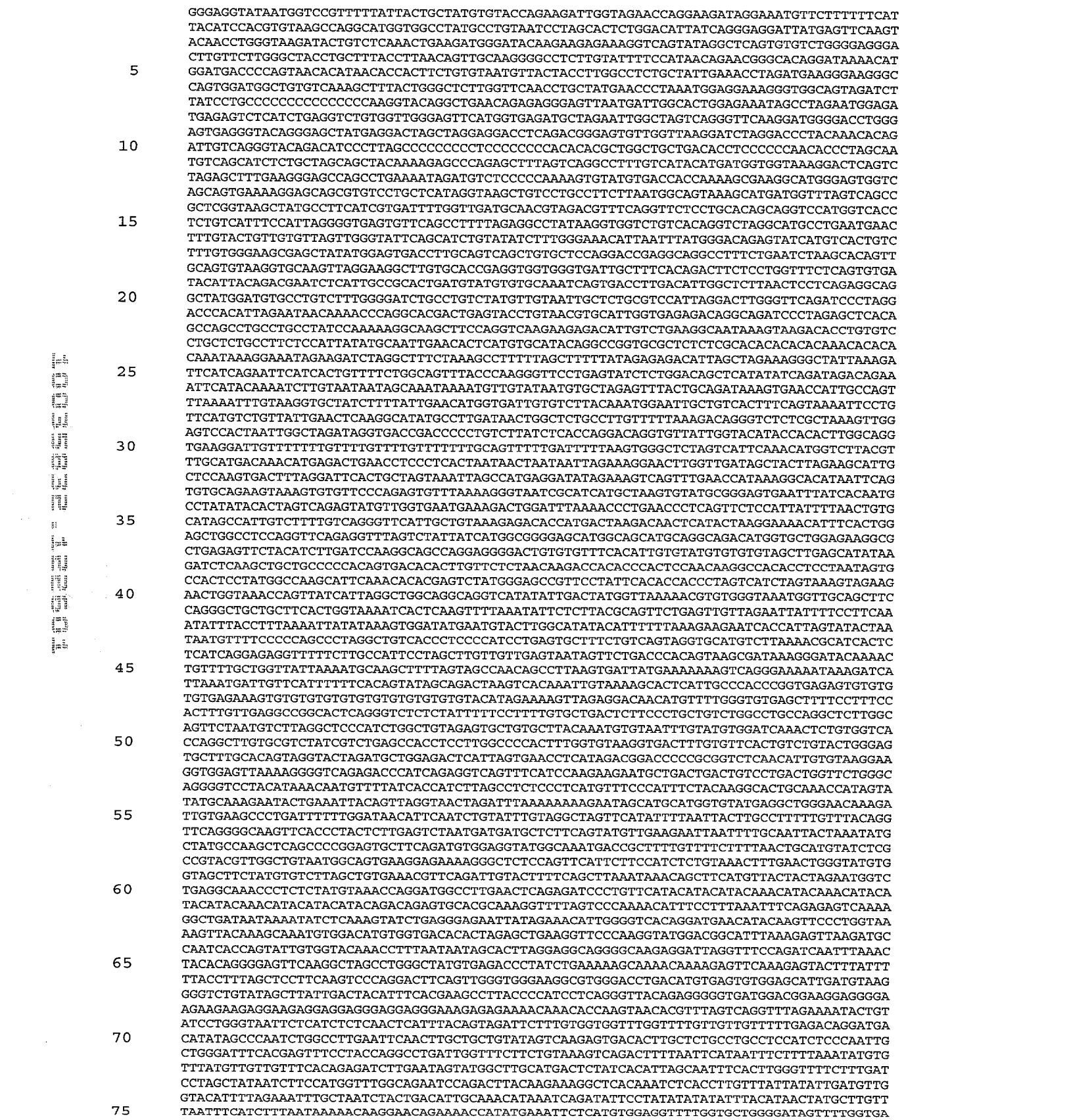


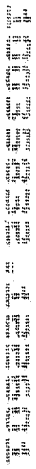
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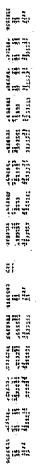




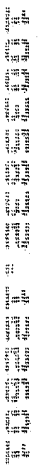
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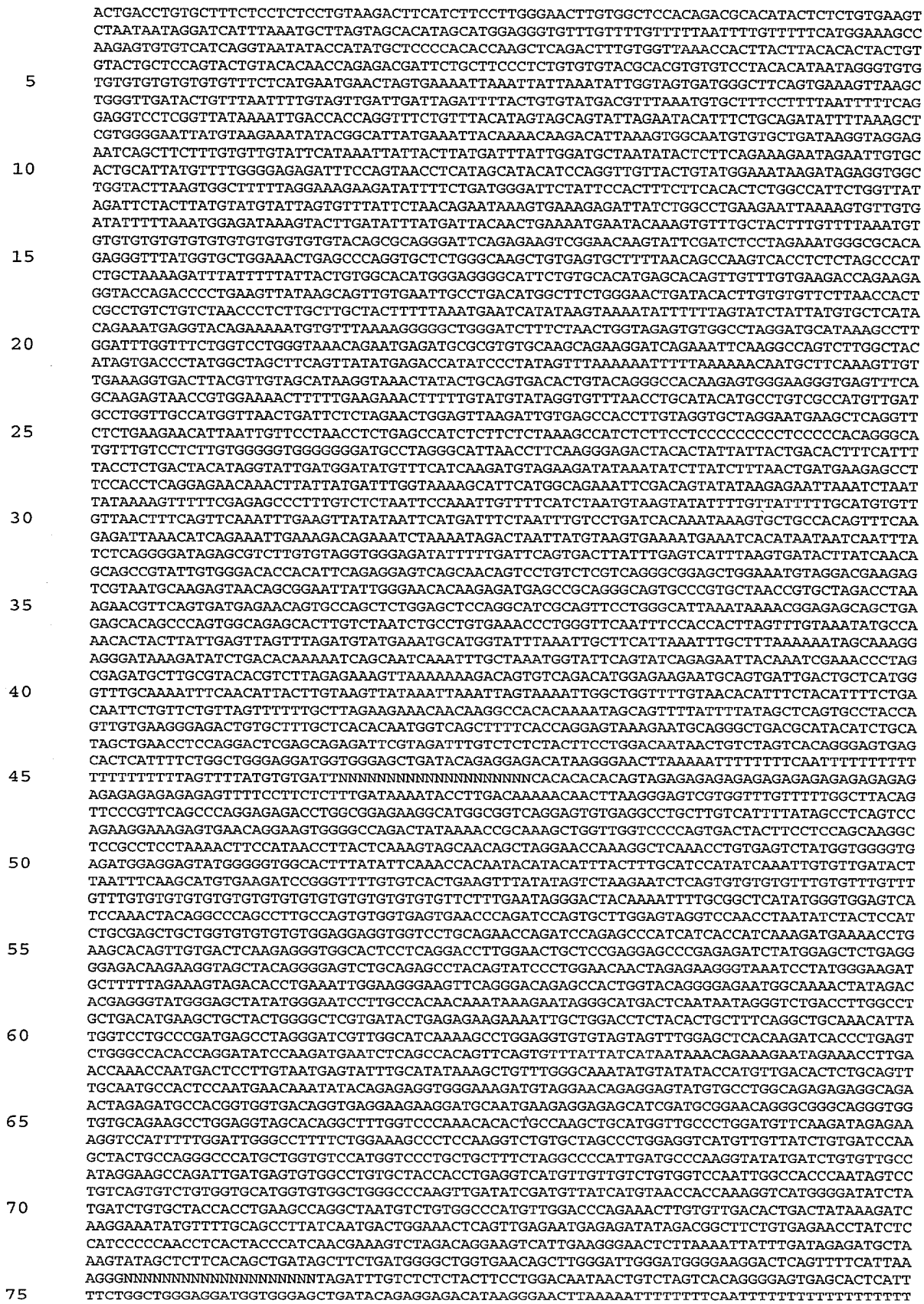


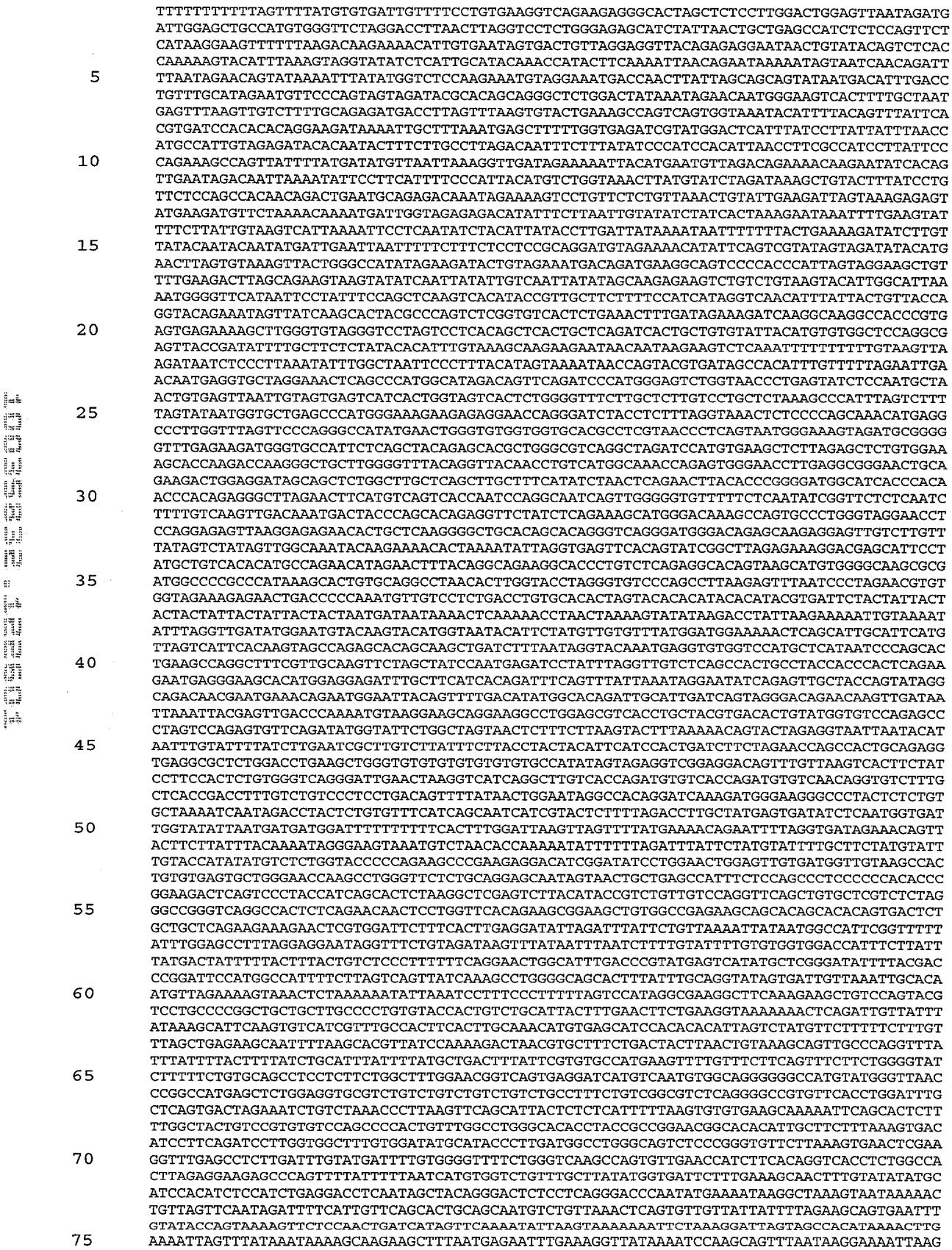


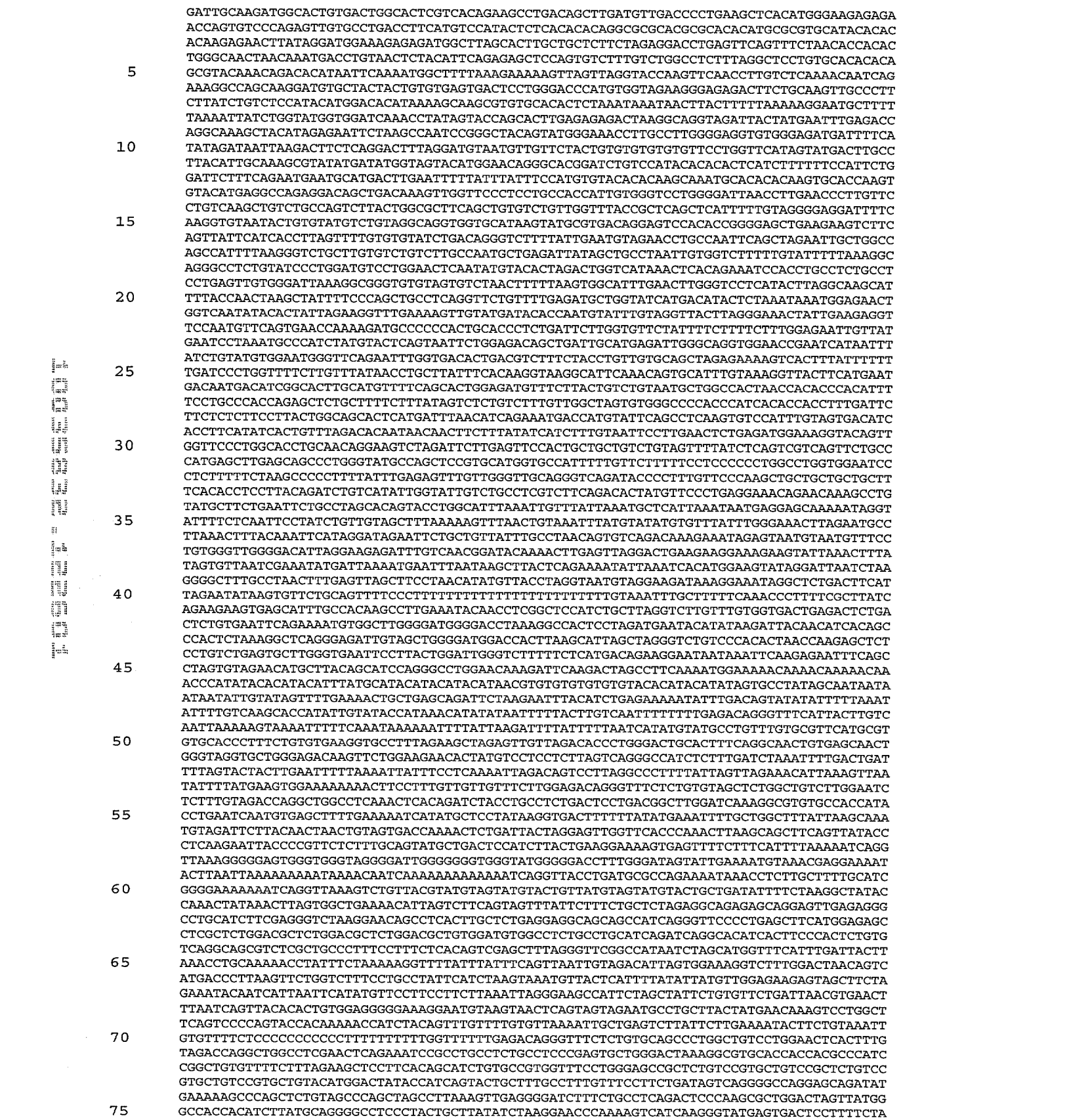


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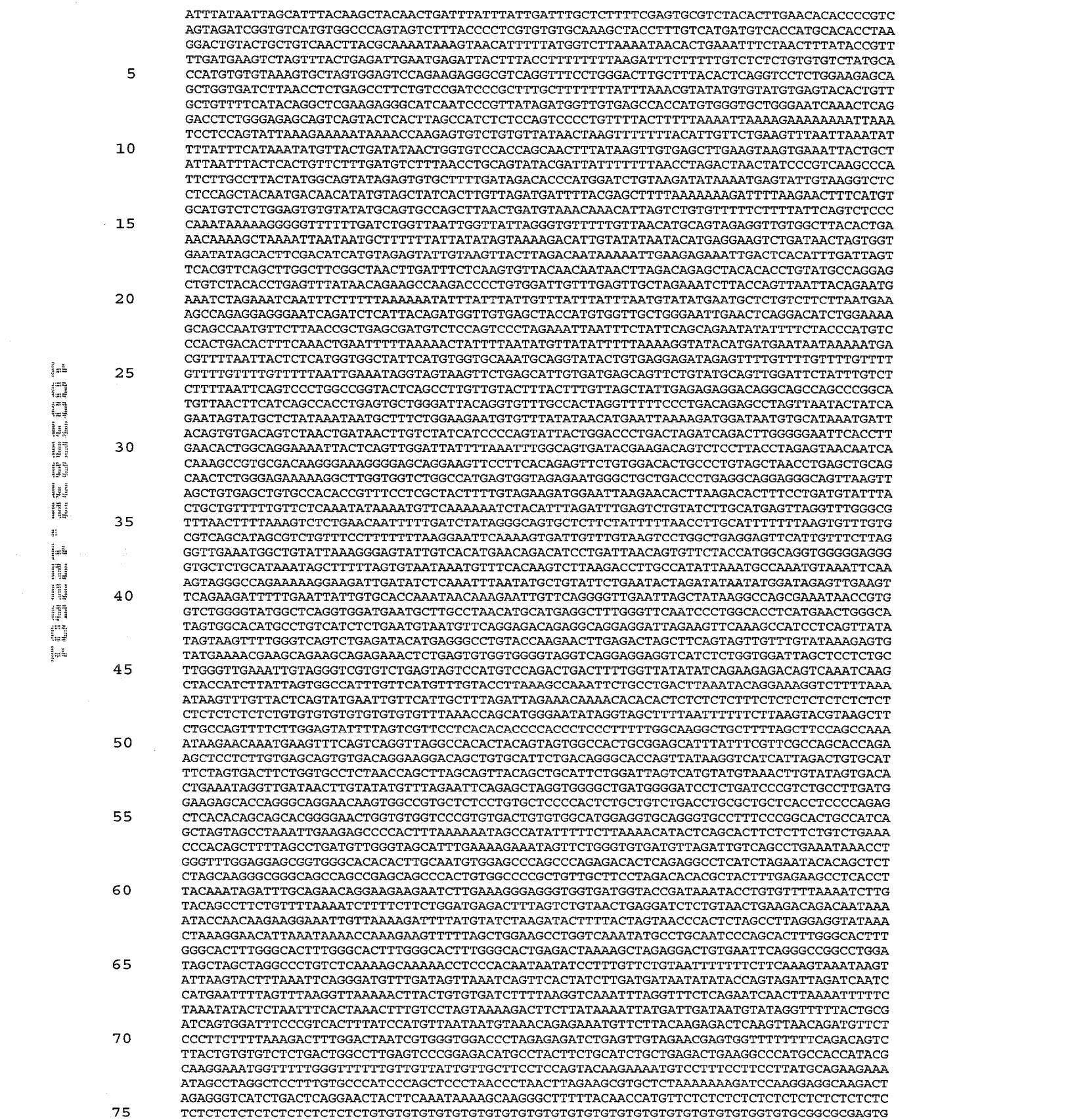


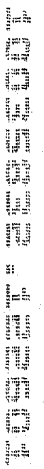






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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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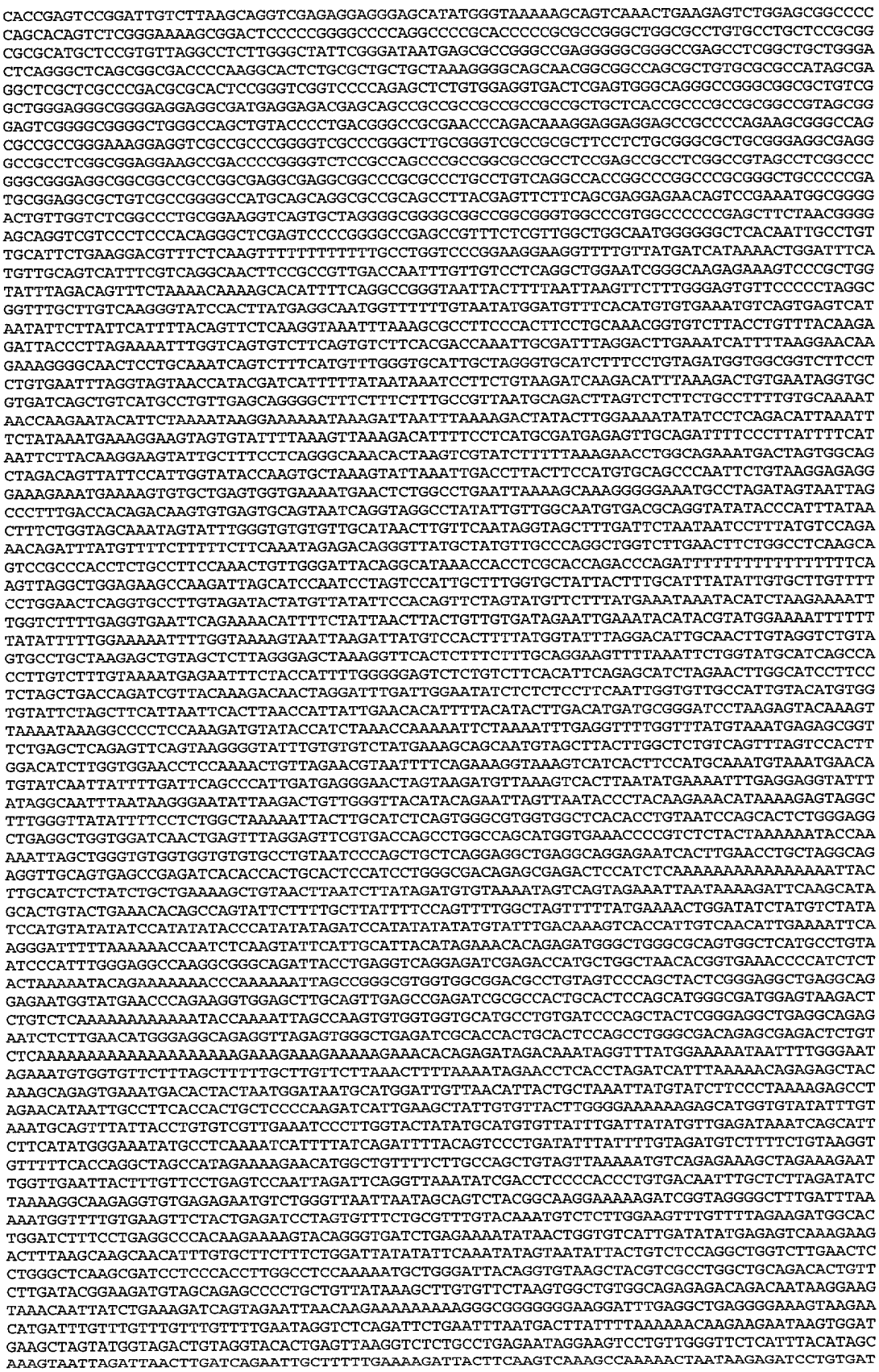
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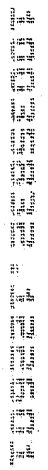
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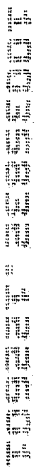
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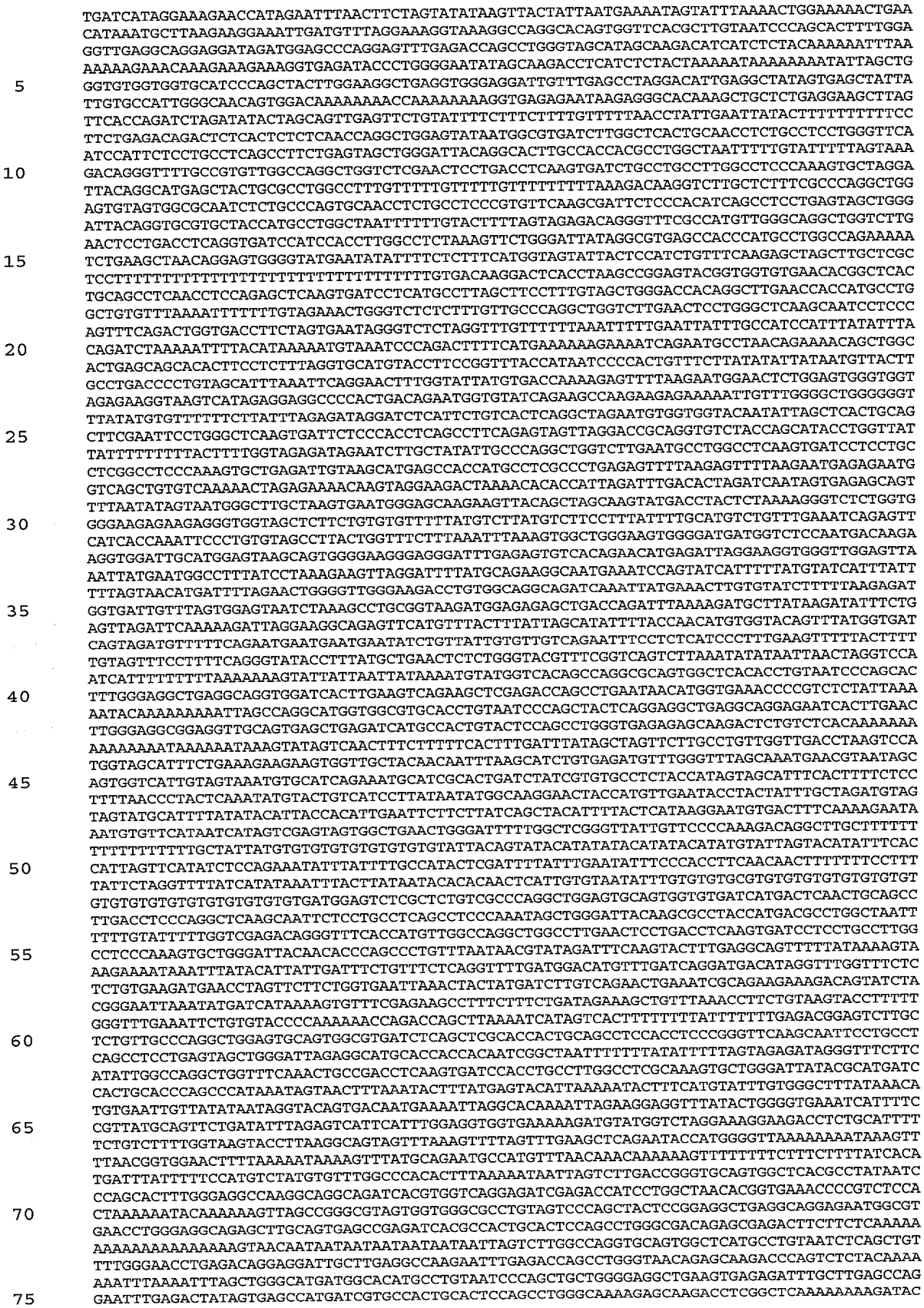
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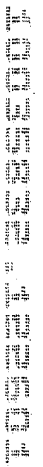
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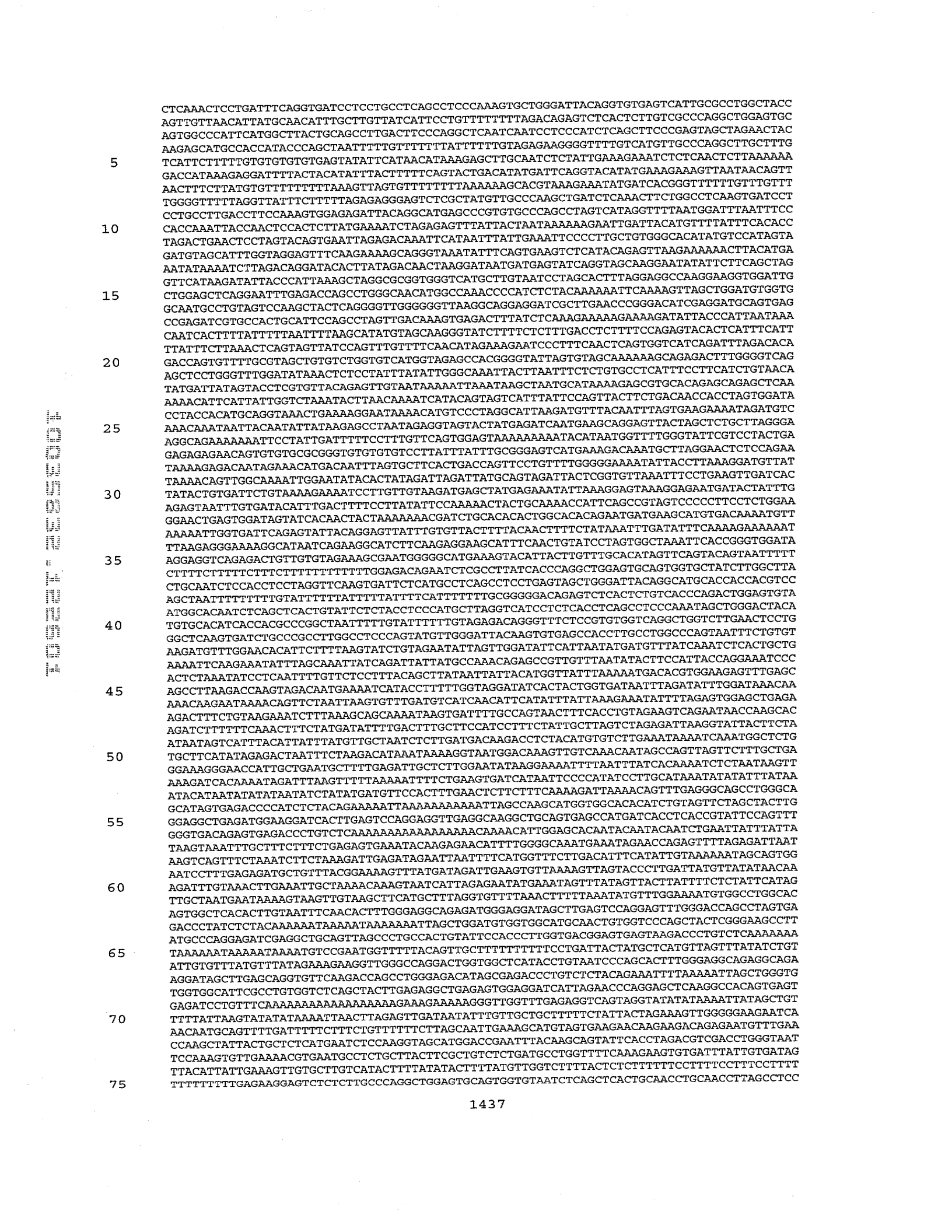
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HUMAN SEQUENCE - mRNA
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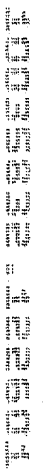
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Table 68

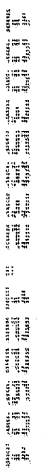
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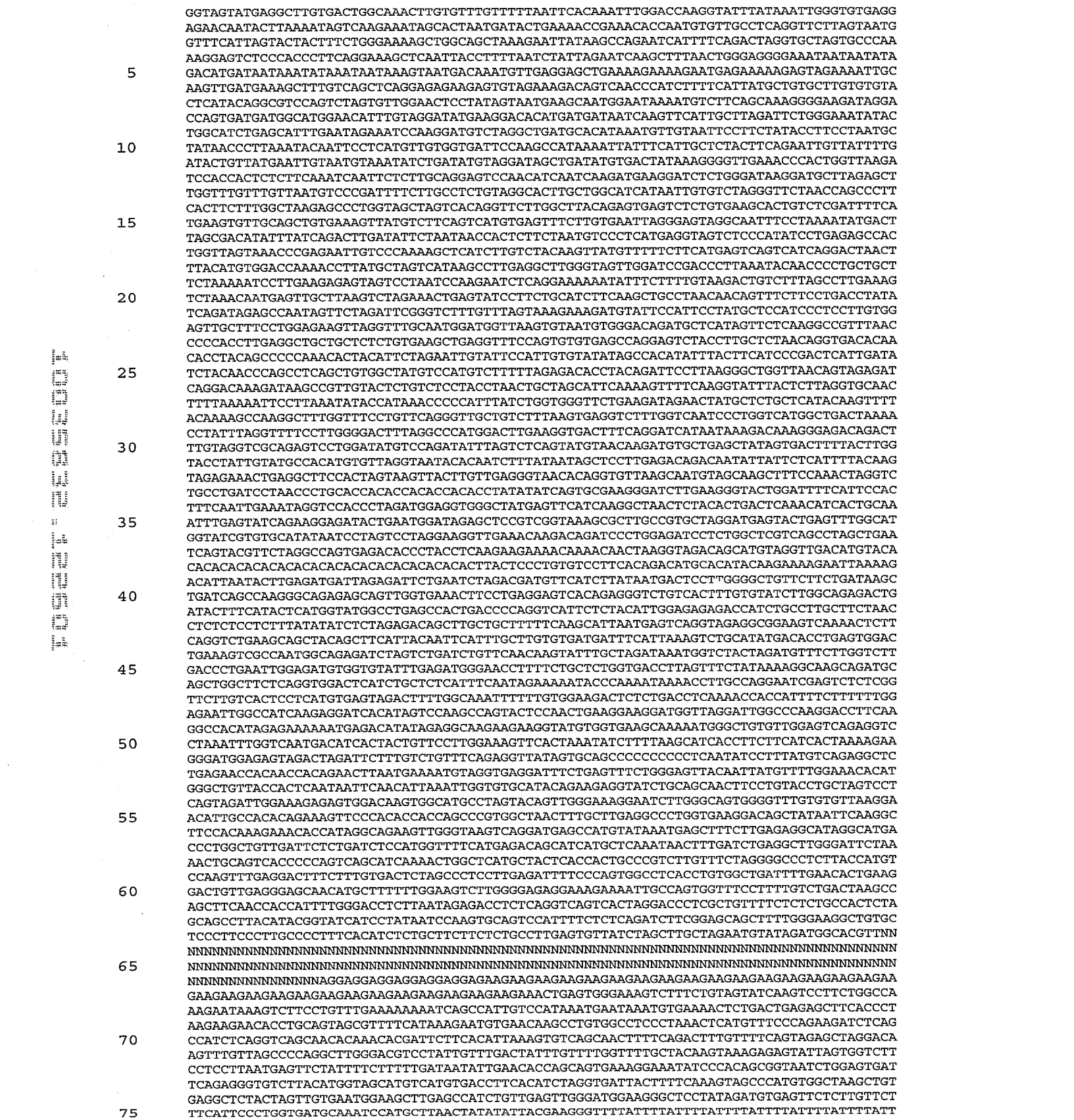
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Sequence Listing

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MOUSE SEQUENCE - mRNA

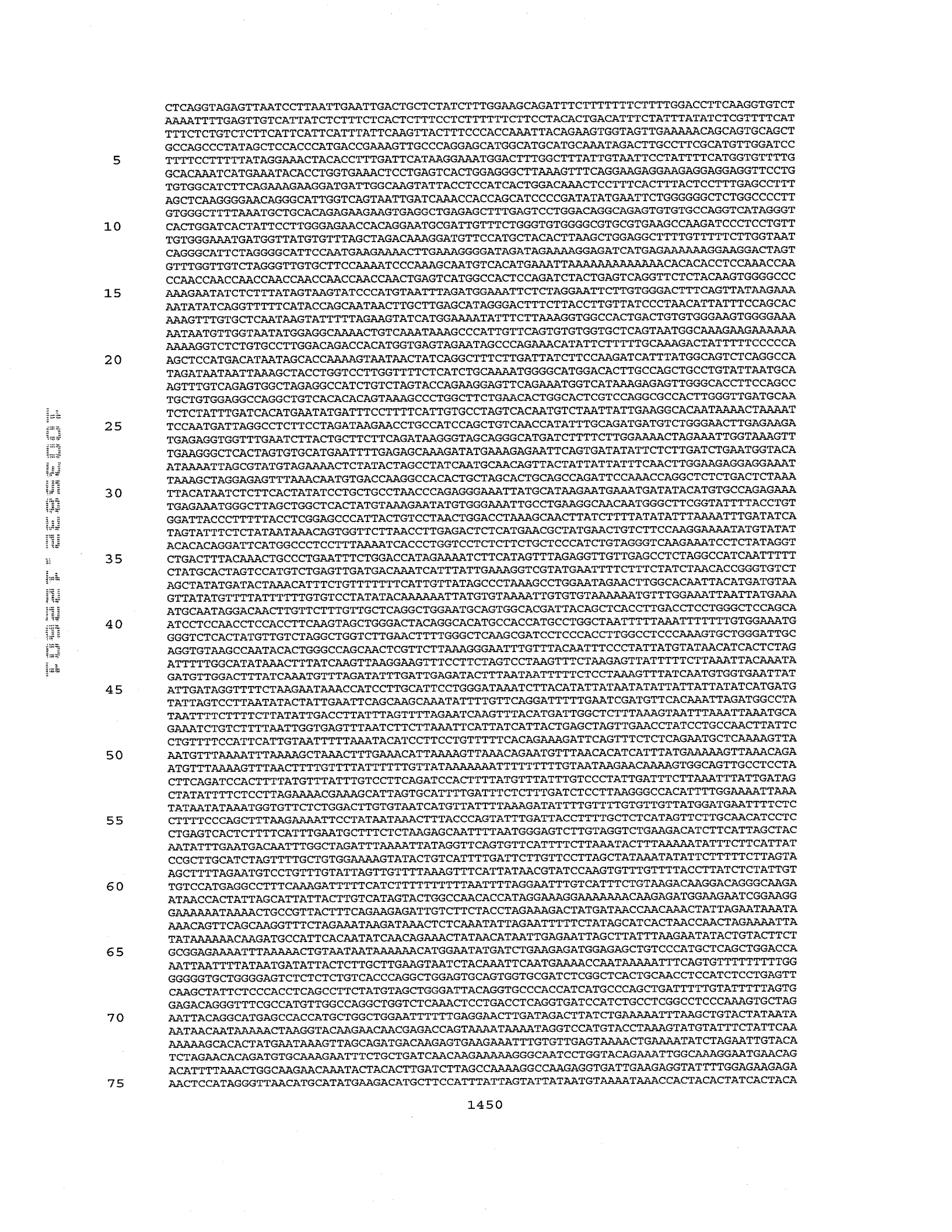
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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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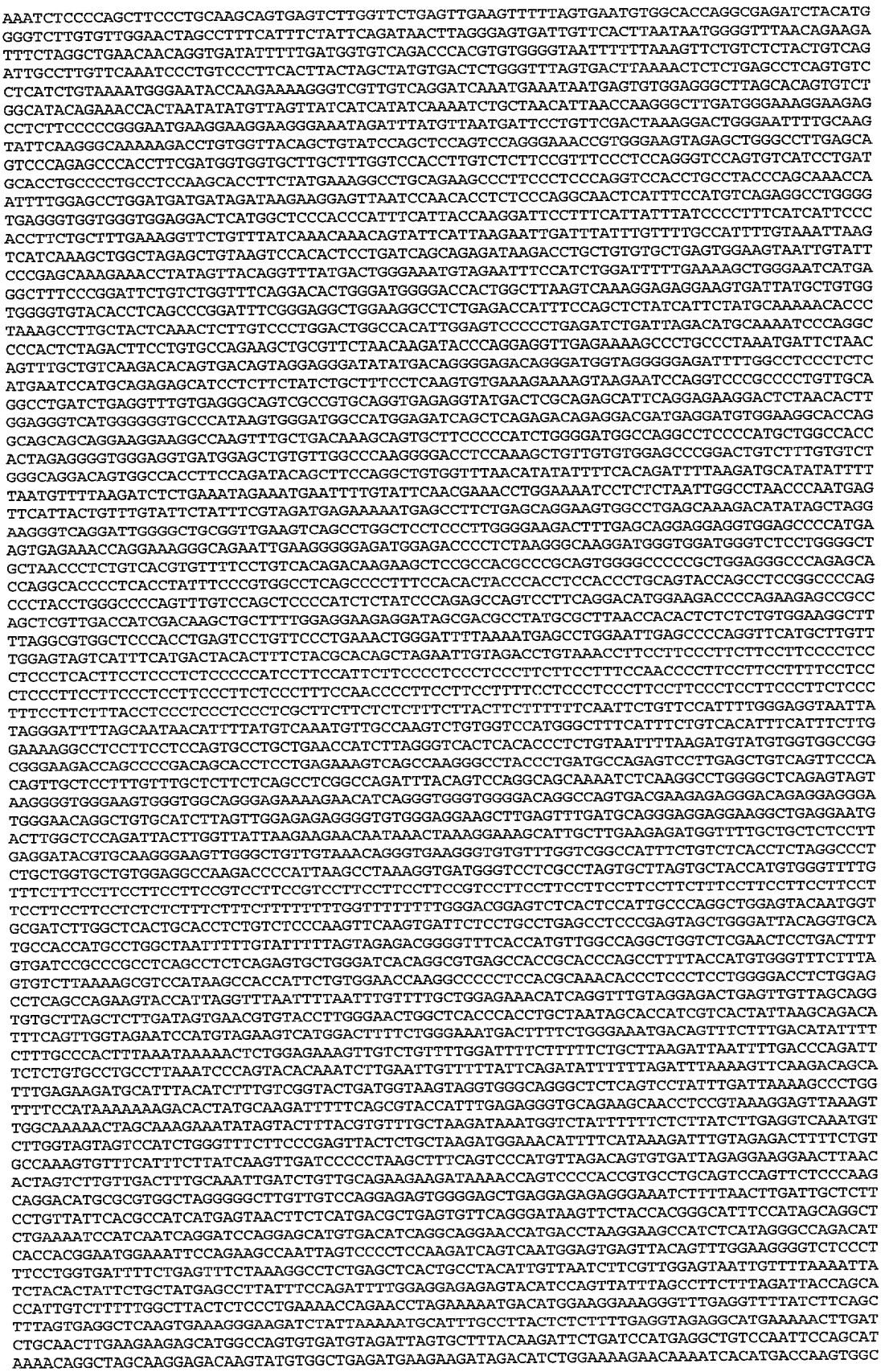
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 69

MOUSE NOMENCLATURE

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Celera	mCG1223

HUMAN NOMENCLATURE

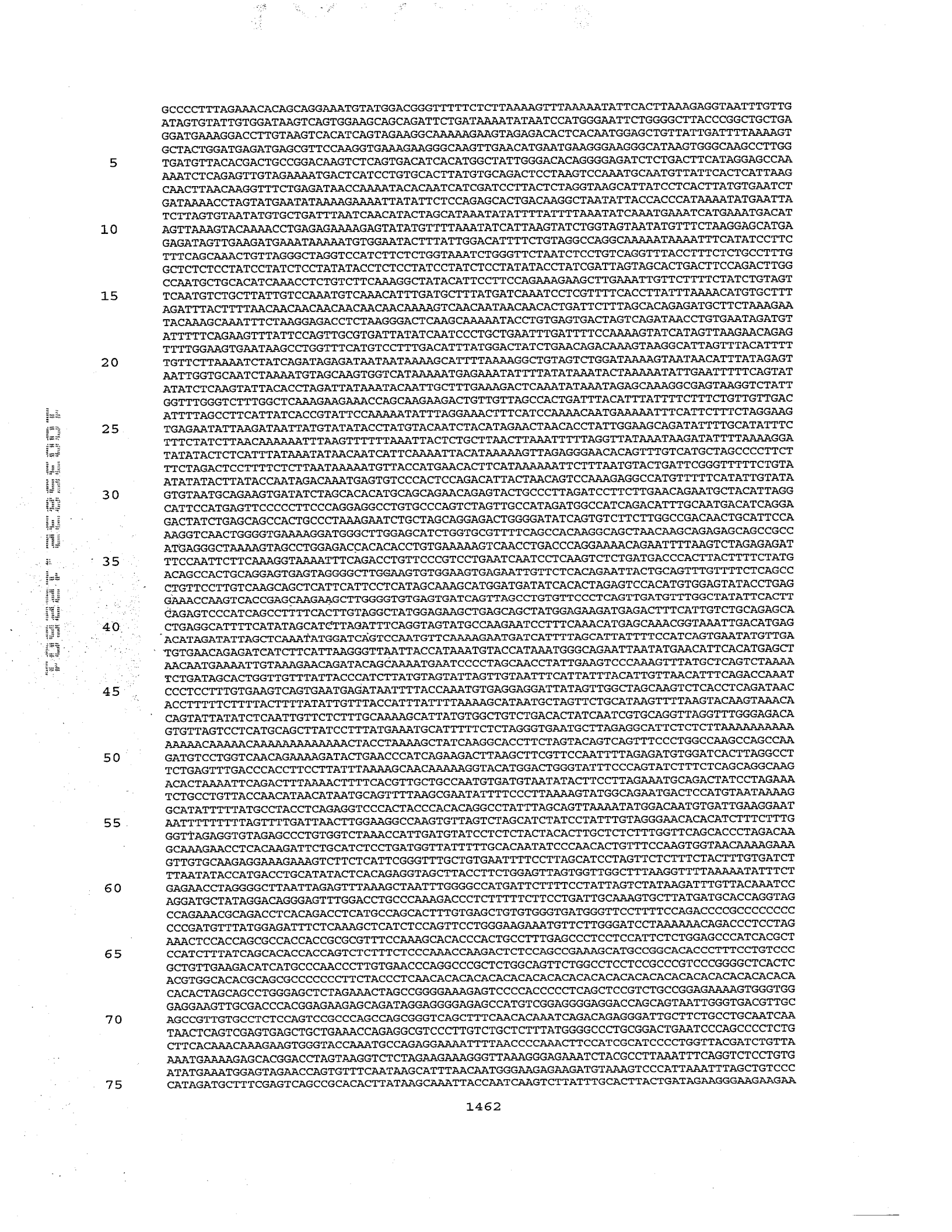
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Celera	hCG36839

MOUSE SEQUENCE - GENOMIC

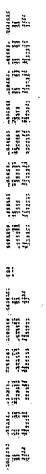
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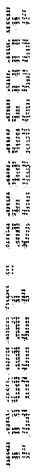
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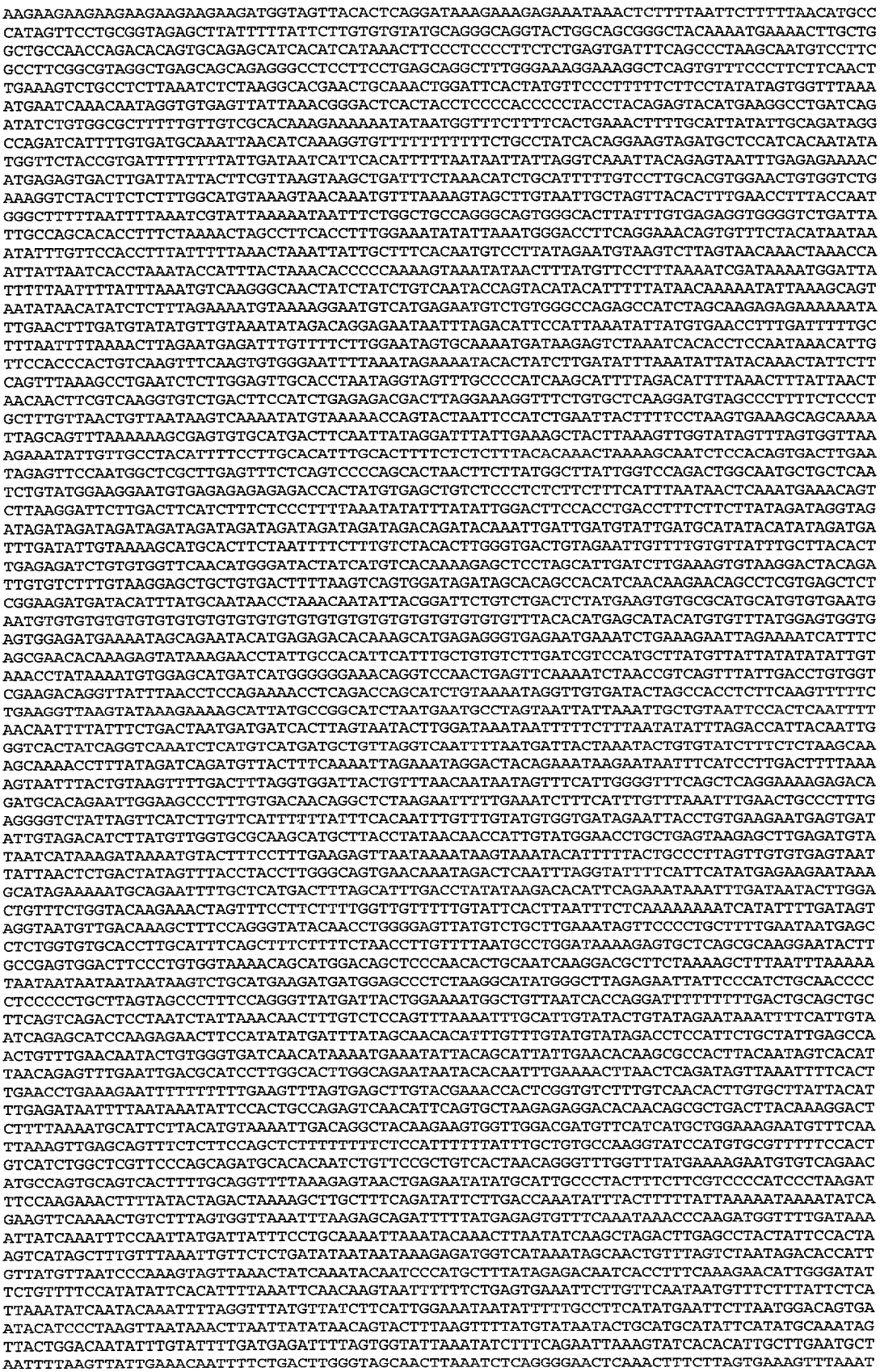
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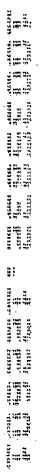


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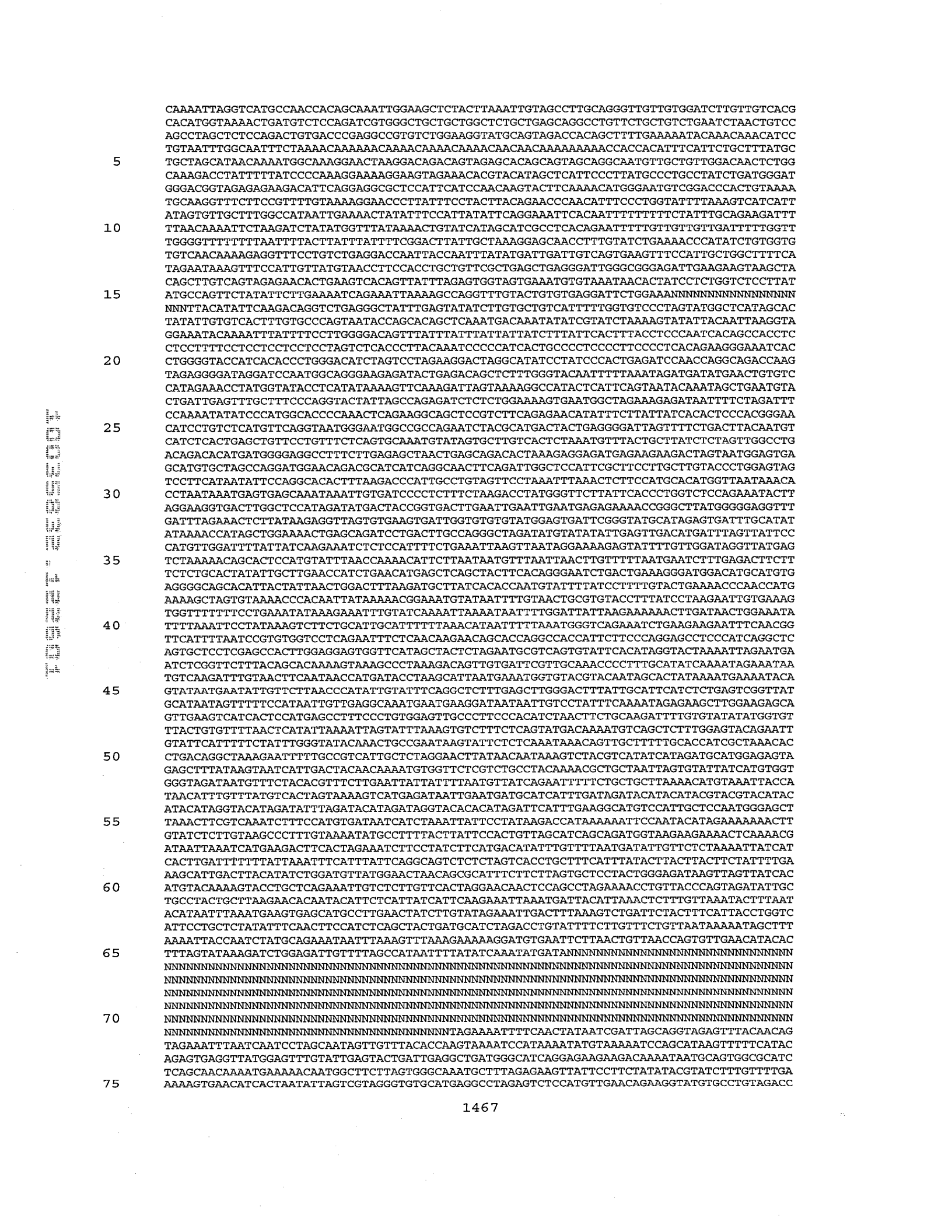


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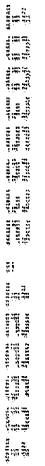




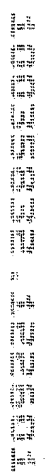
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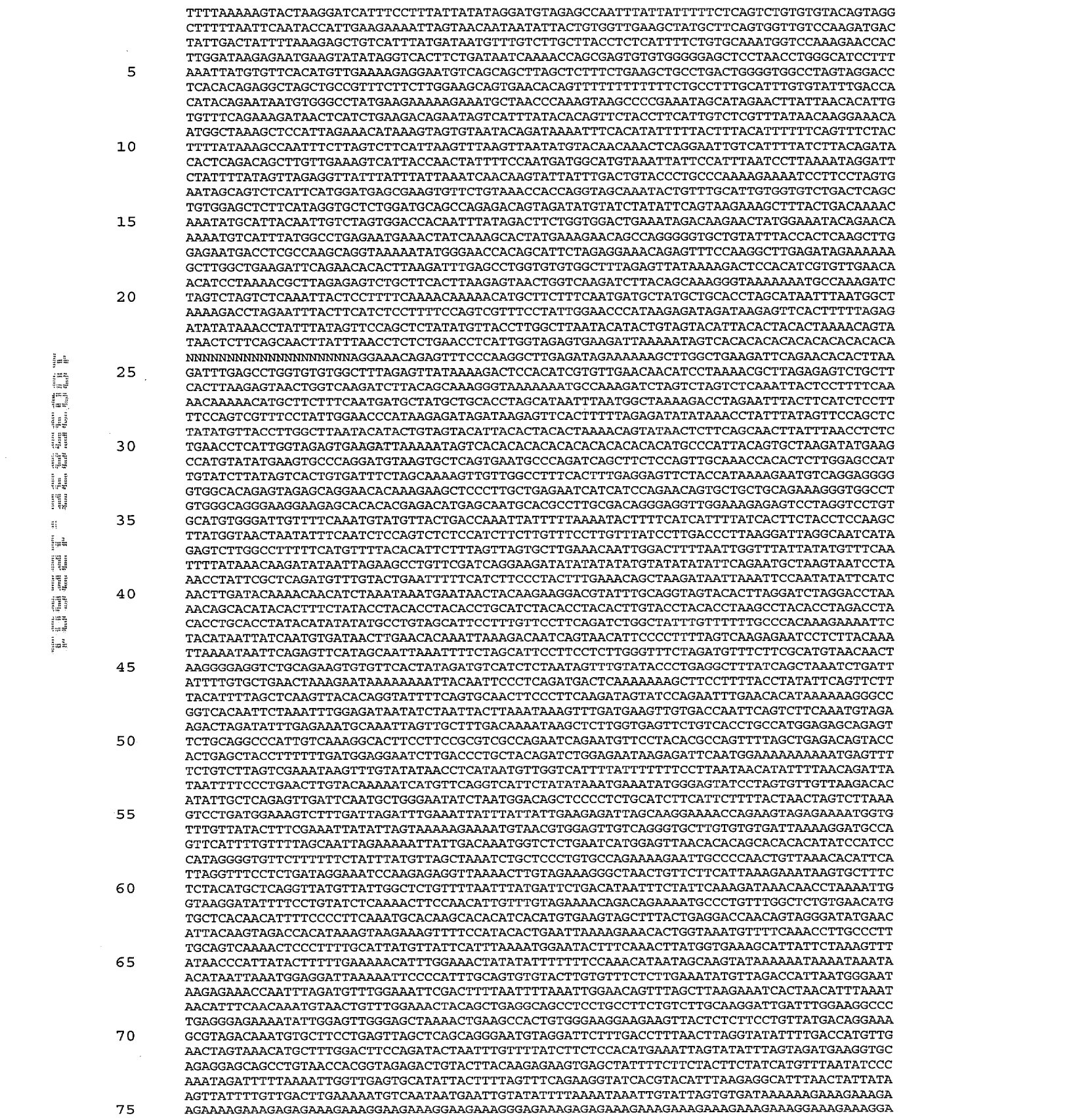
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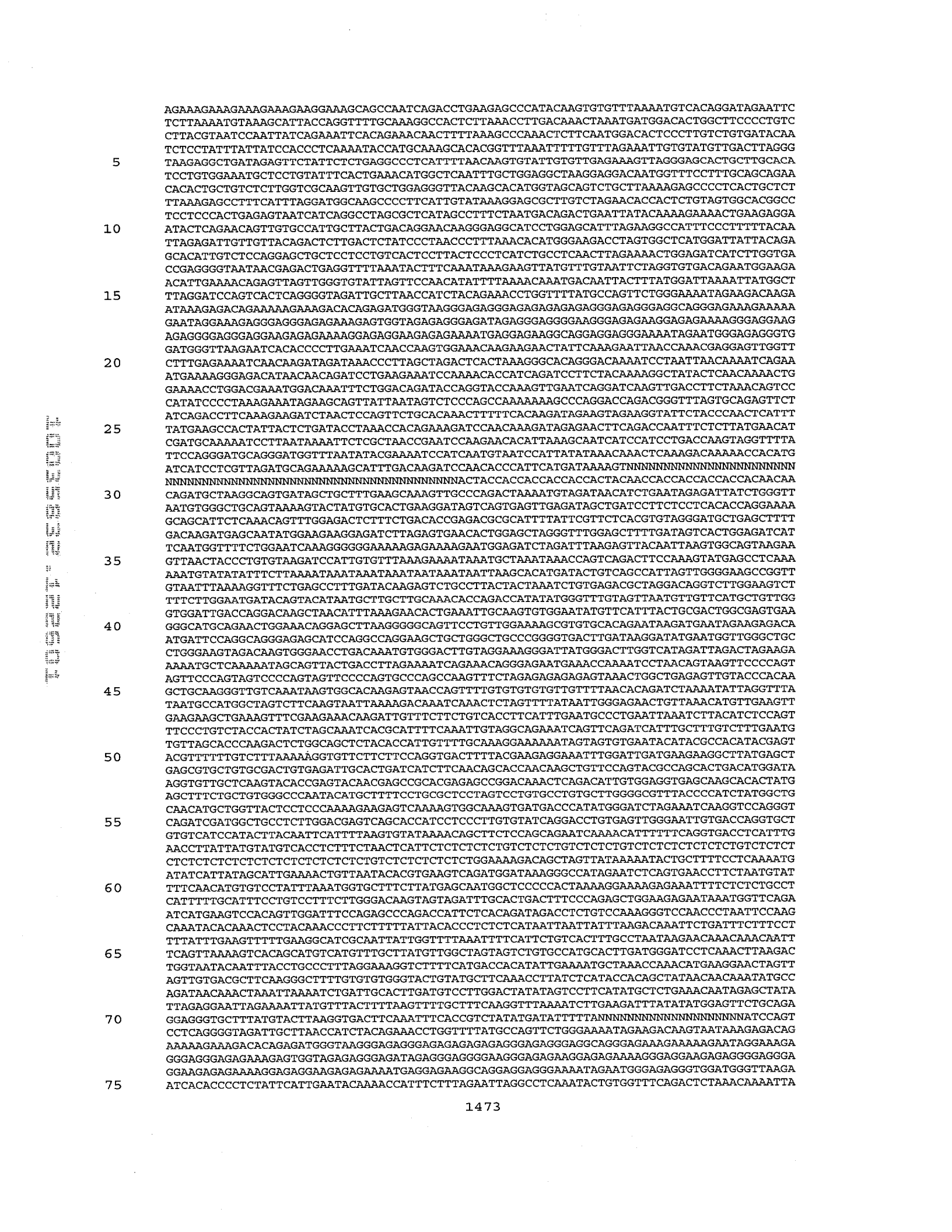


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Please see the Sequence Listing

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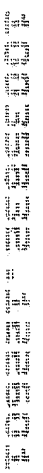
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MOUSE SEQUENCE - CODING
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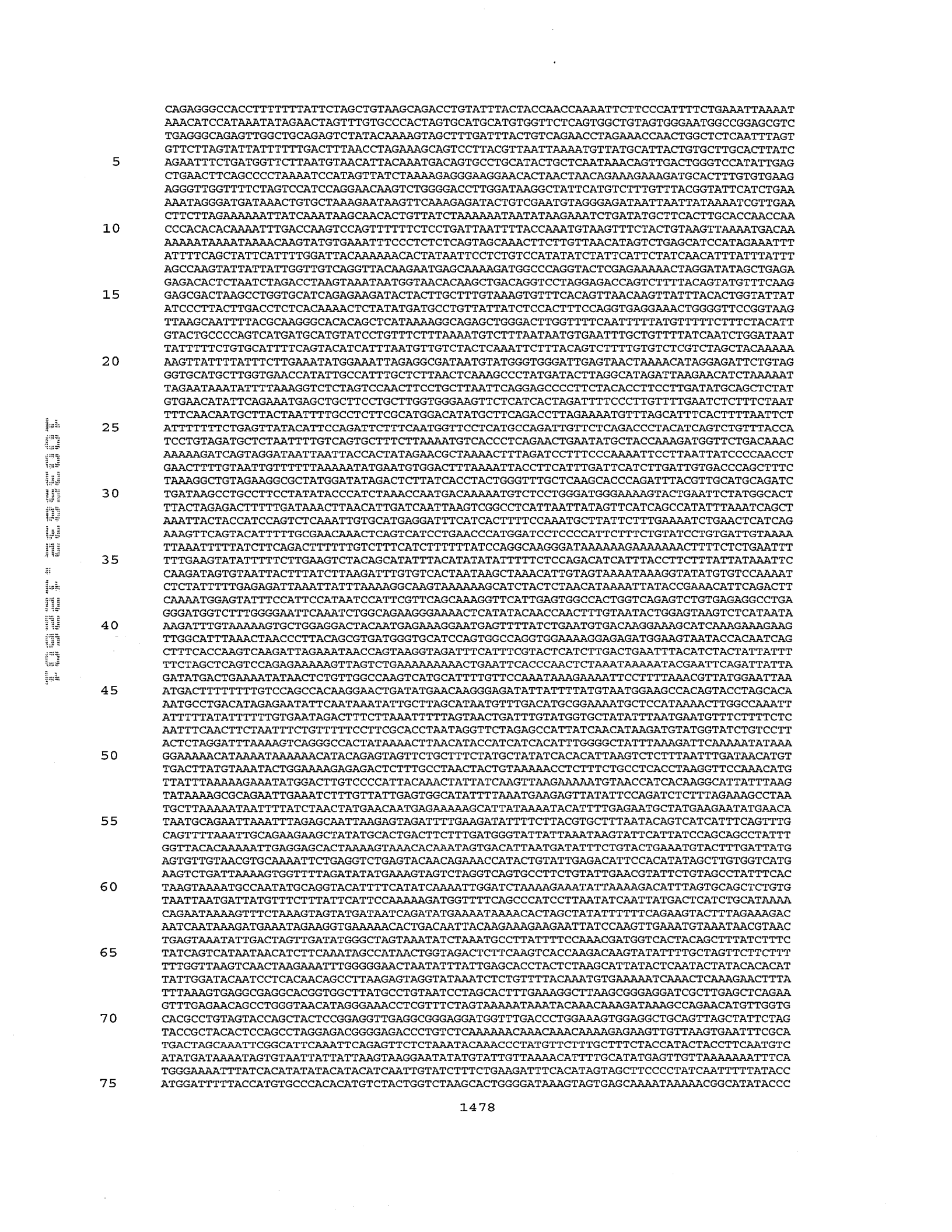
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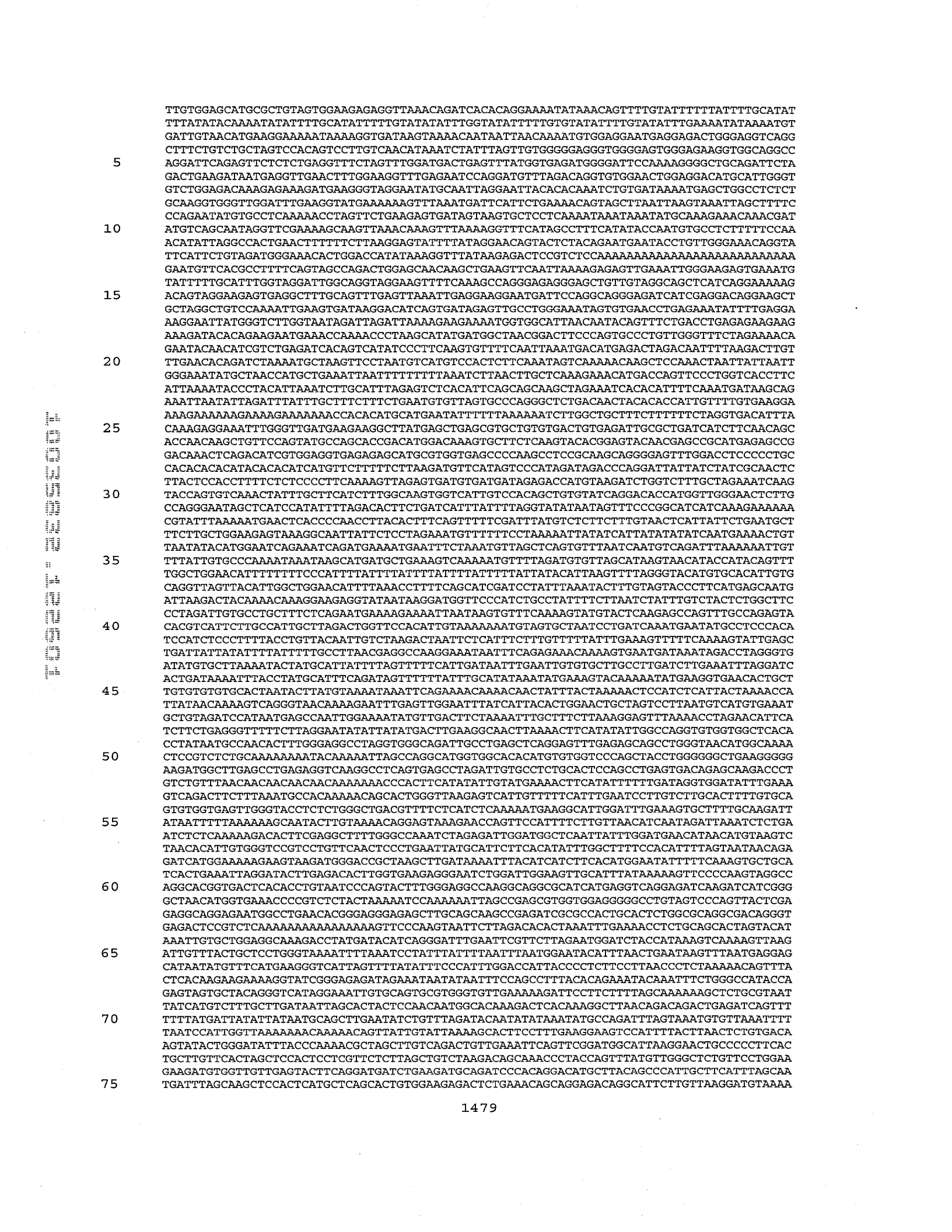
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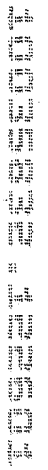
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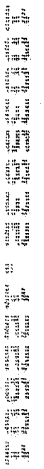
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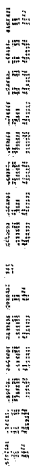
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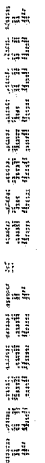
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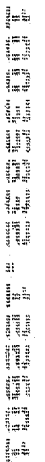


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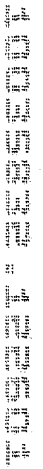


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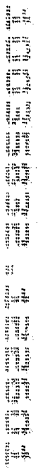
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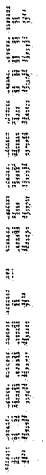
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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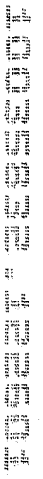
Table 70

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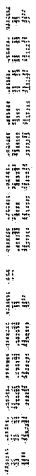
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MOUSE SEQUENCE - GENOMIC

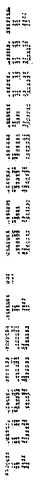
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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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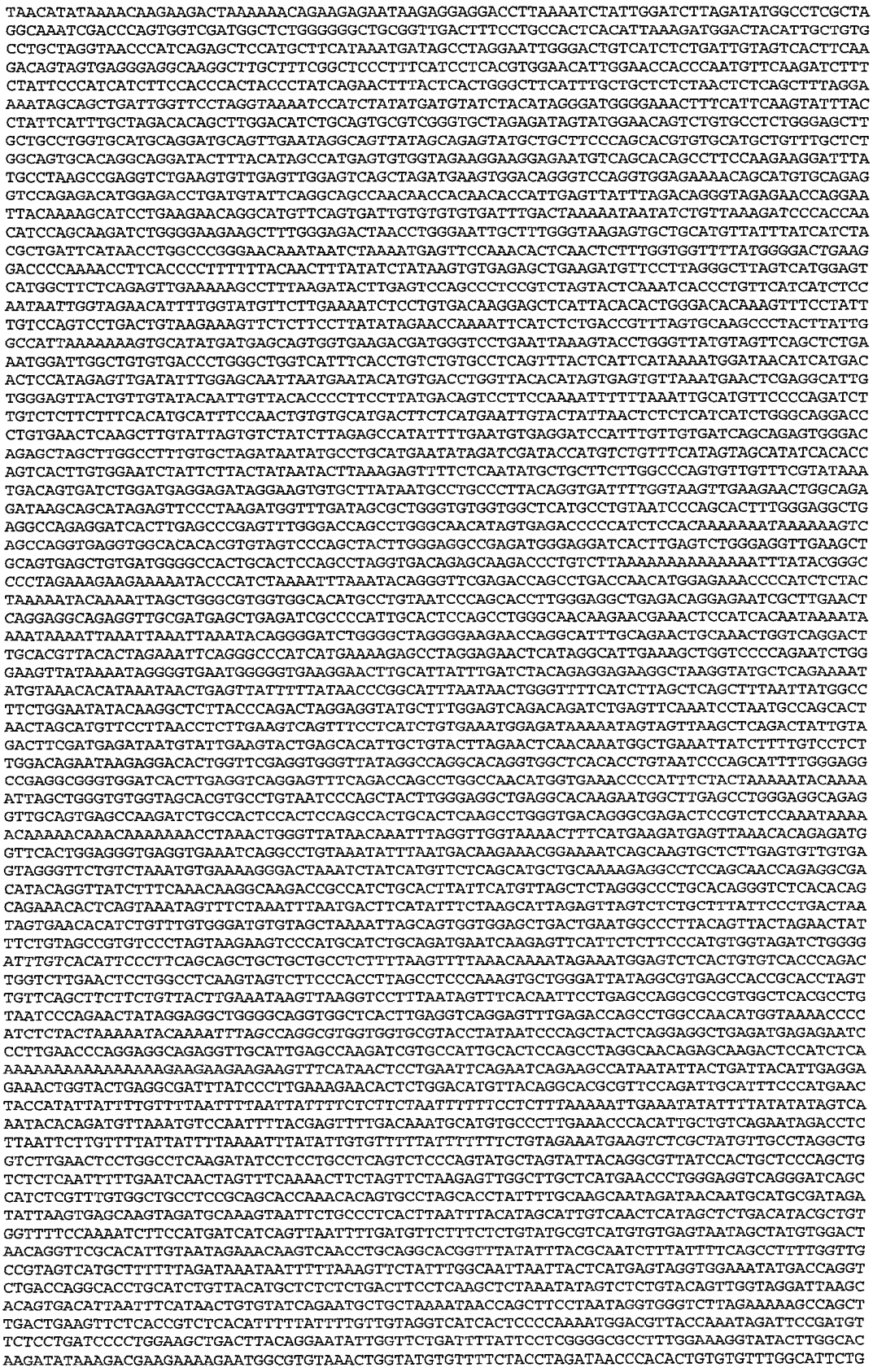
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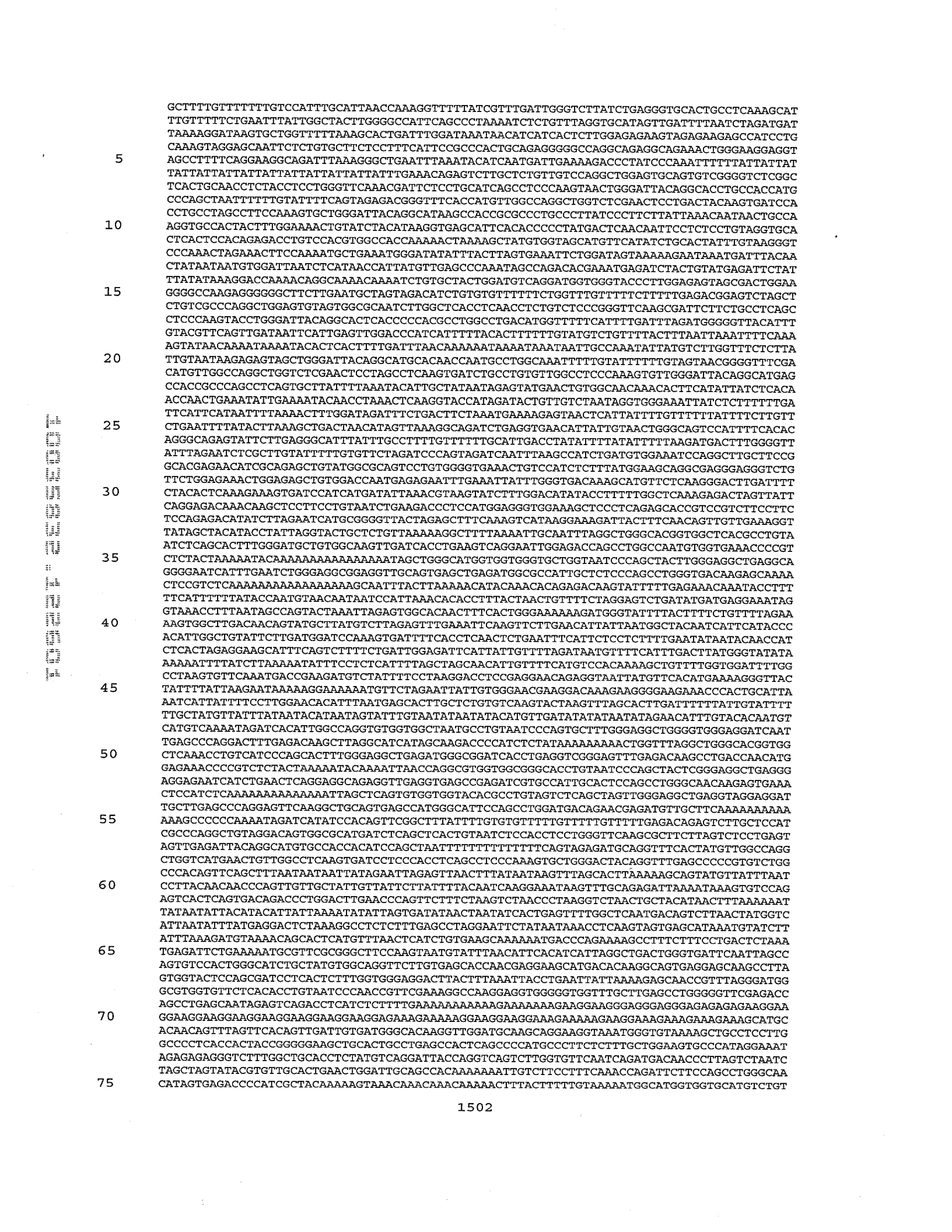


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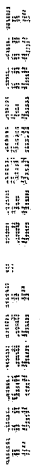


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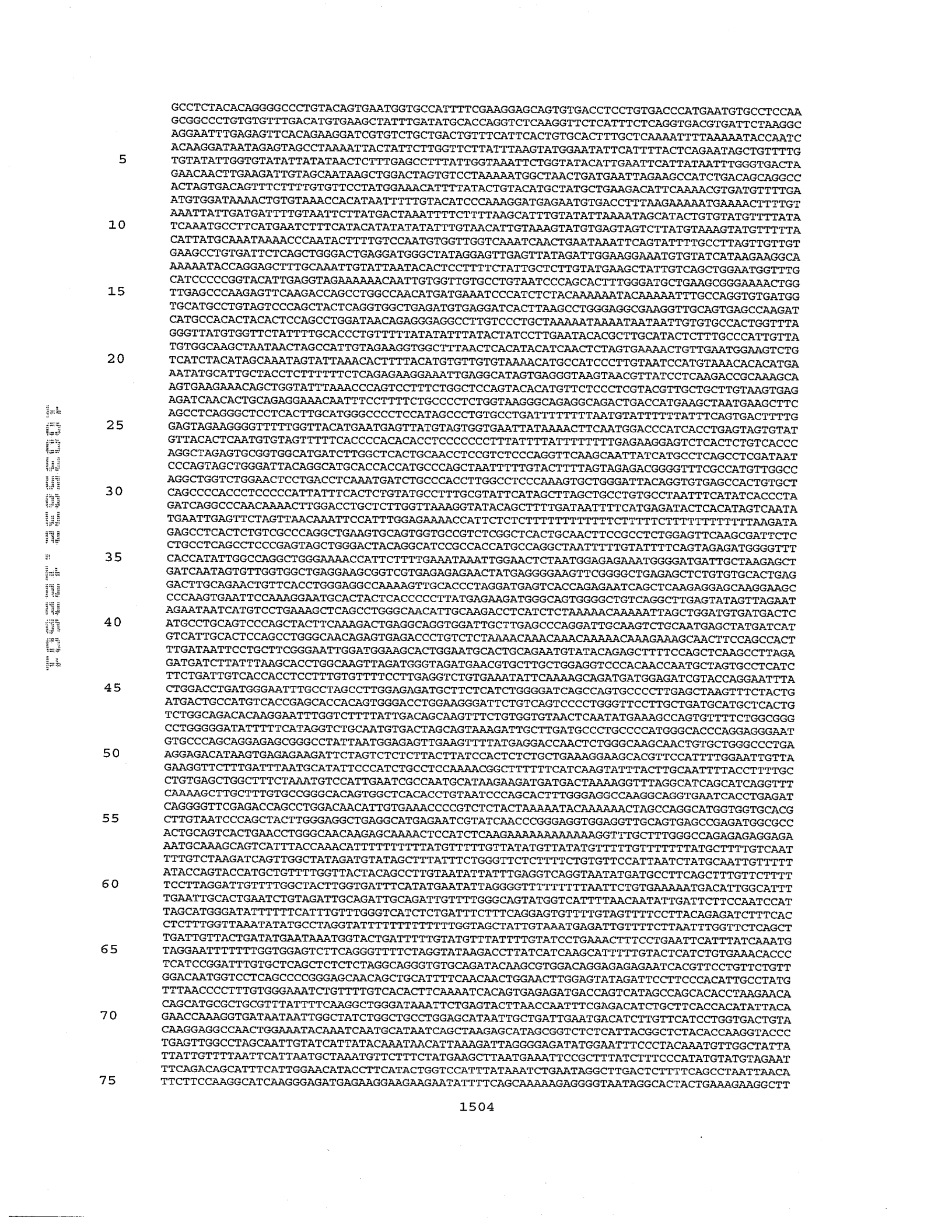




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55 HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 71

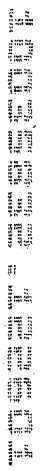
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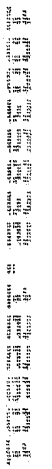
MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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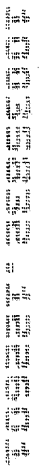
MOUSE SEQUENCE - CODING

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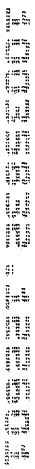
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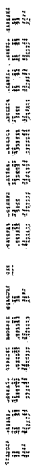
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 72

MOUSE NOMENCLATURE
ICSGNM Cbx8
Celera mCG13904

HUMAN NOMENCLATURE
HGNC CBX8
Celera hCG28570

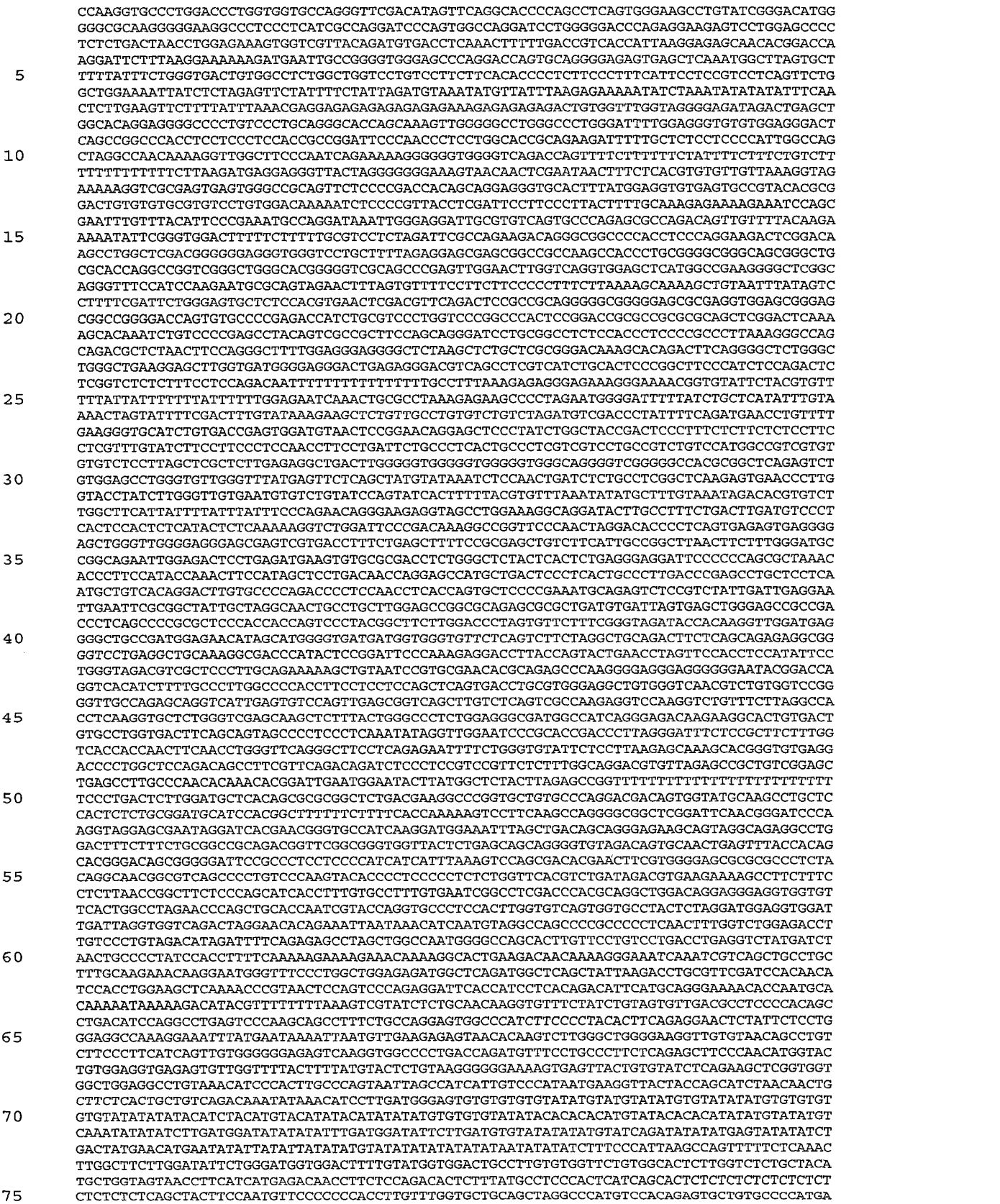
MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 73

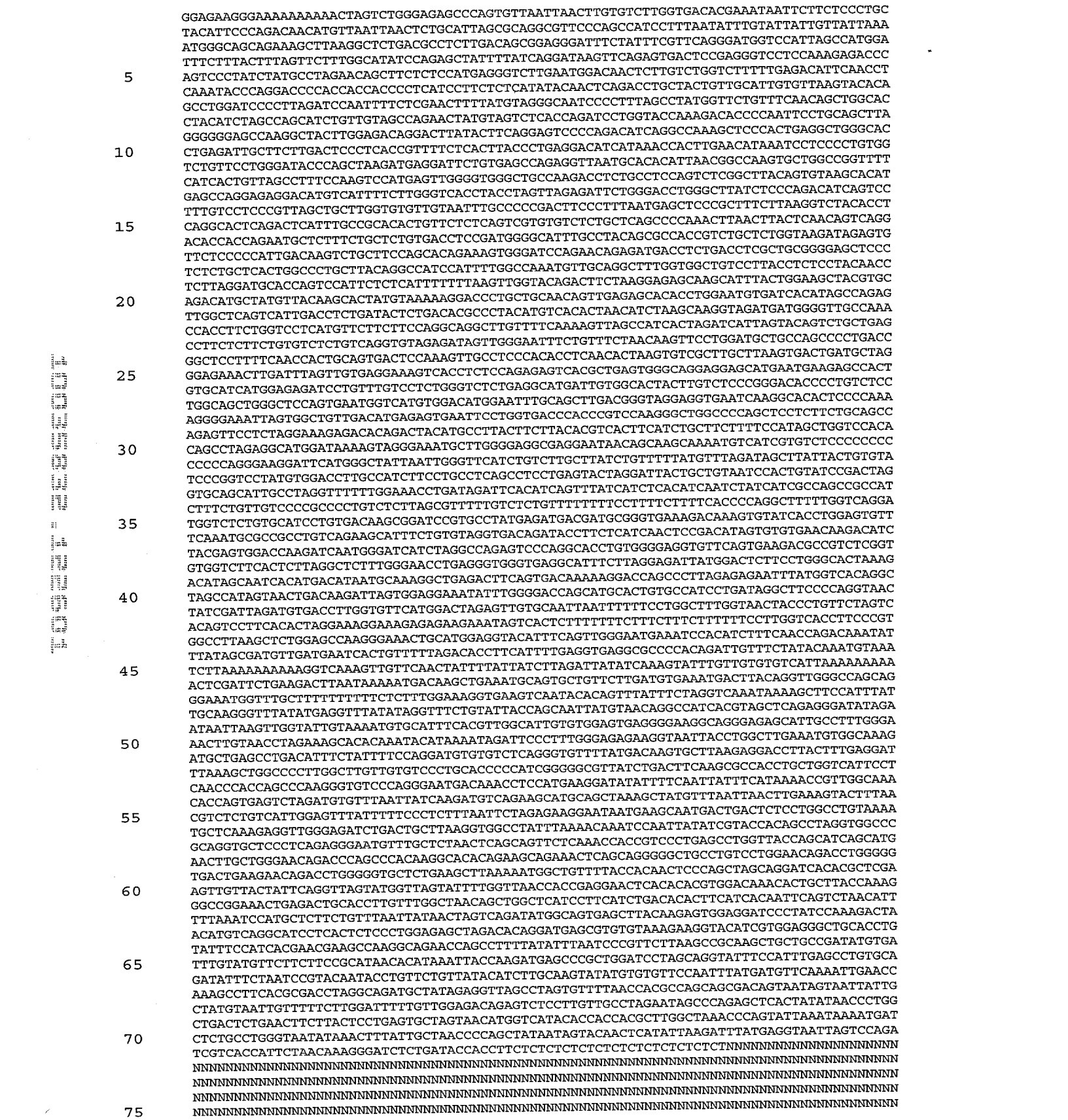
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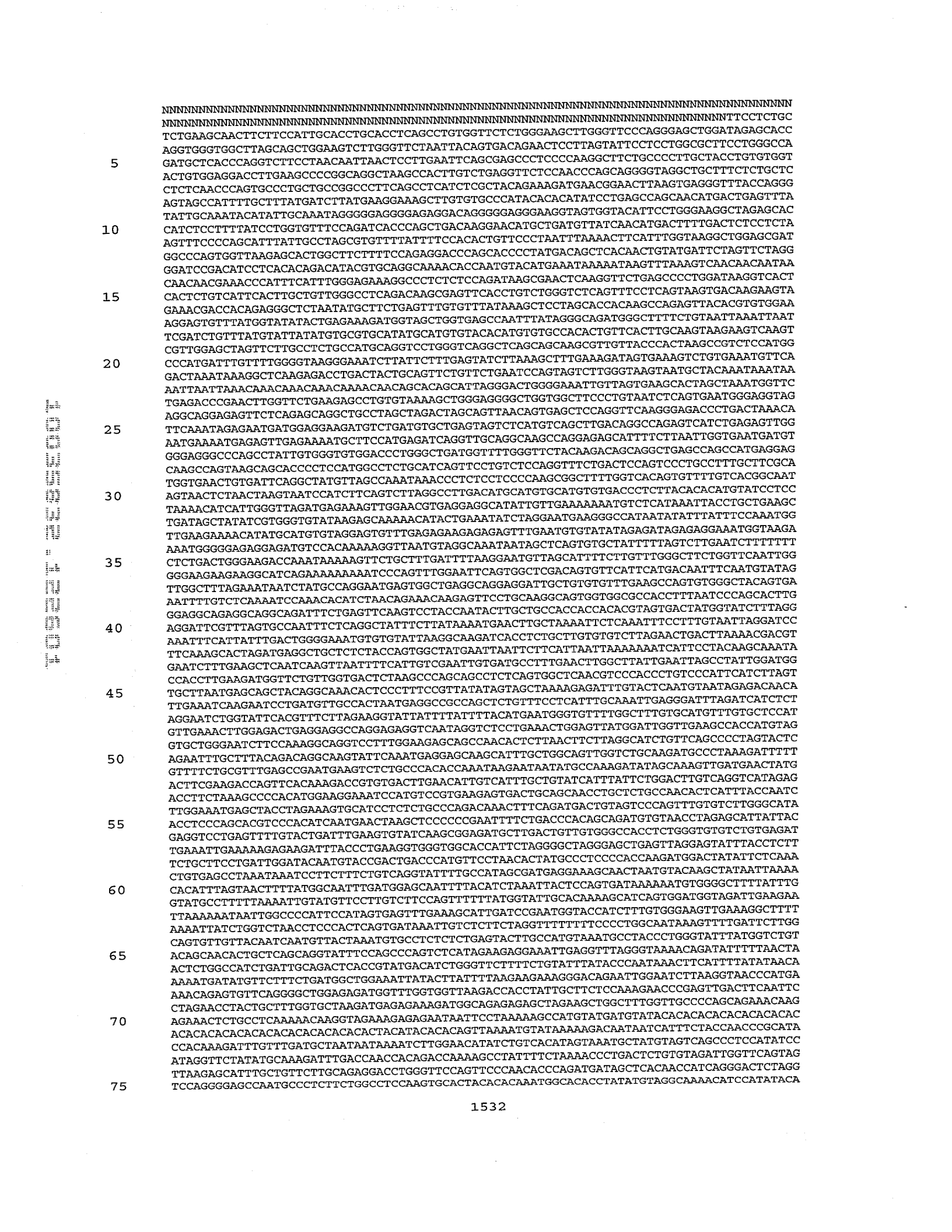
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MOUSE SEQUENCE - GENOMIC

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NNNN

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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

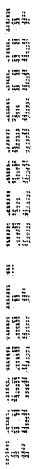
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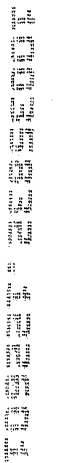
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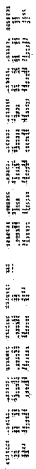


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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 74

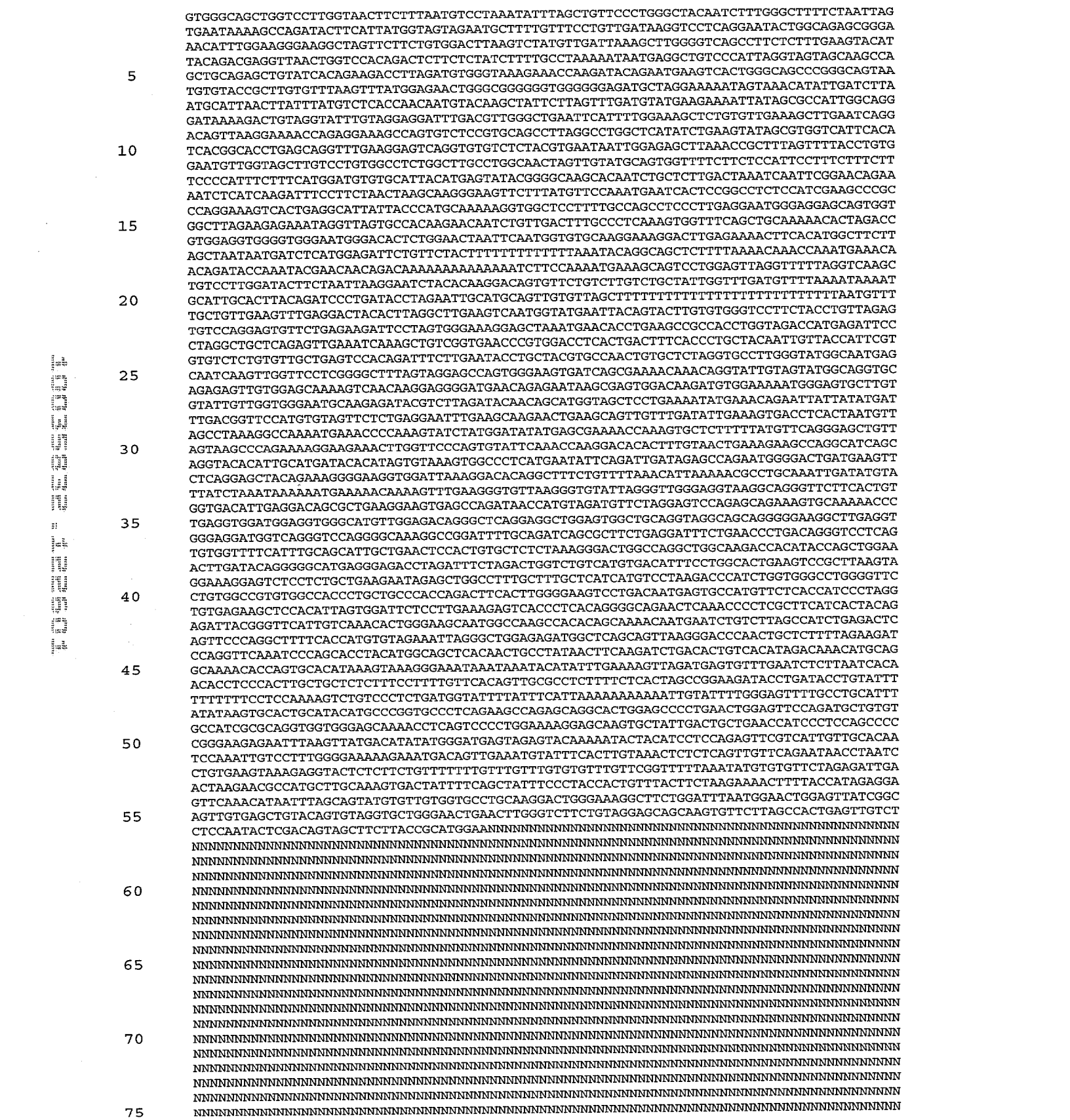
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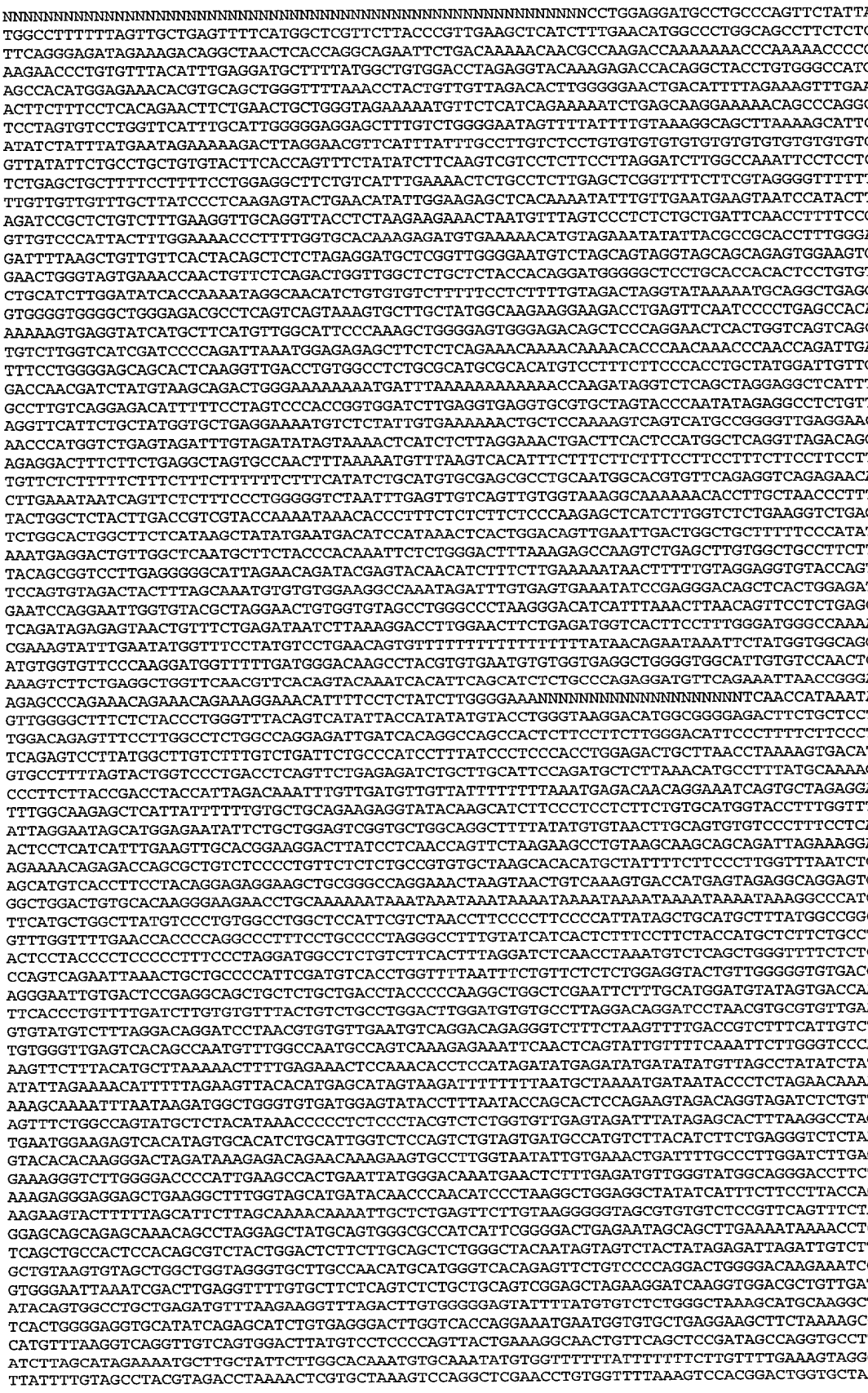
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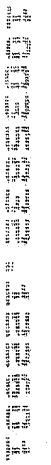
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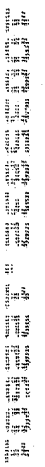


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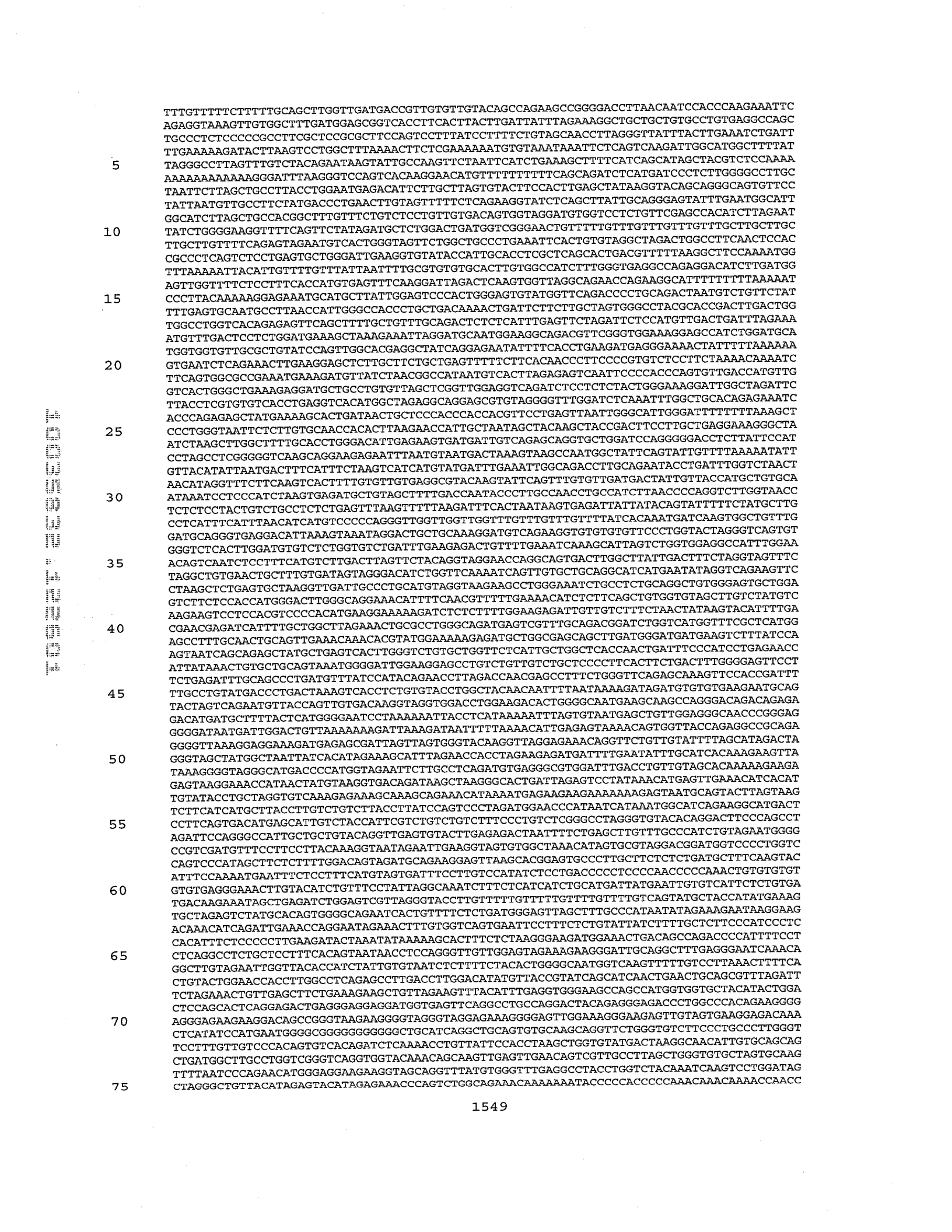




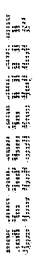
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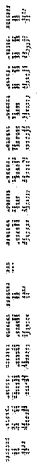
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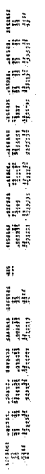
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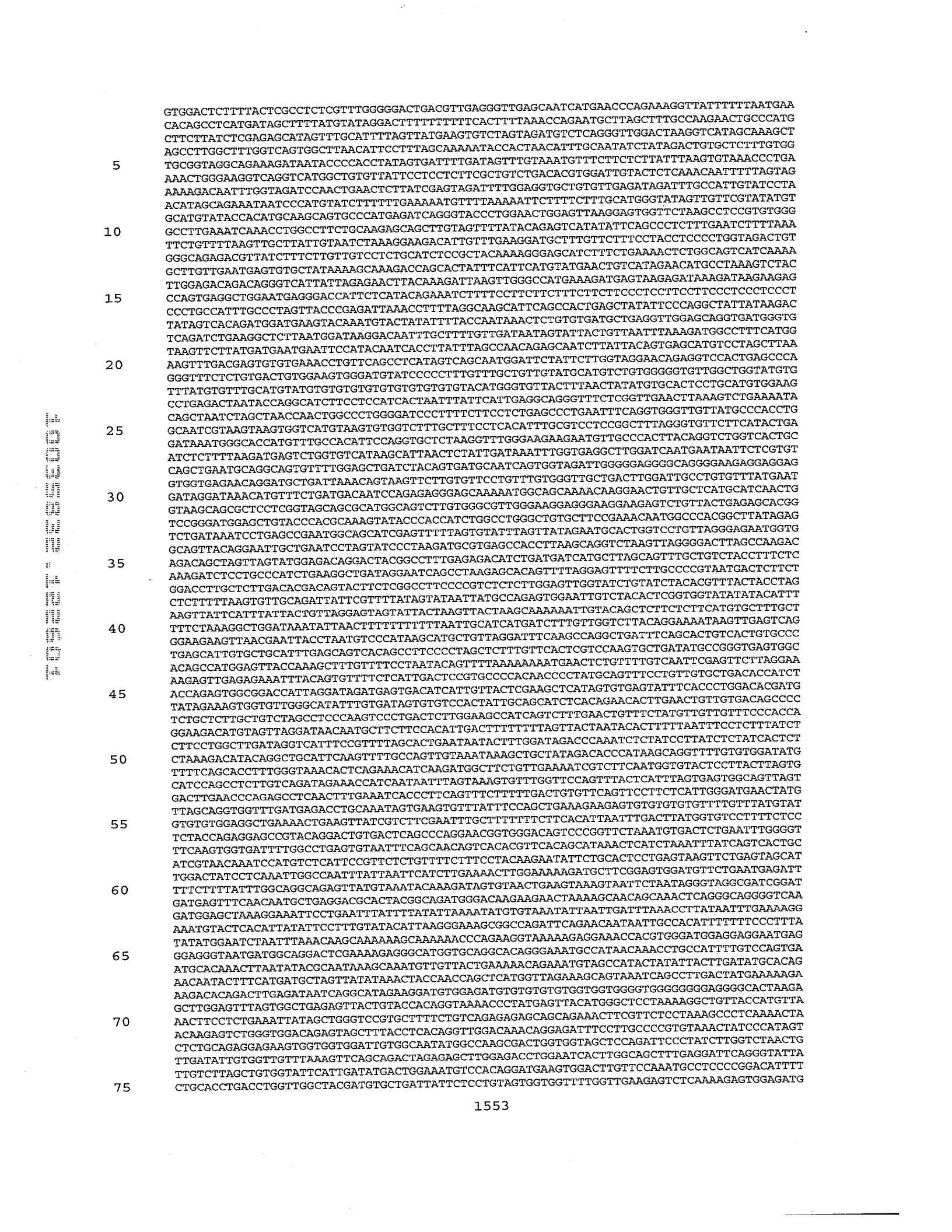
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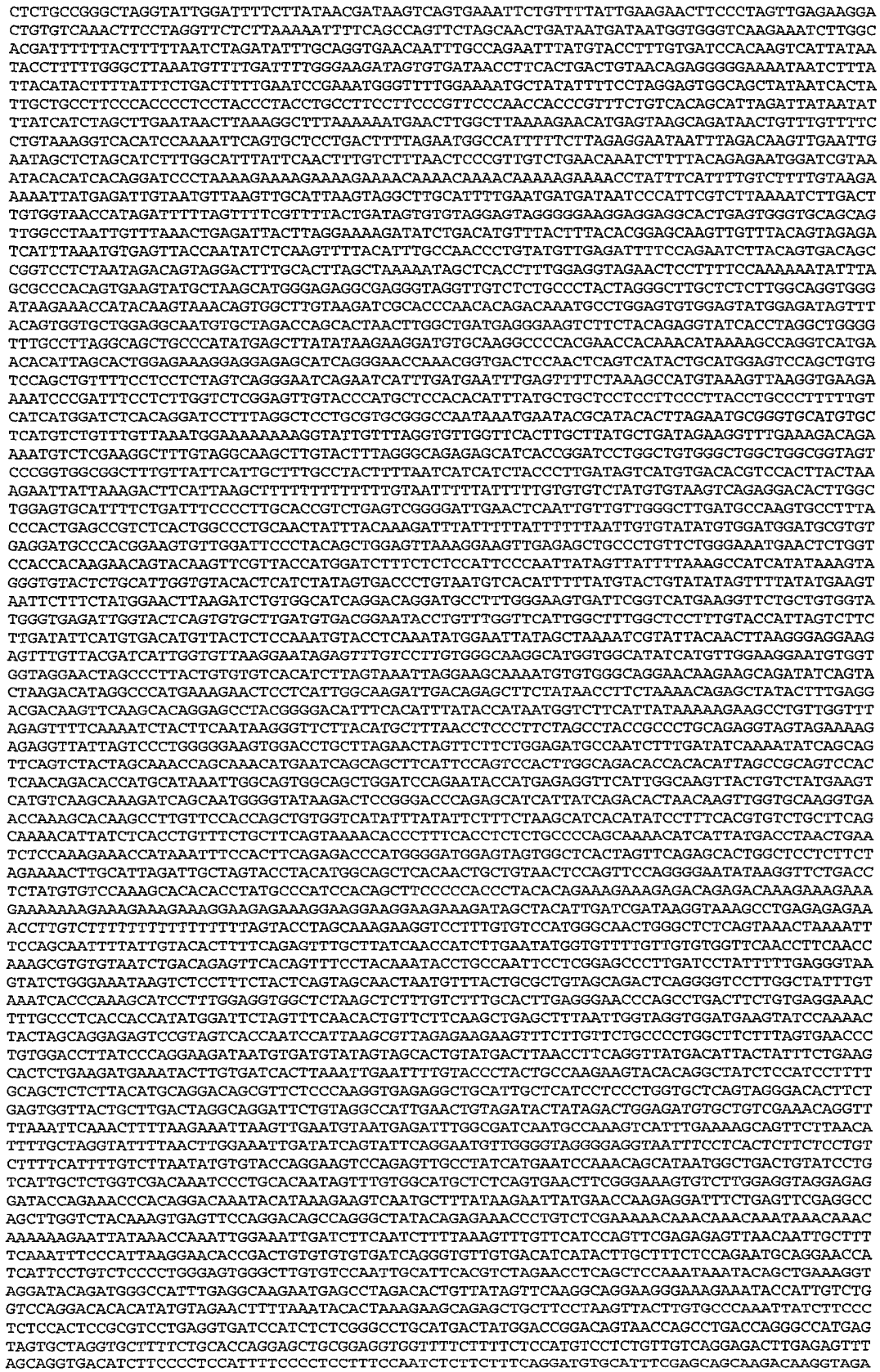


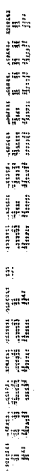
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Replacement Sheet - 2nd Set of Sequence Listing

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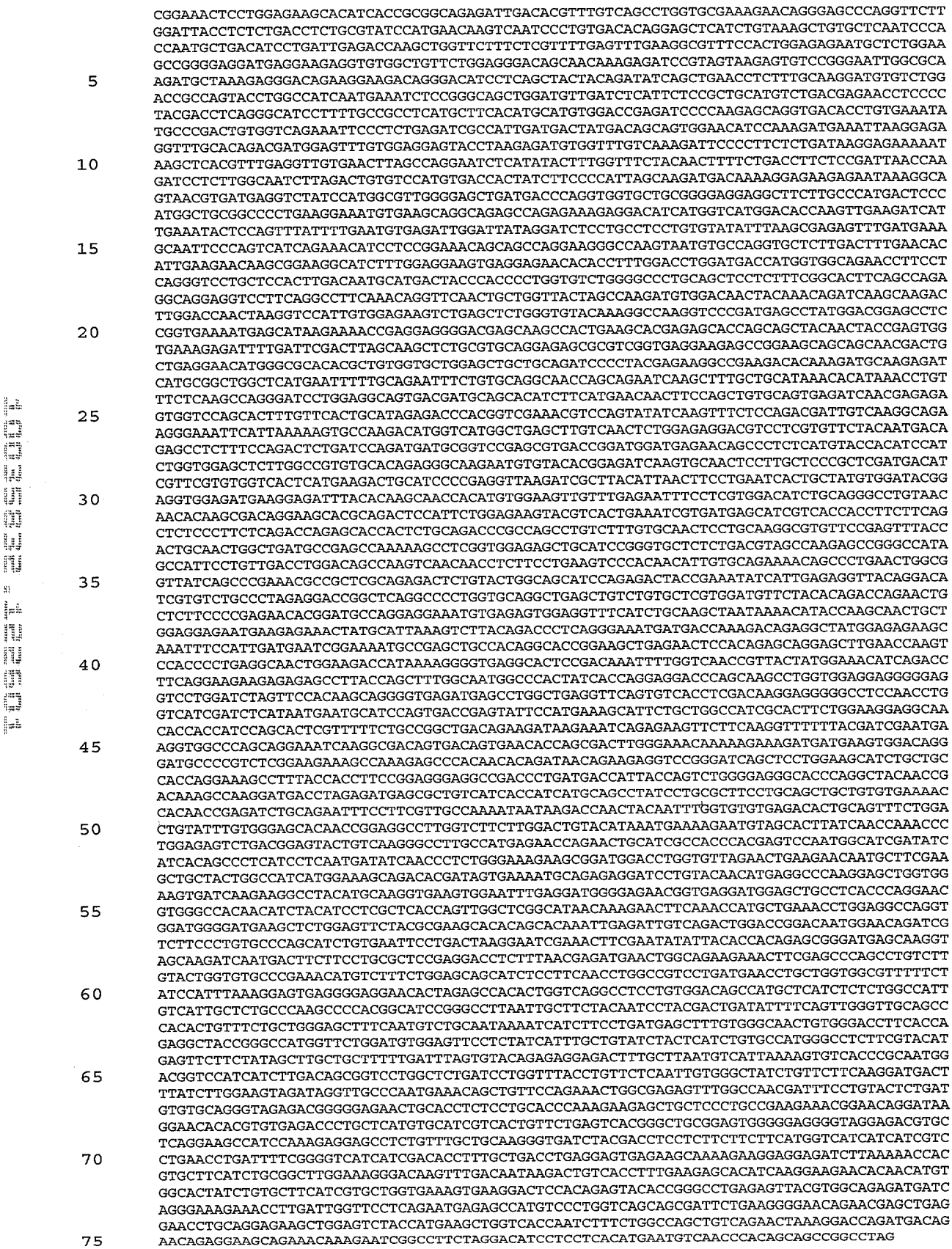
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MOUSE SEQUENCE - mRNA
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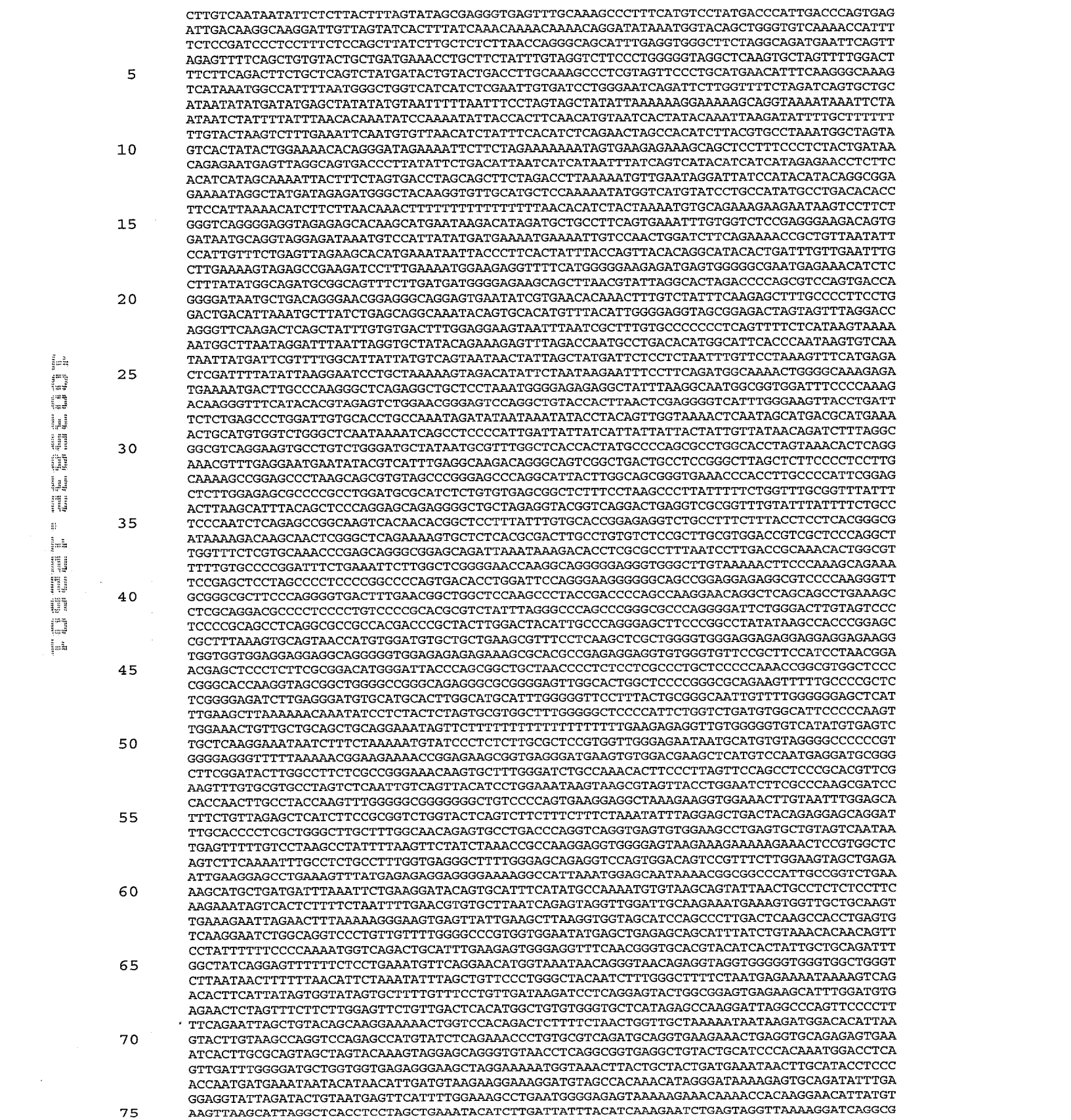
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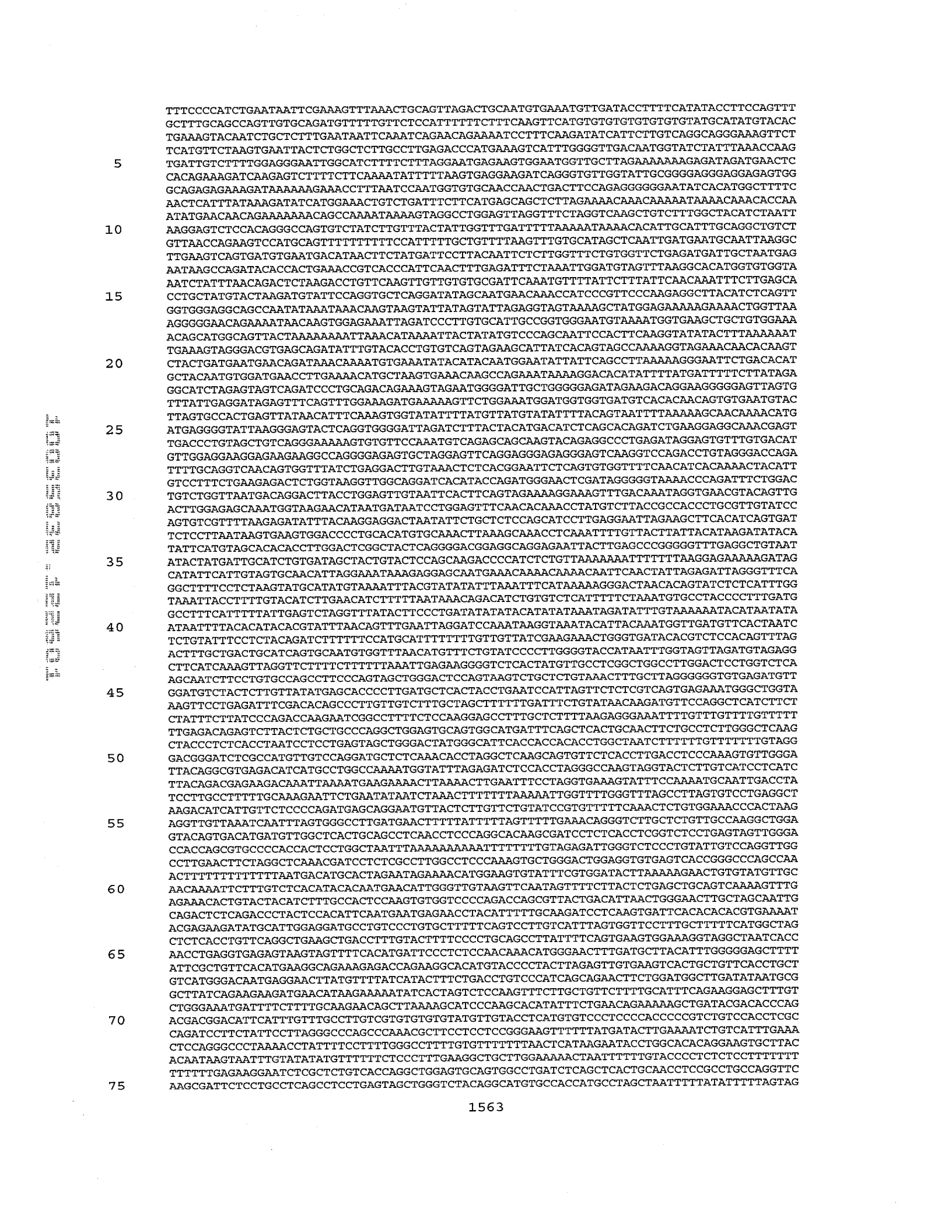
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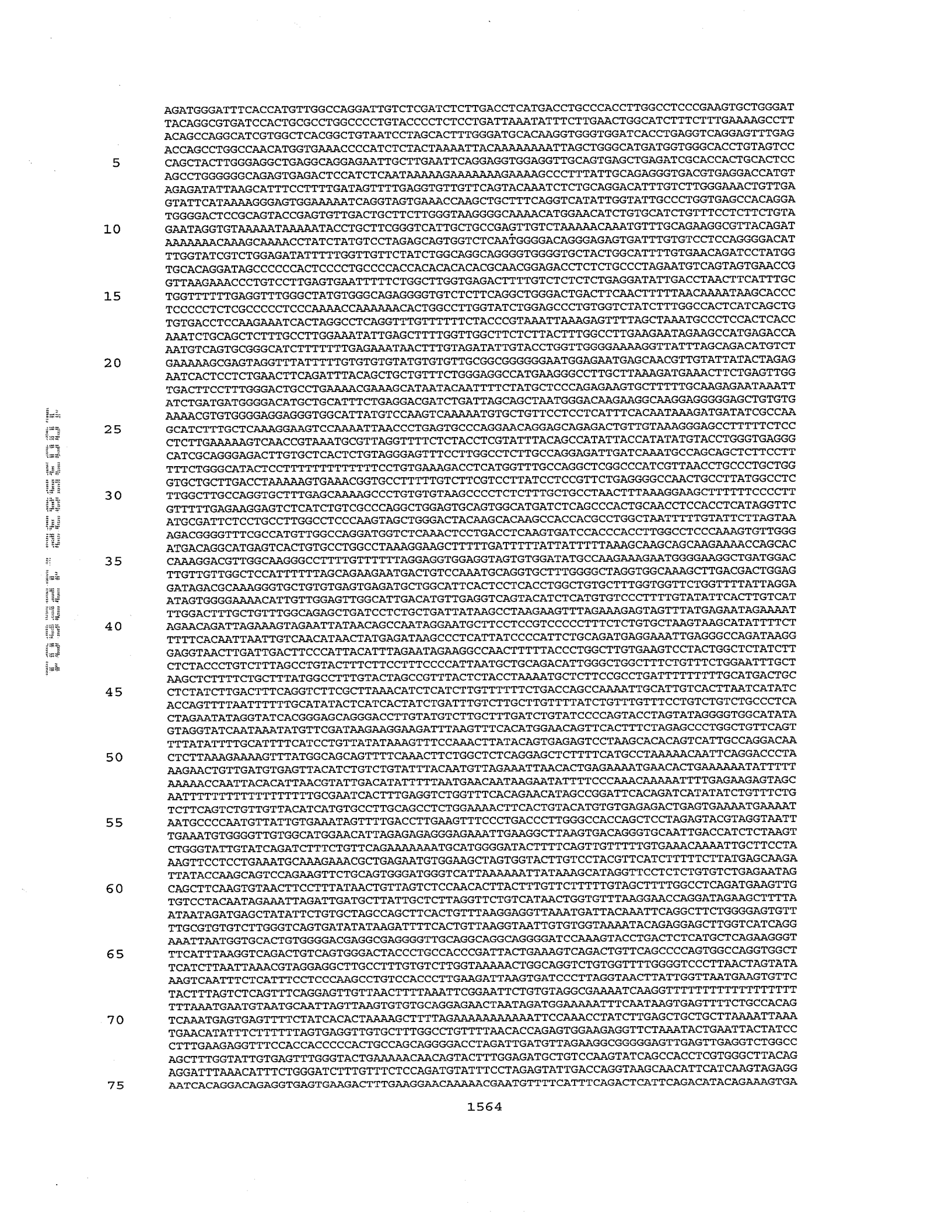
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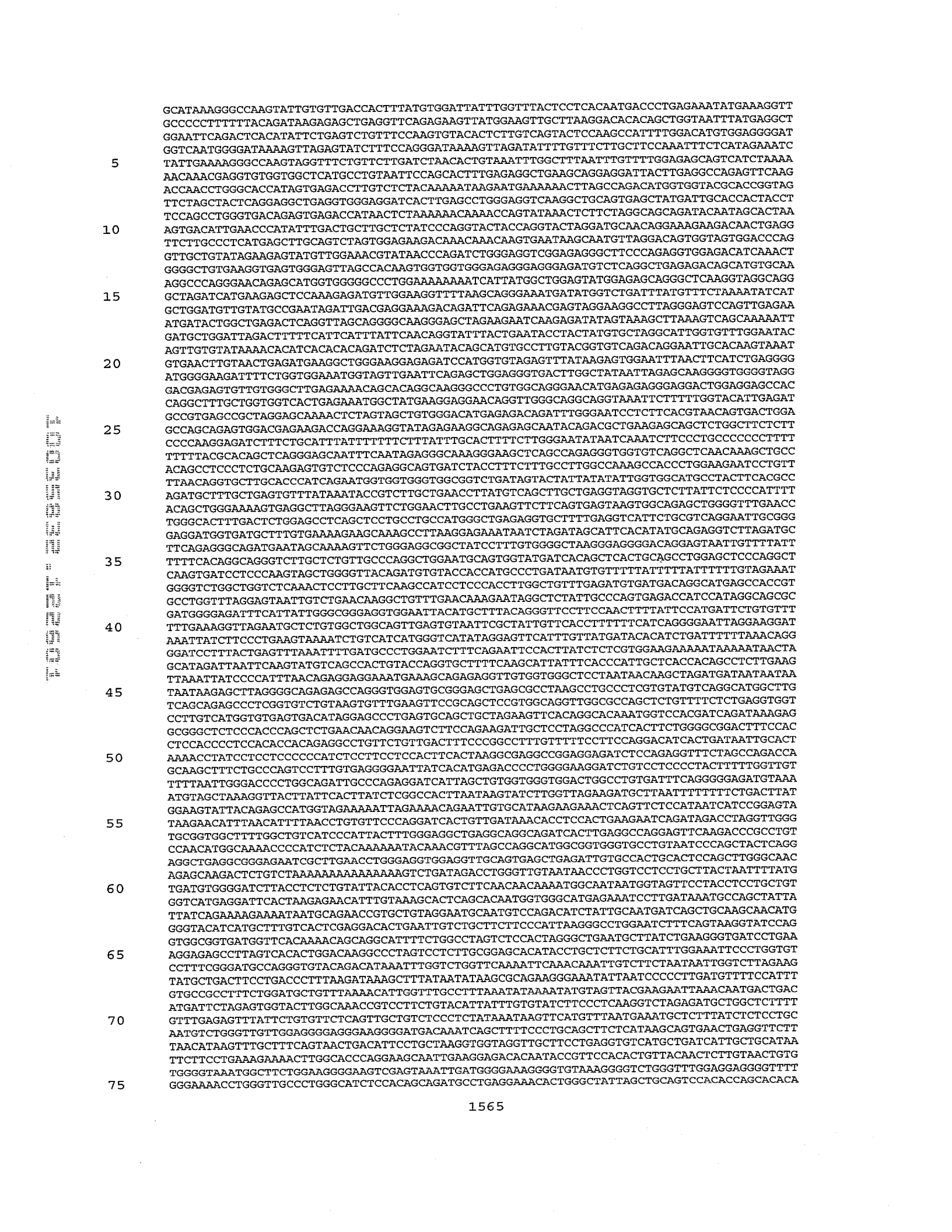
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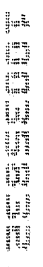




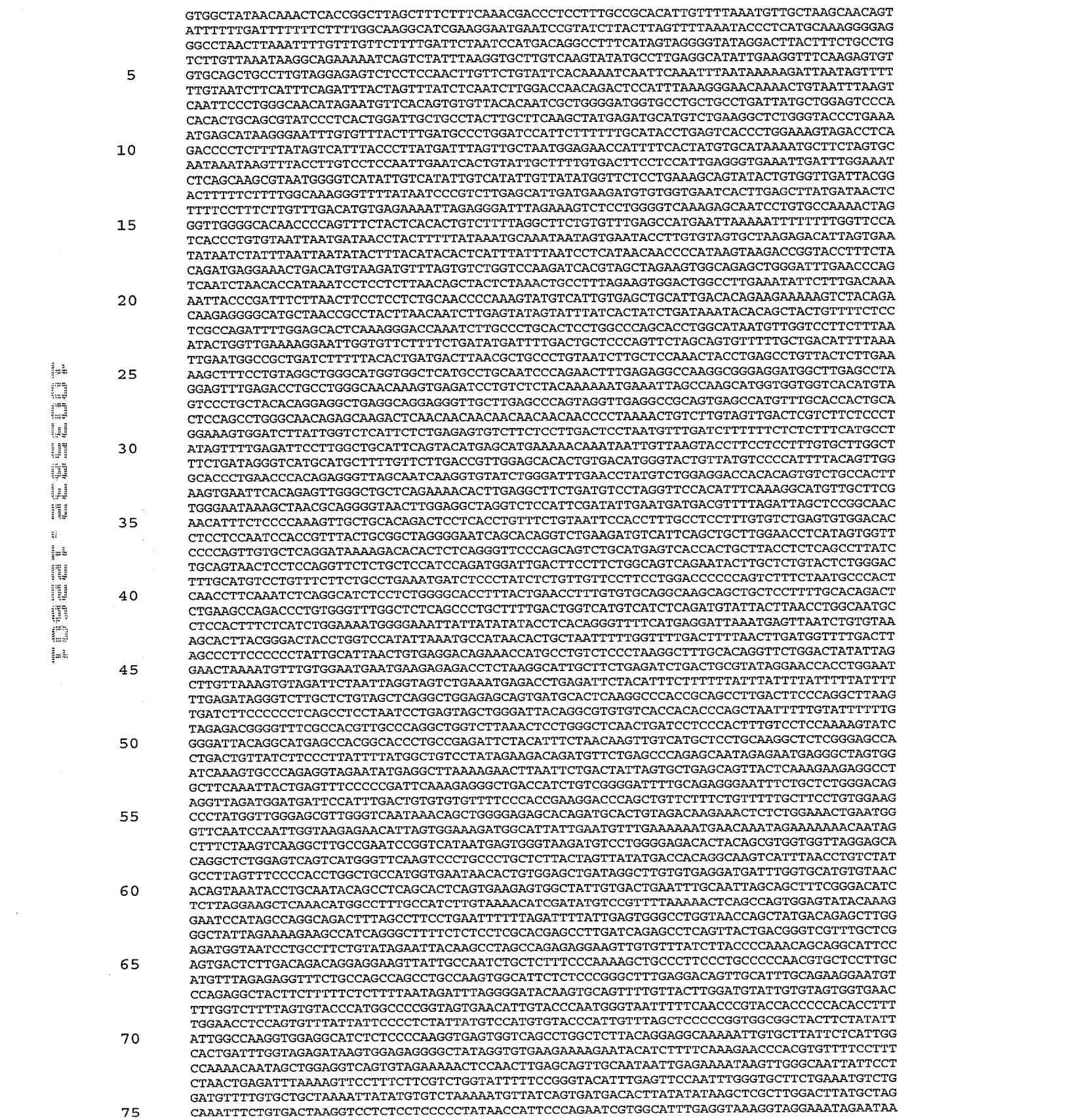
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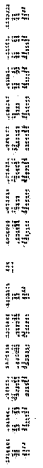
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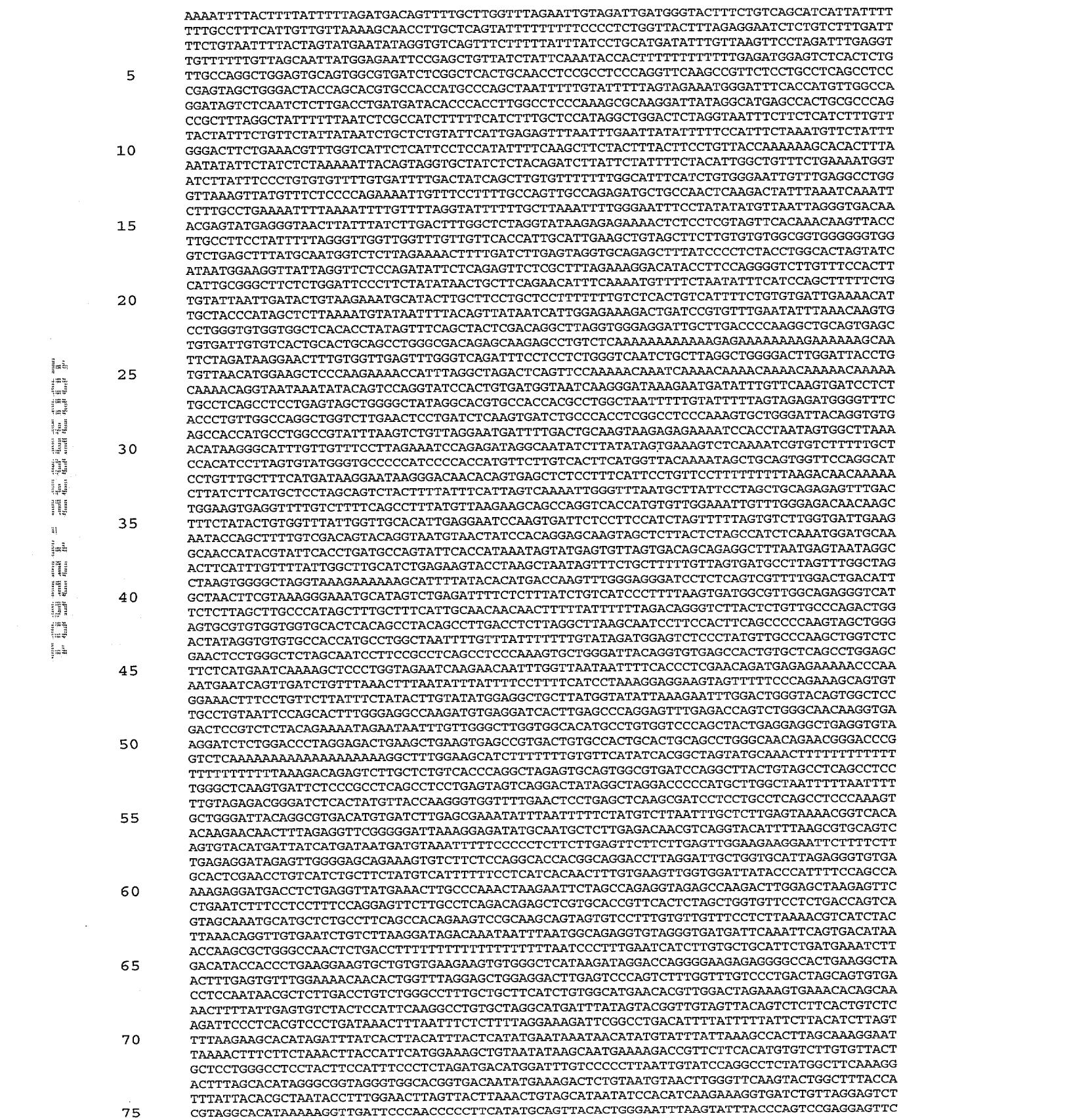


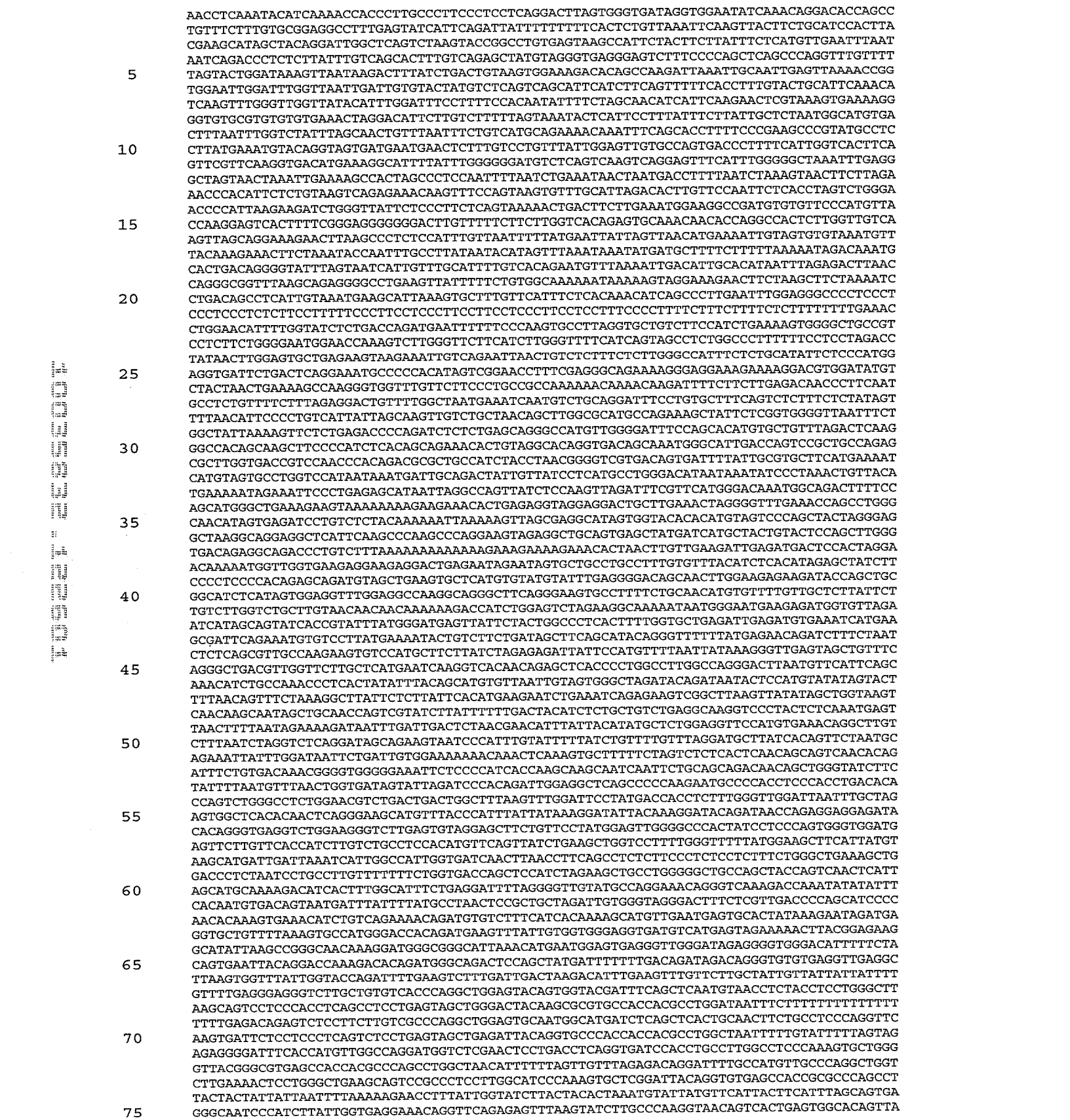
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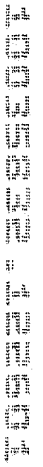




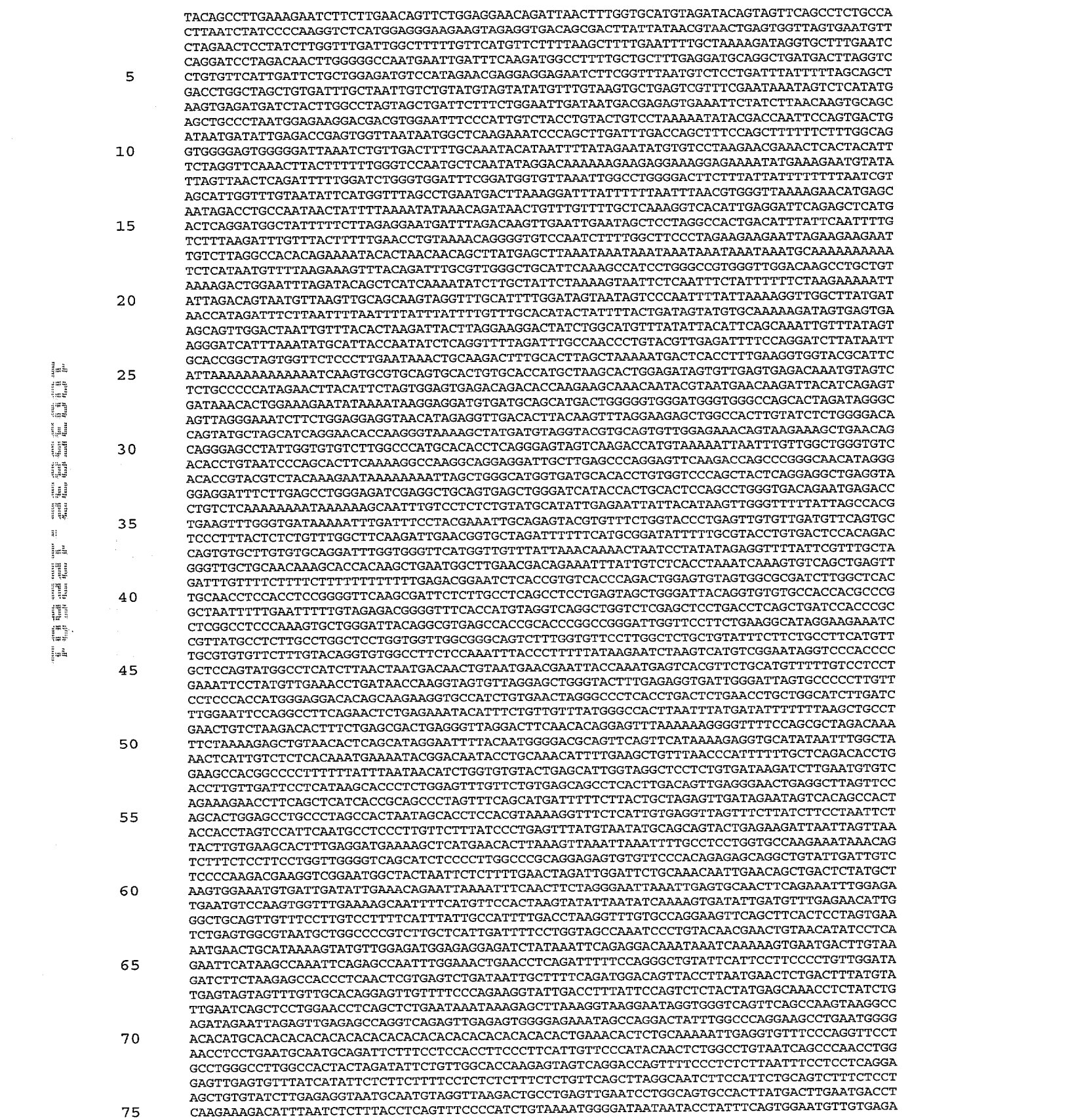
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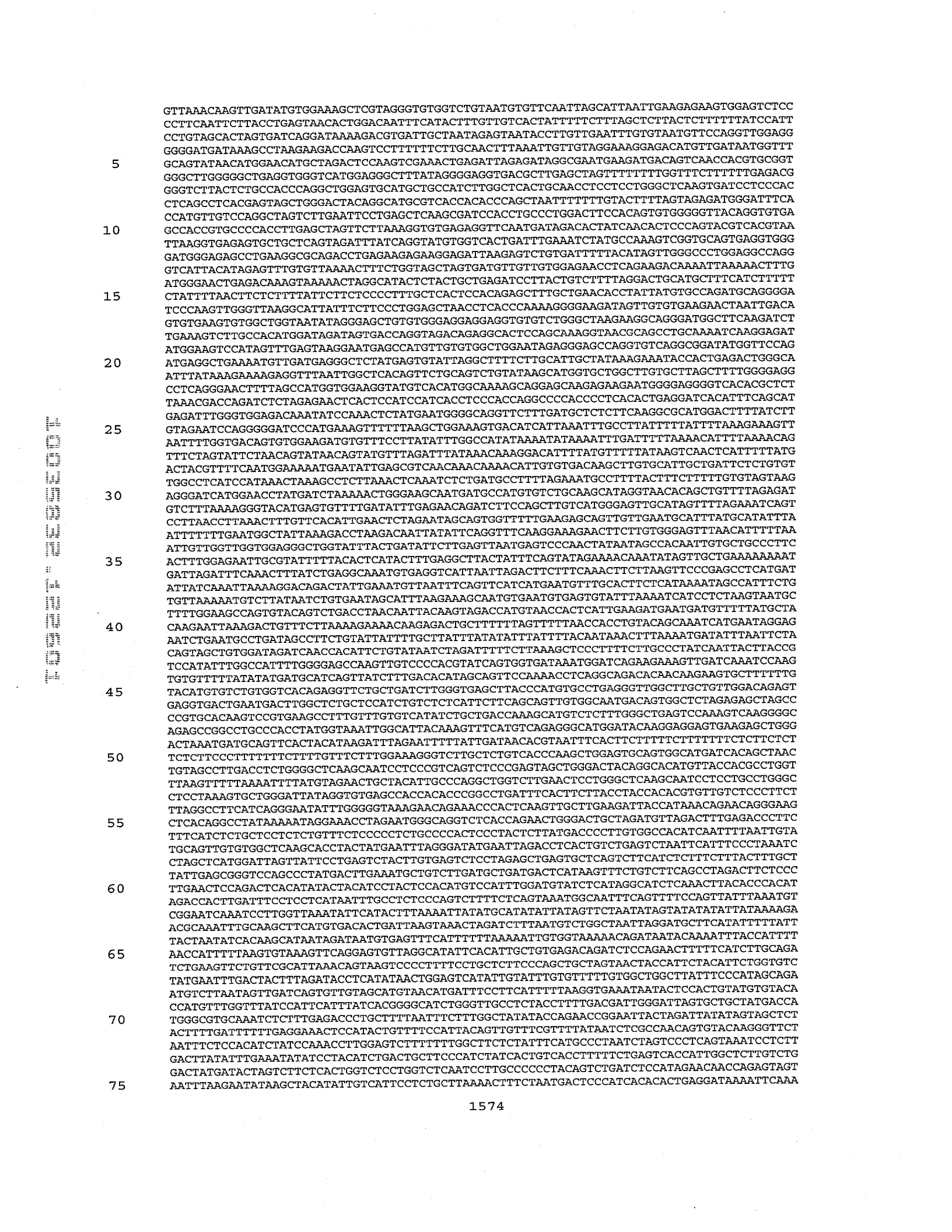


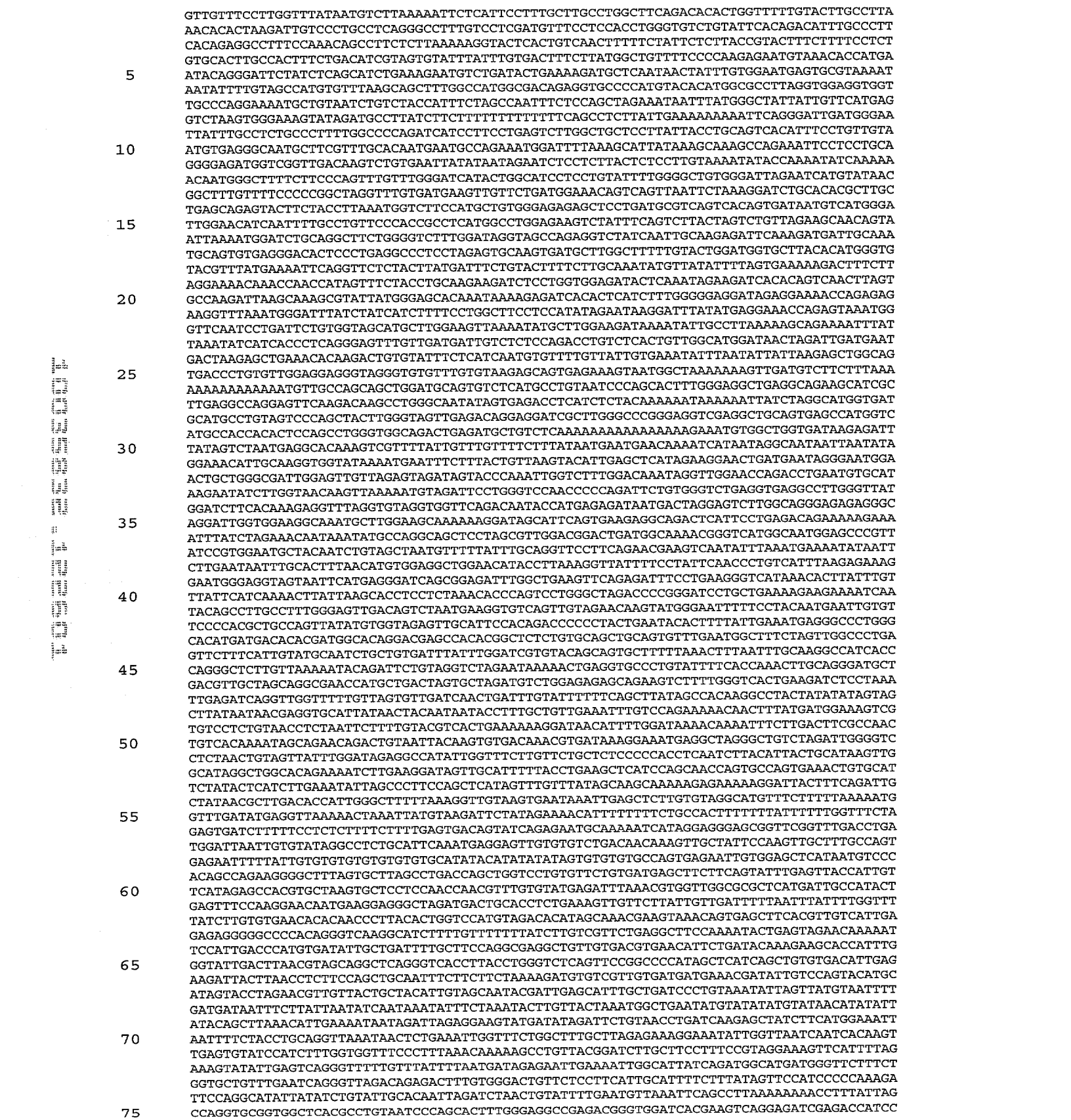


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HUMAN SEQUENCE - mRNA

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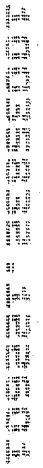
Table 75

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Celera mCG9377

HUMAN NOMENCLATURE
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Celera hCG37088

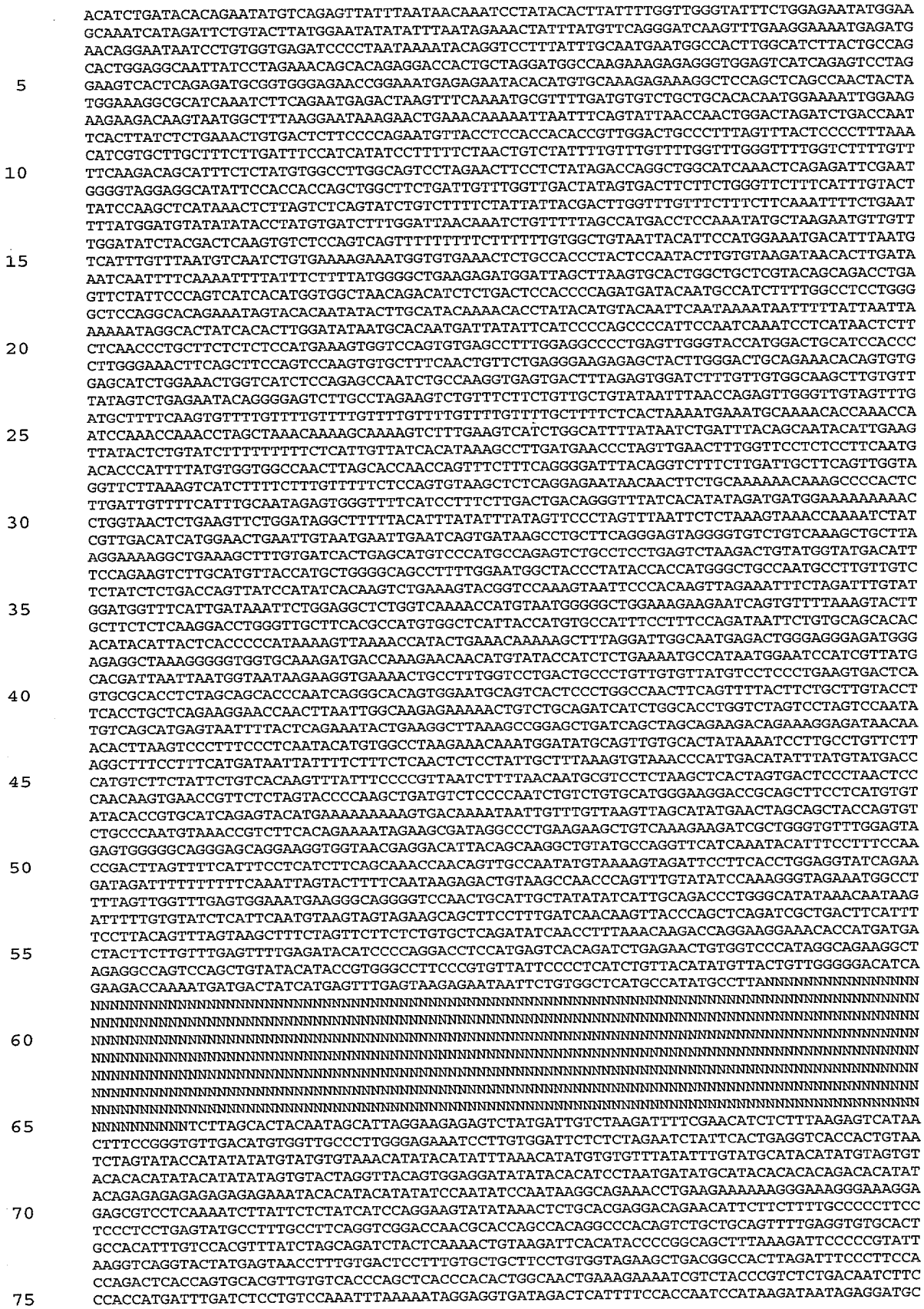
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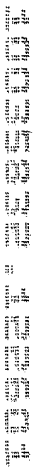
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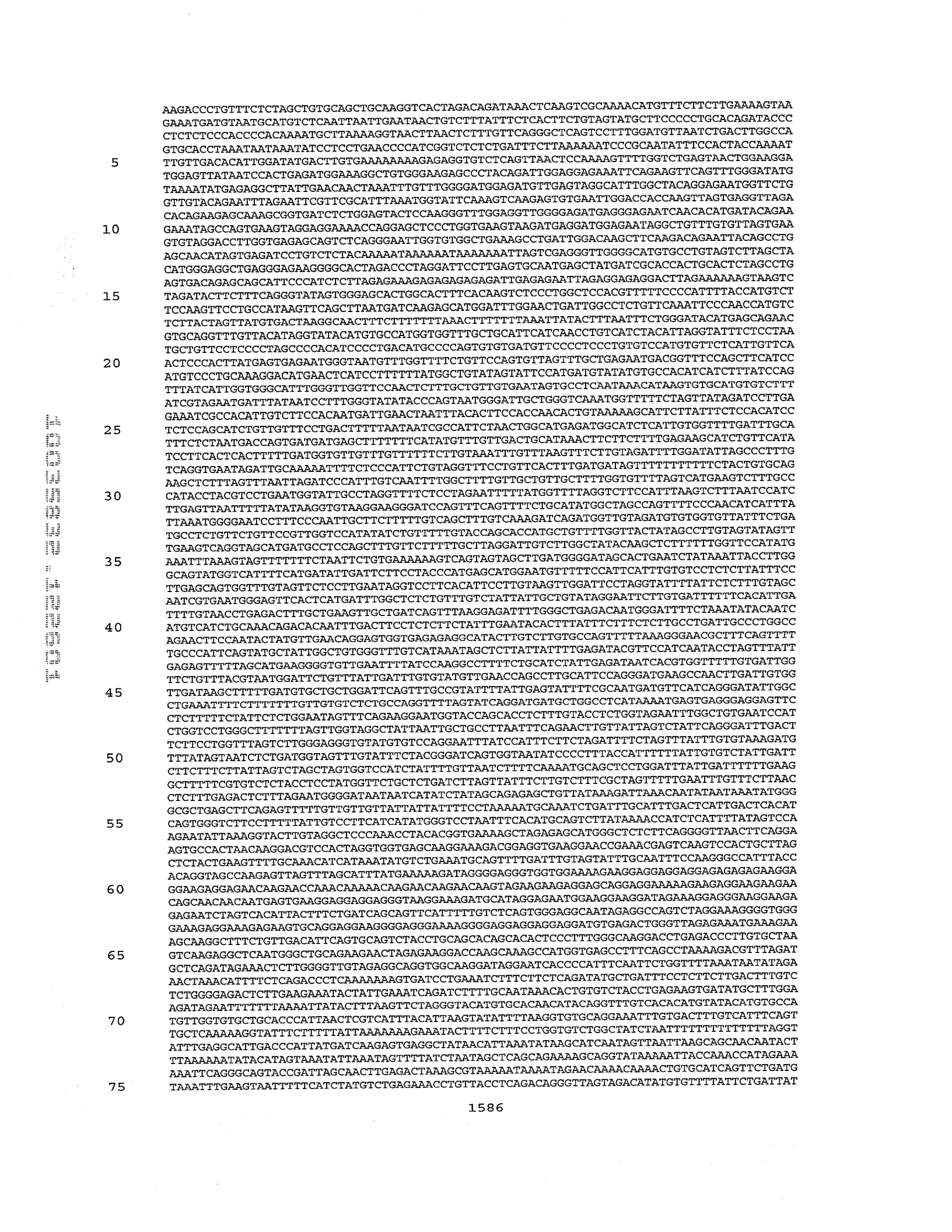
MOUSE SEQUENCE - mRNA

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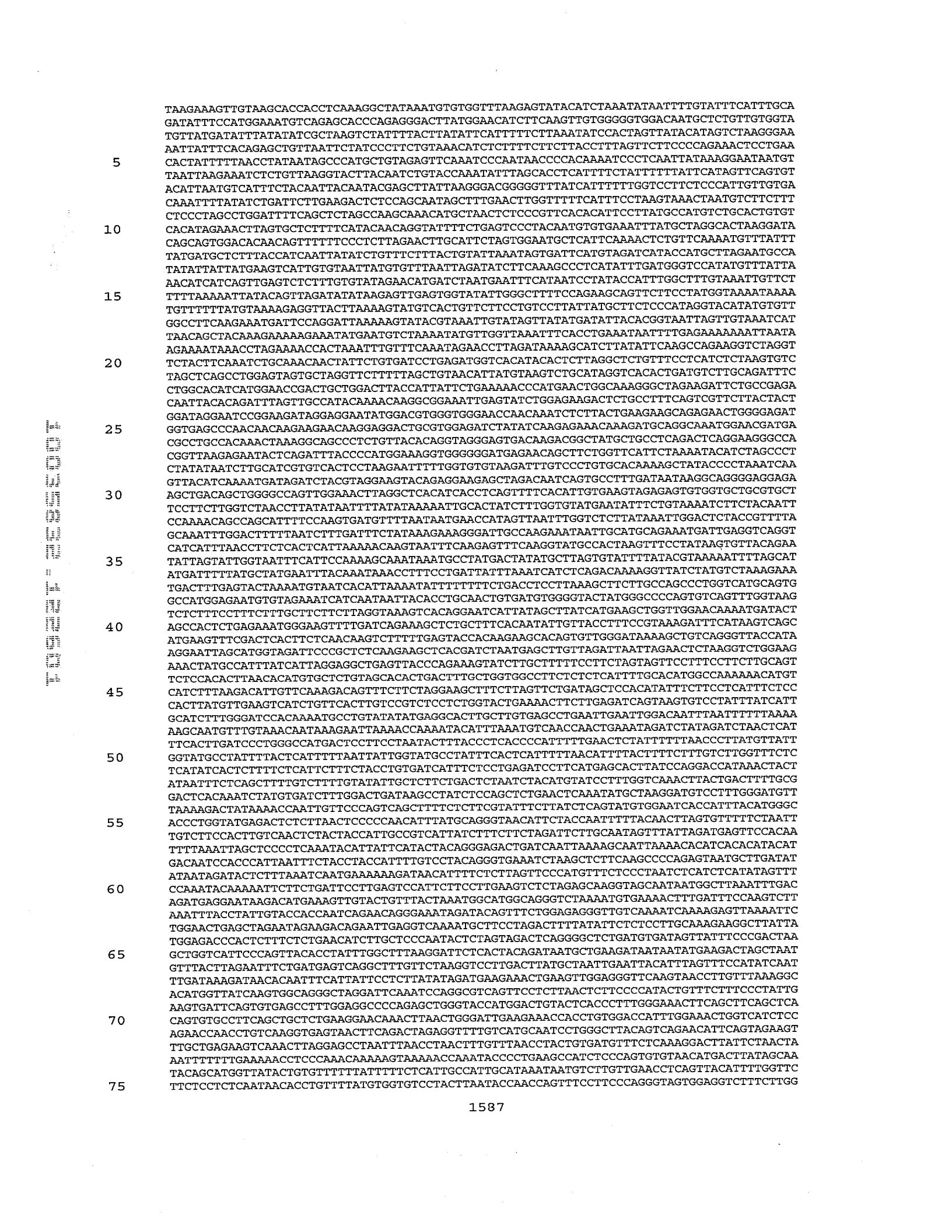
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MOUSE SEQUENCE - CODING
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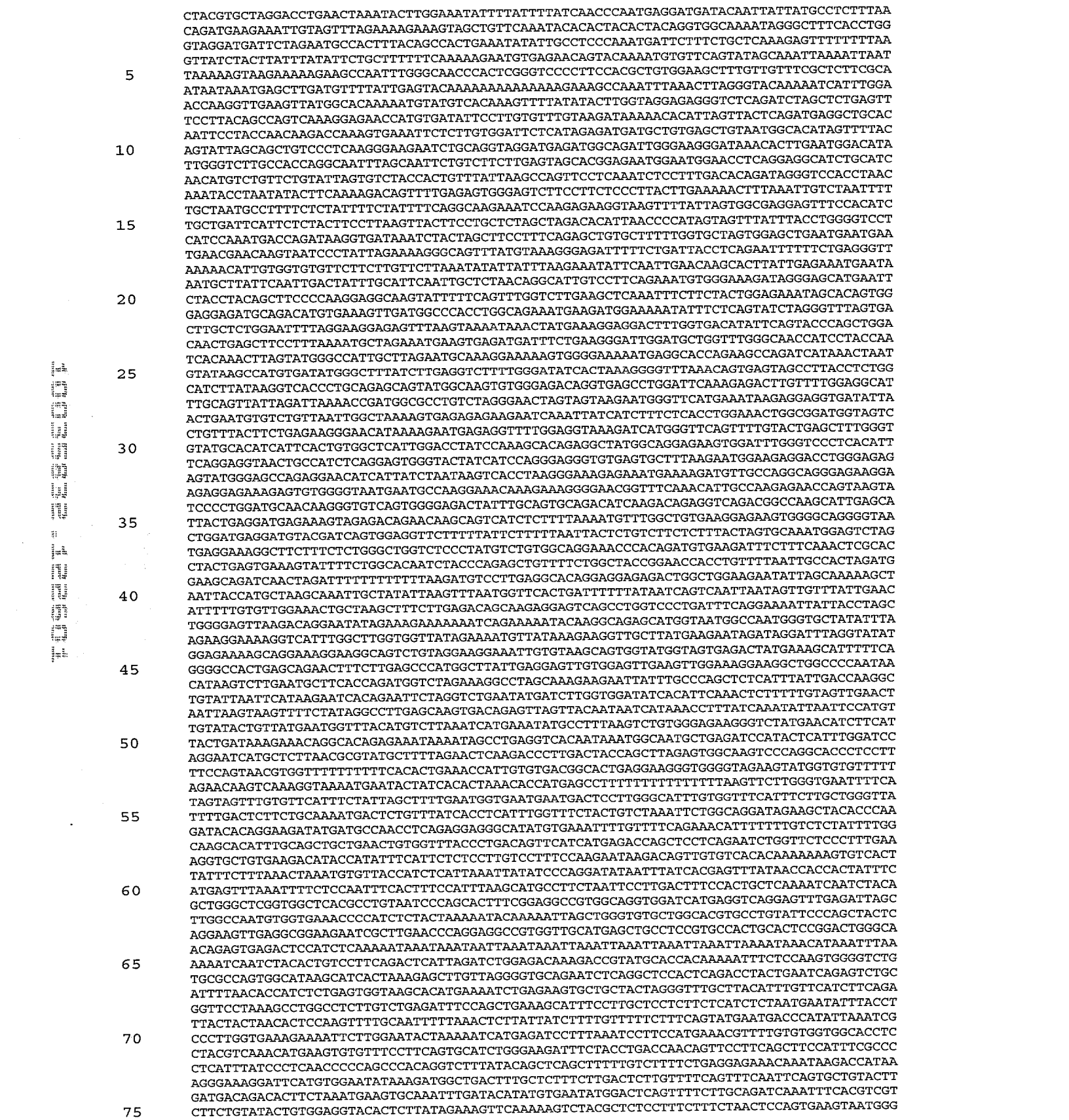
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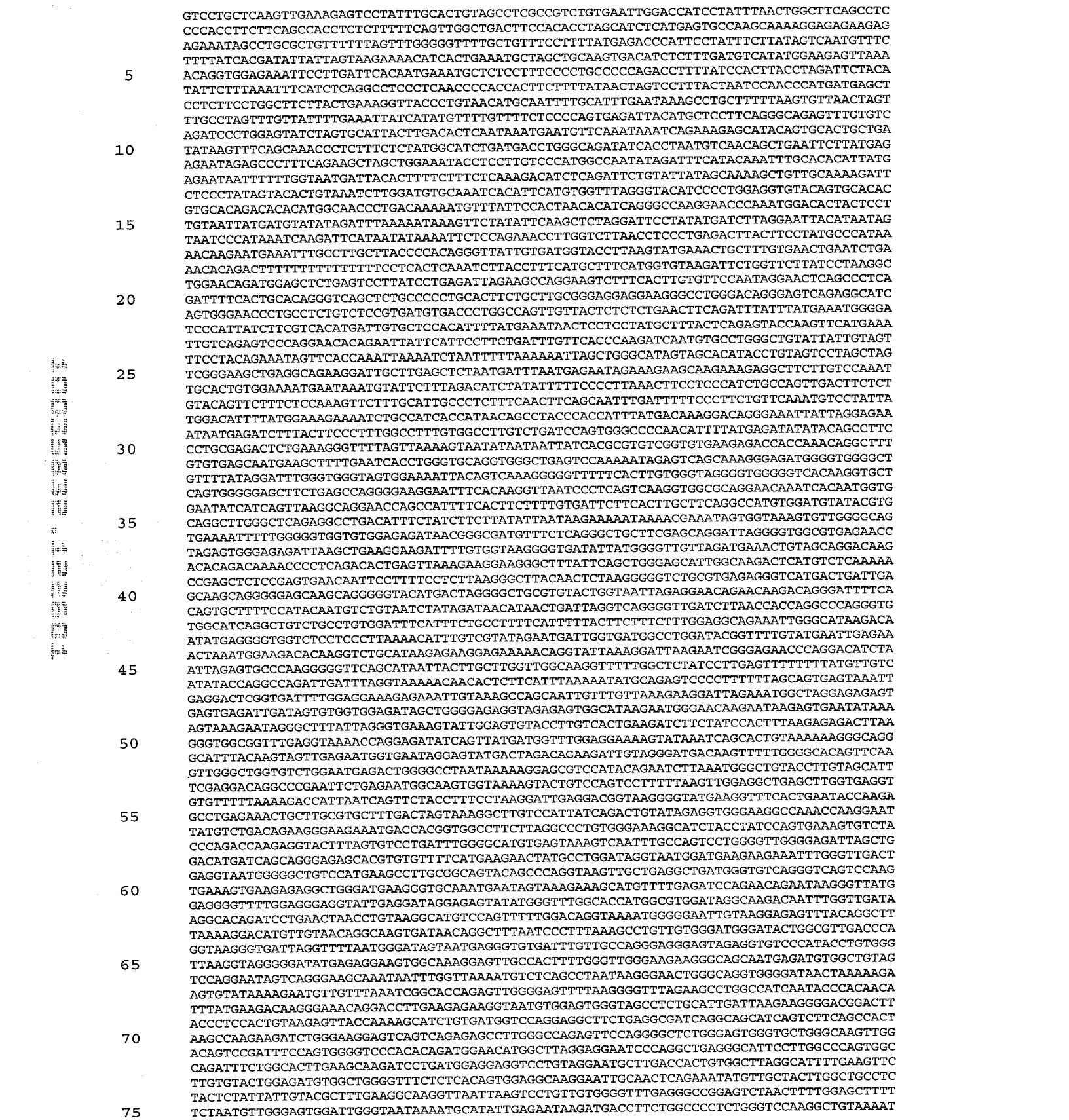


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HUMAN SEQUENCE - mRNA
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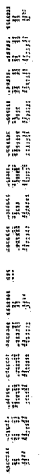
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Table 76

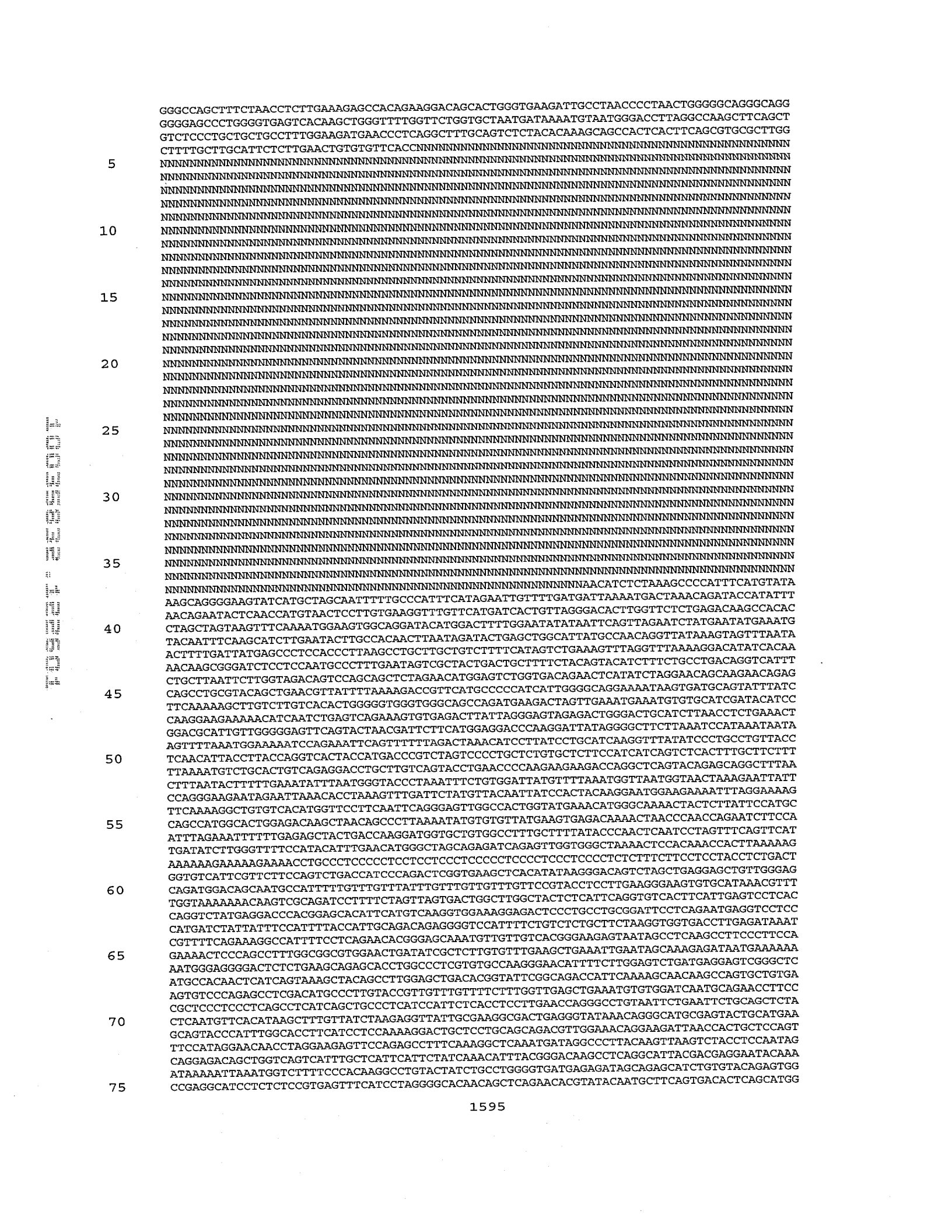
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MOUSE SEQUENCE - GENOMIC
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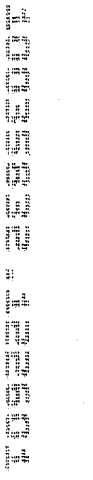


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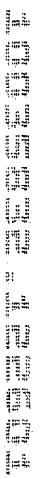


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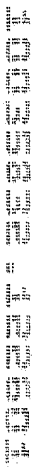
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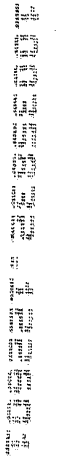
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MOUSE SEQUENCE - mRNA
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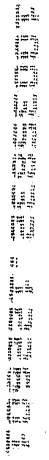
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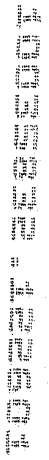


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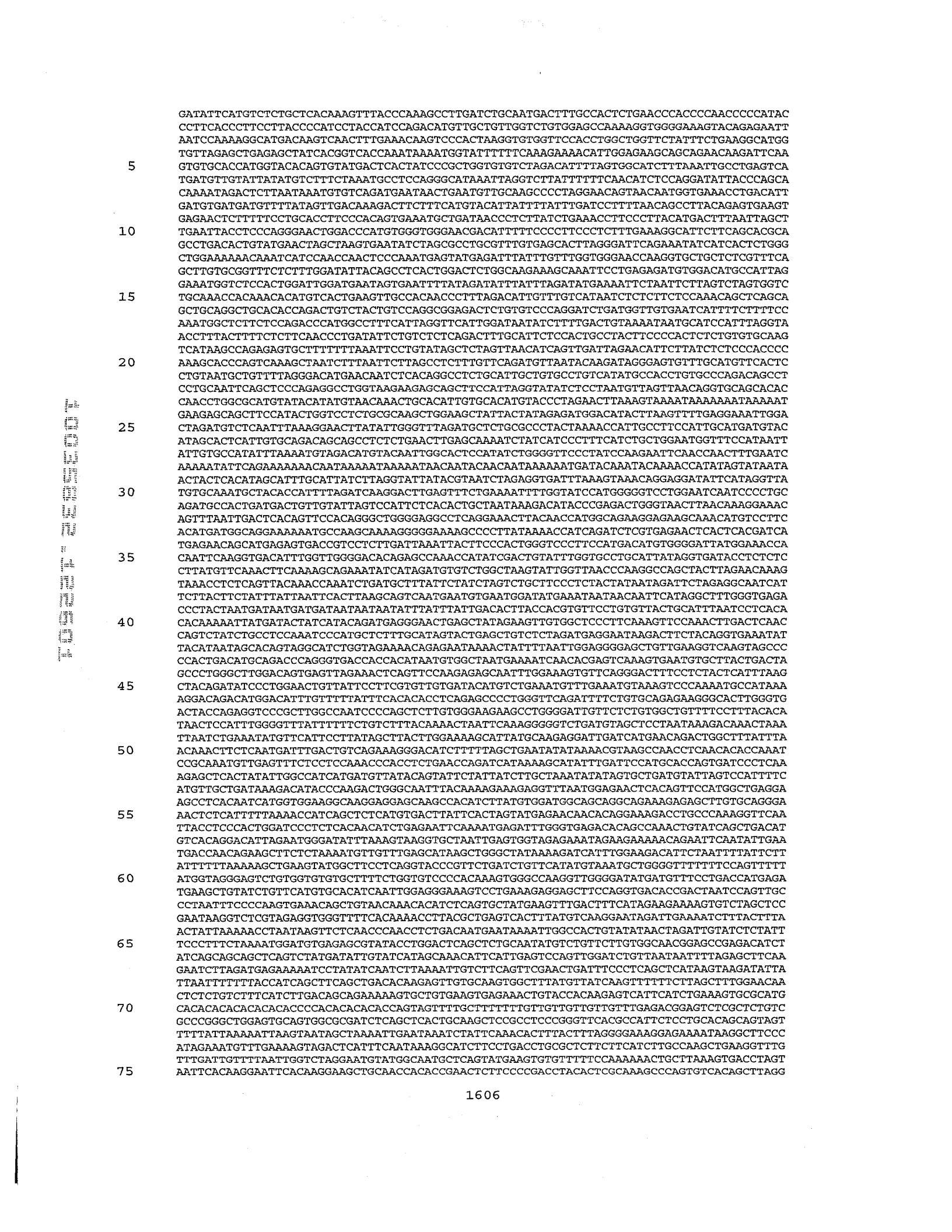
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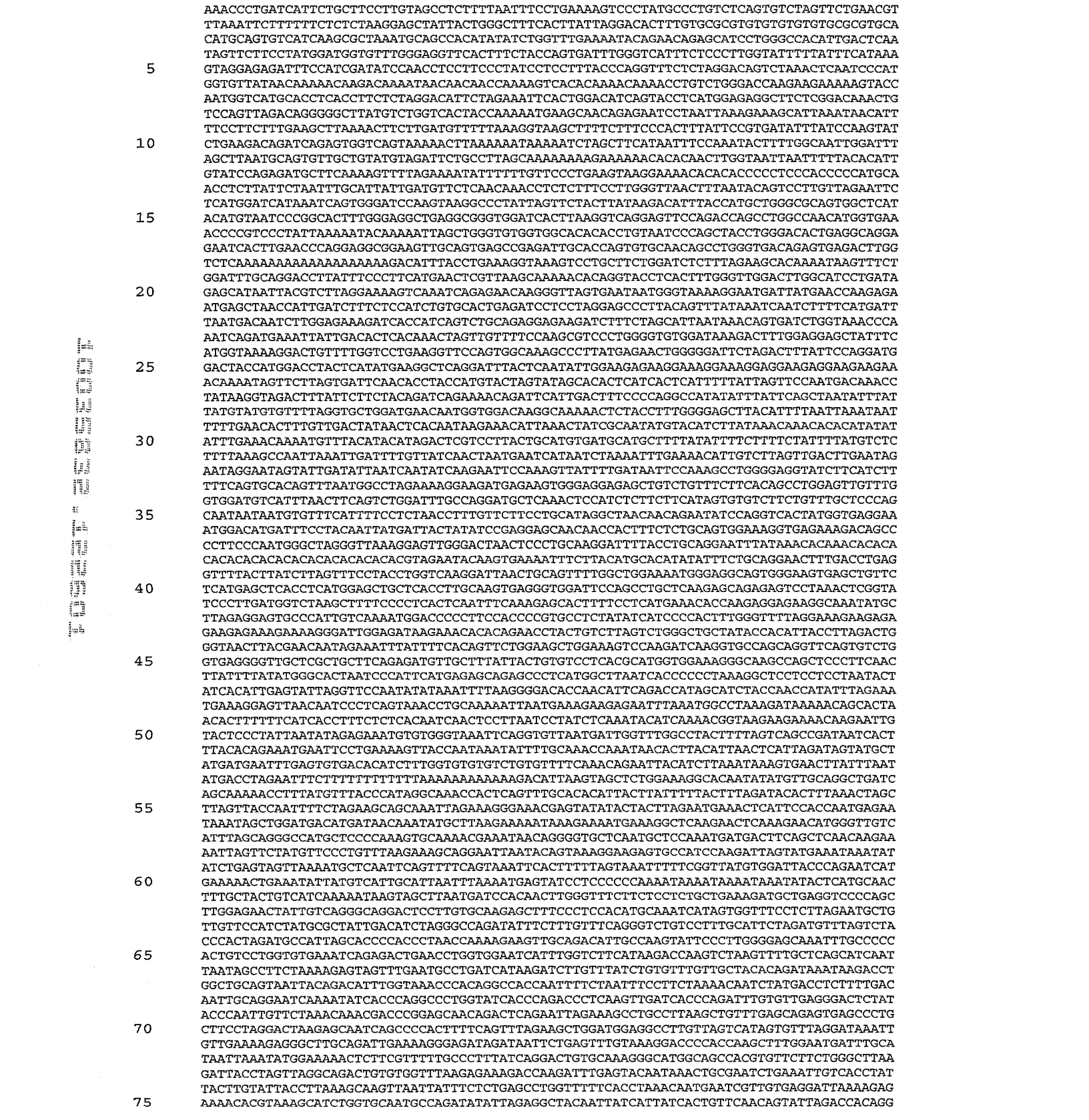
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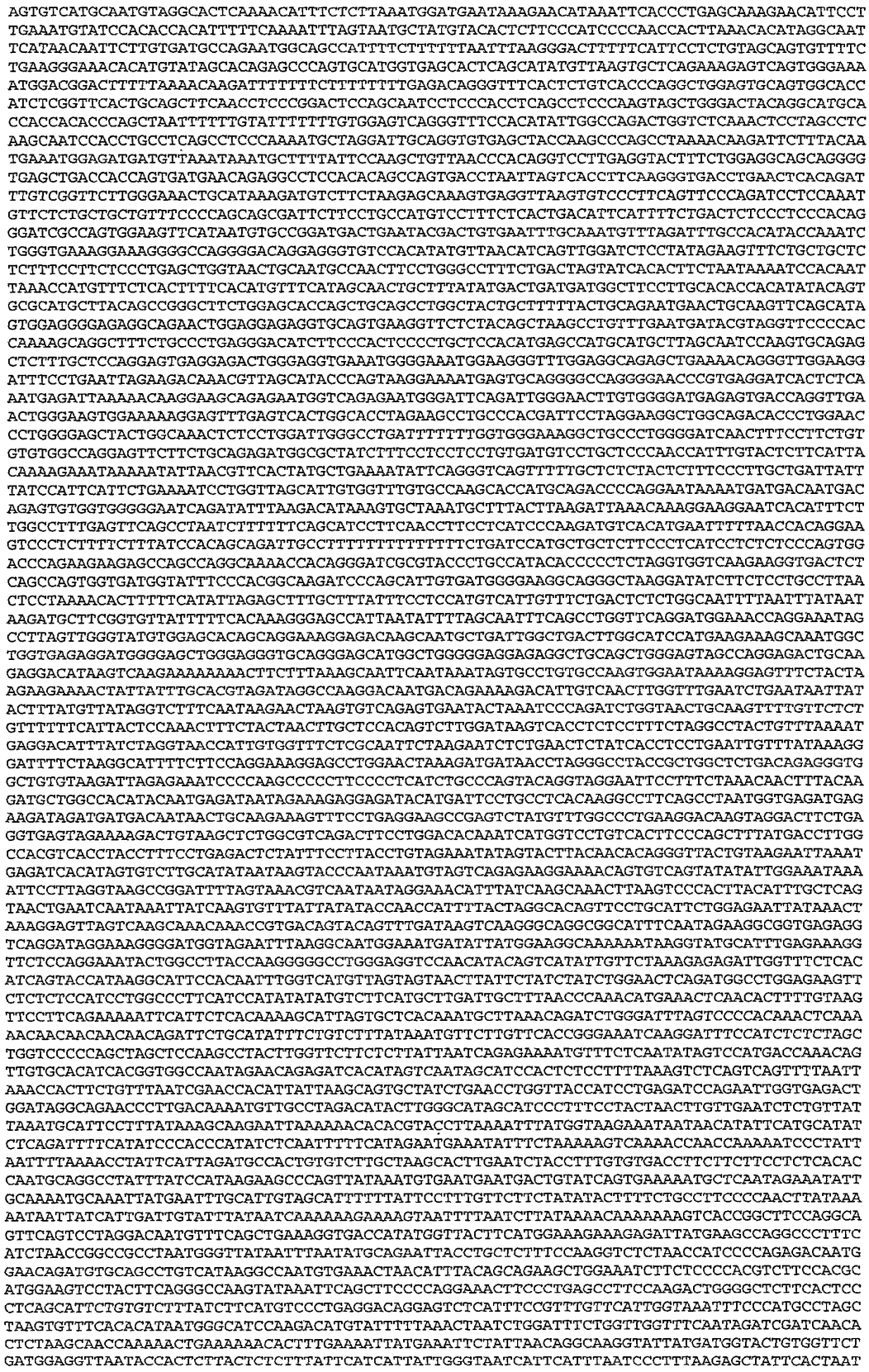


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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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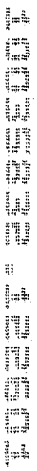


Table 77

MOUSE NOMENCLATURE
ICSGNM Pap
Celera mCG18370

HUMAN NOMENCLATURE
HGNC PAP
Celera hCG39519

MOUSE SEQUENCE - GENOMIC

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Sequence Listing

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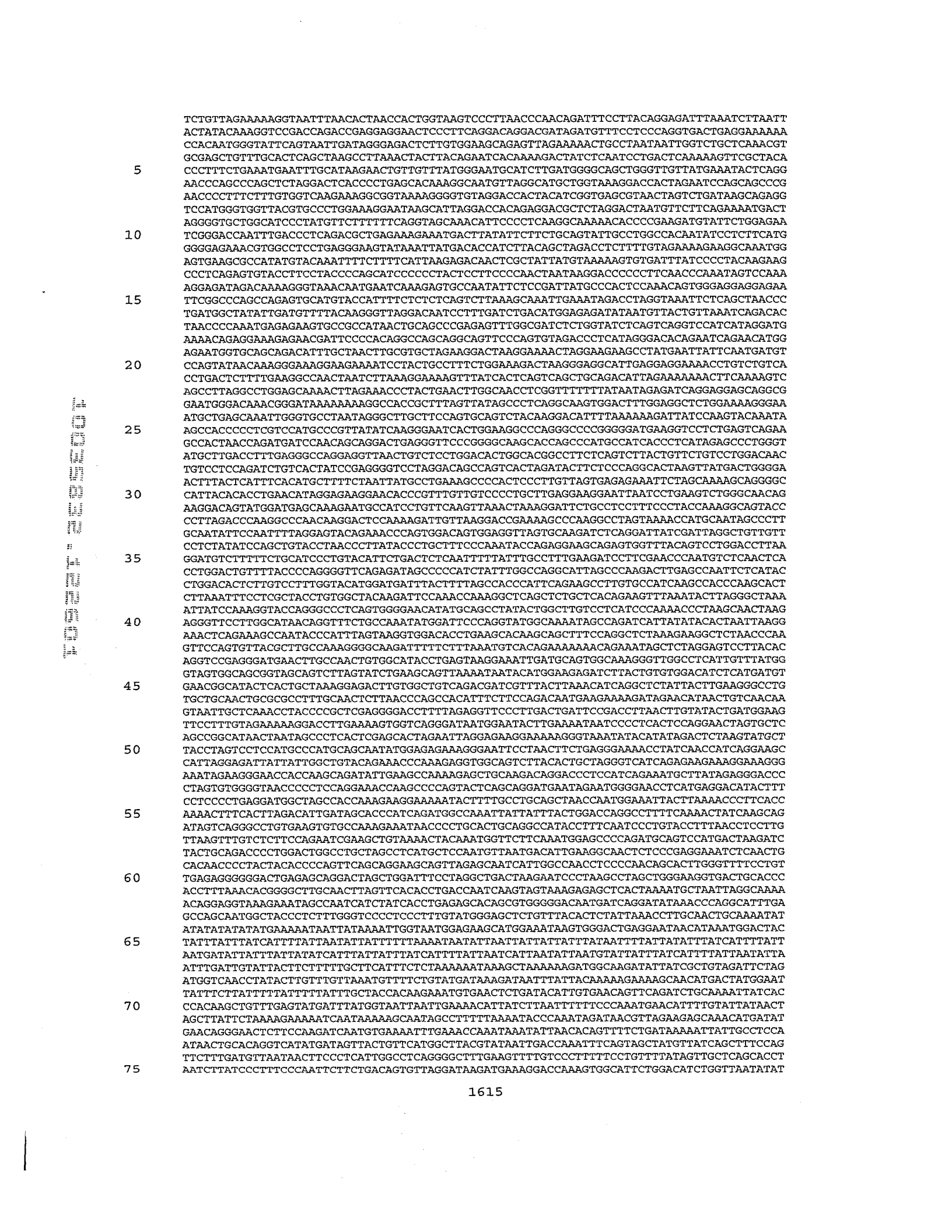
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MOUSE SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 78

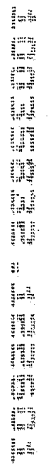
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HUMAN NOMENCLATURE
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MOUSE SEQUENCE - GENOMIC

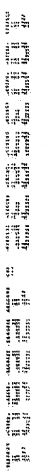
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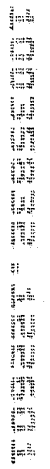
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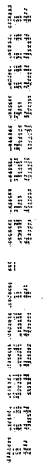
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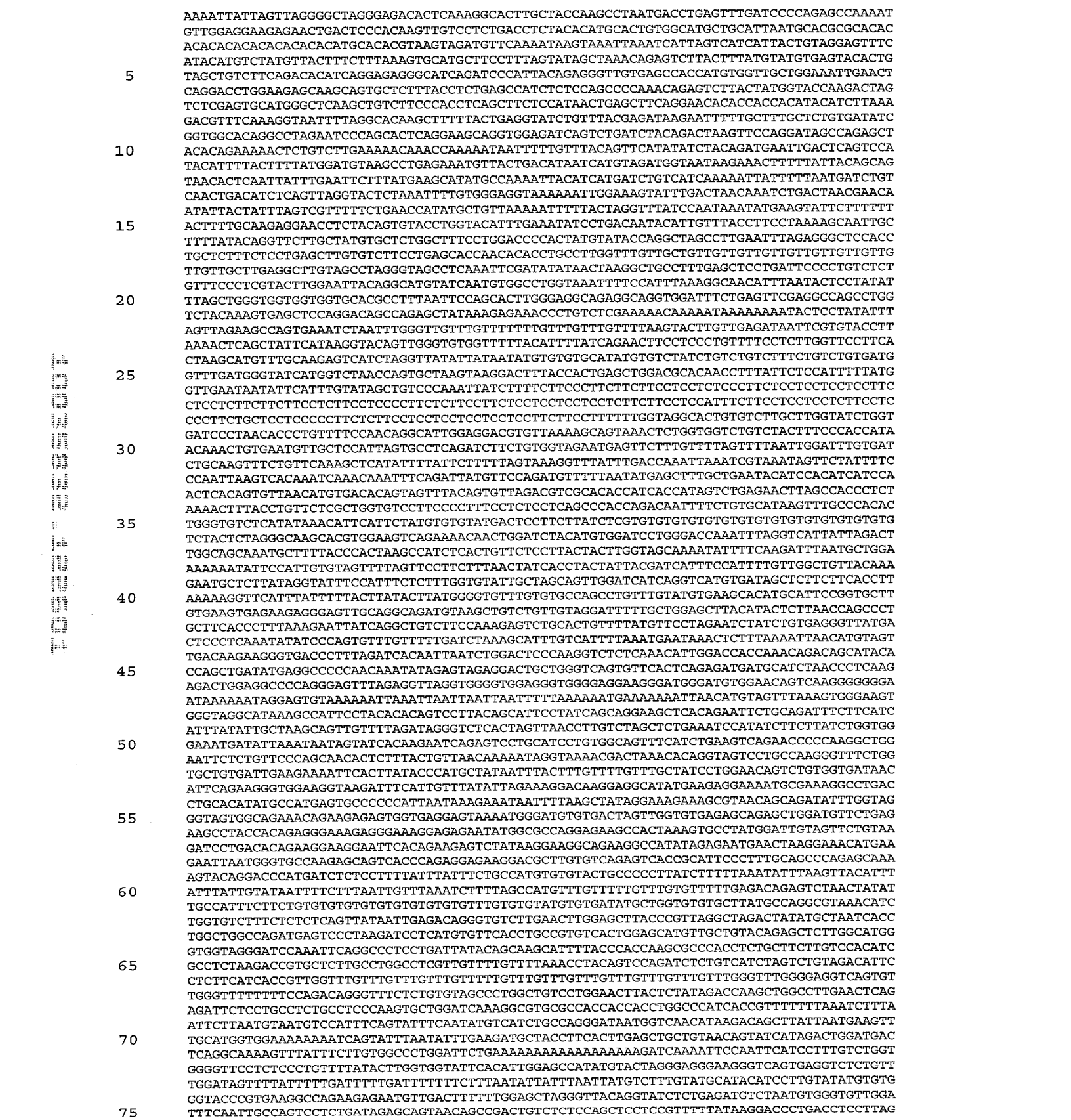
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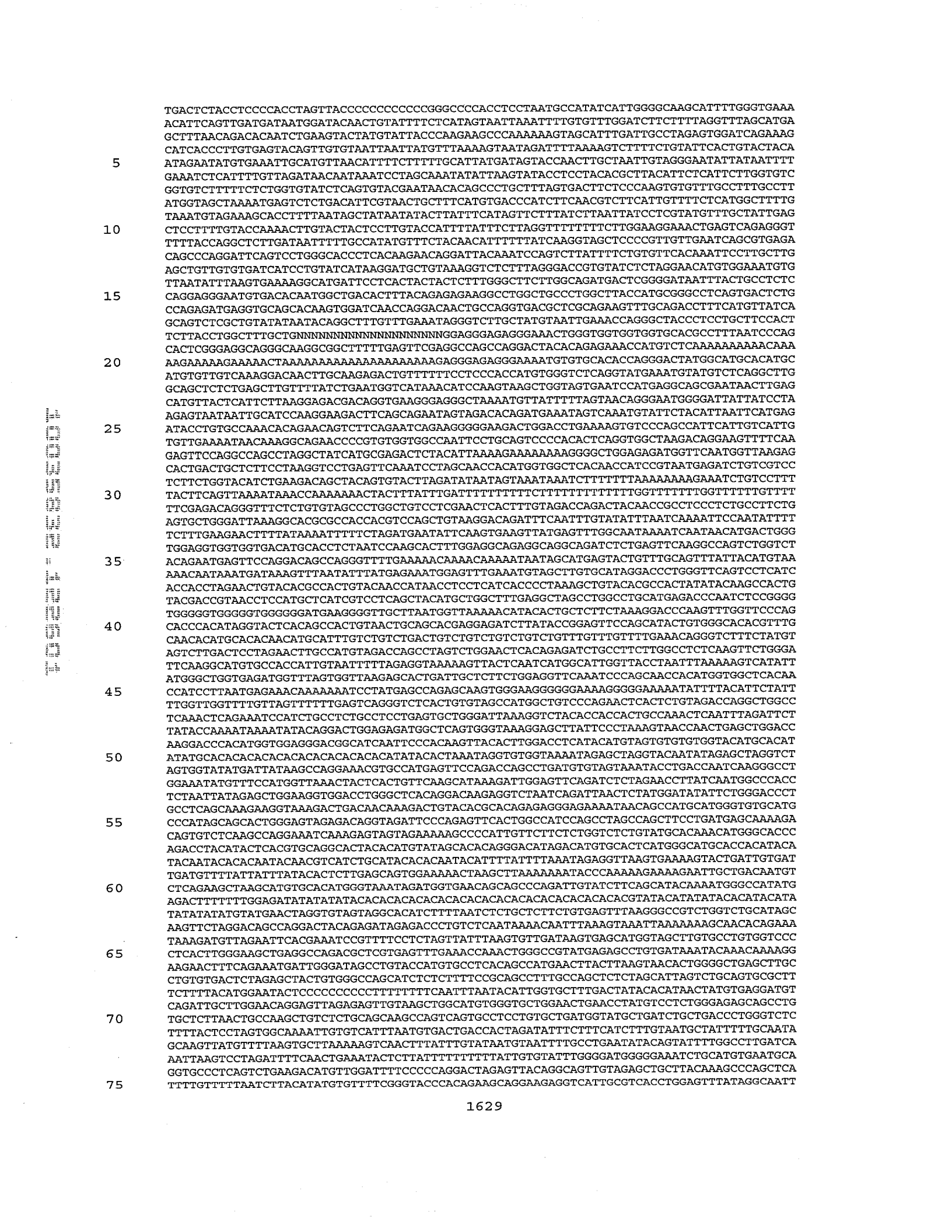


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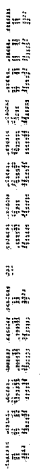




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MOUSE SEQUENCE - mRNA
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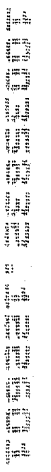
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HUMAN SEQUENCE - GENOMIC
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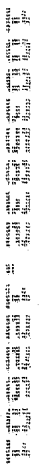
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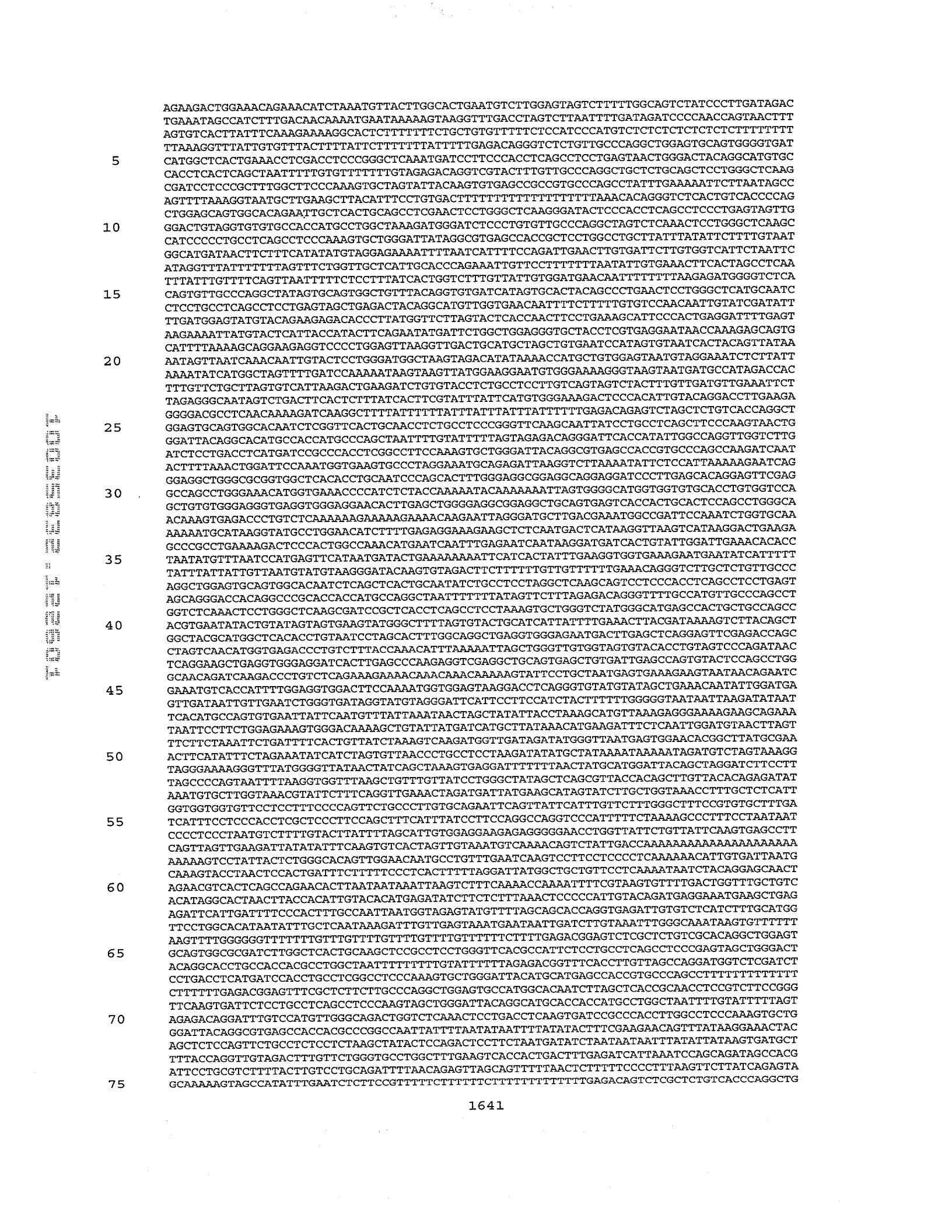
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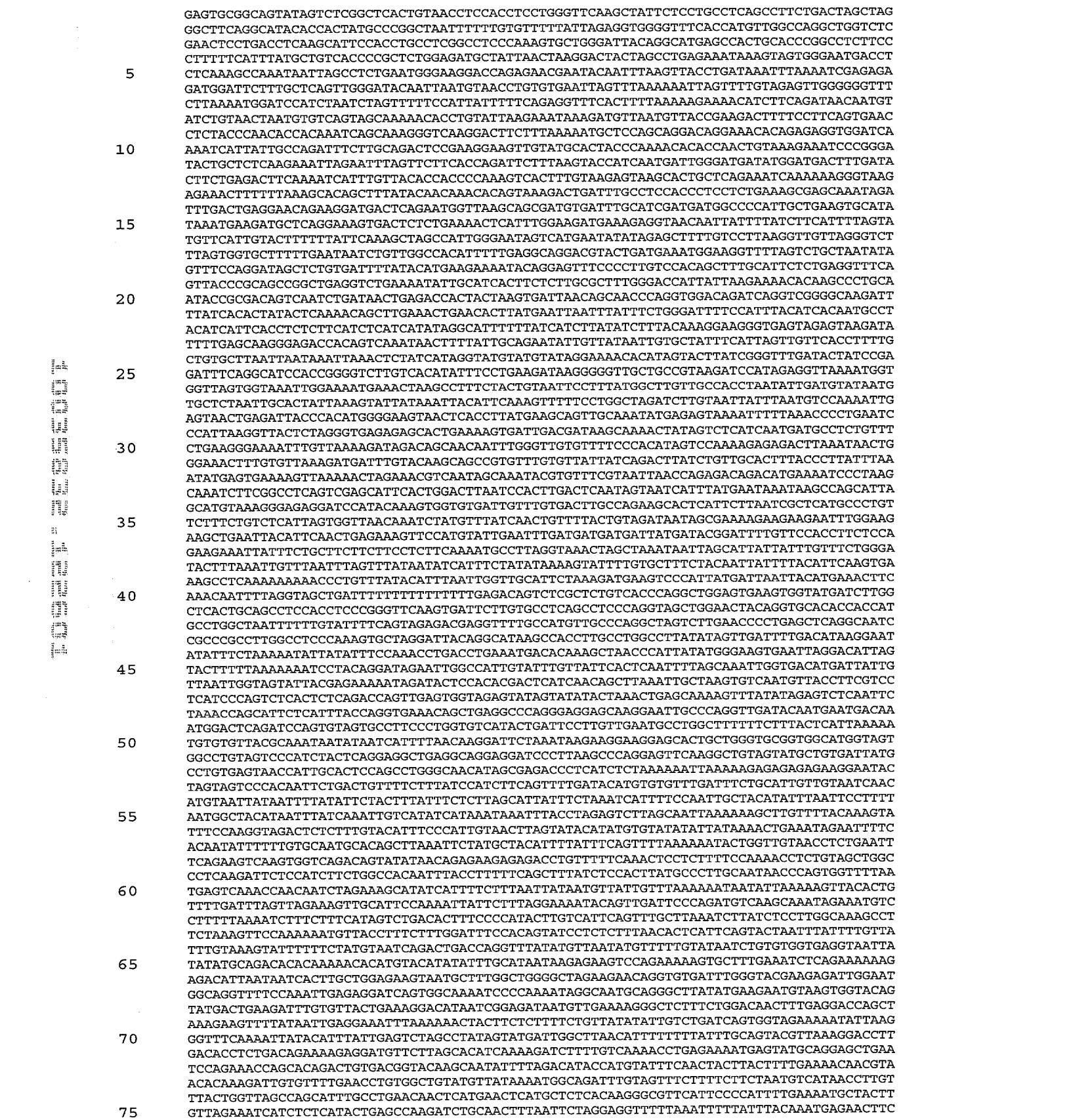


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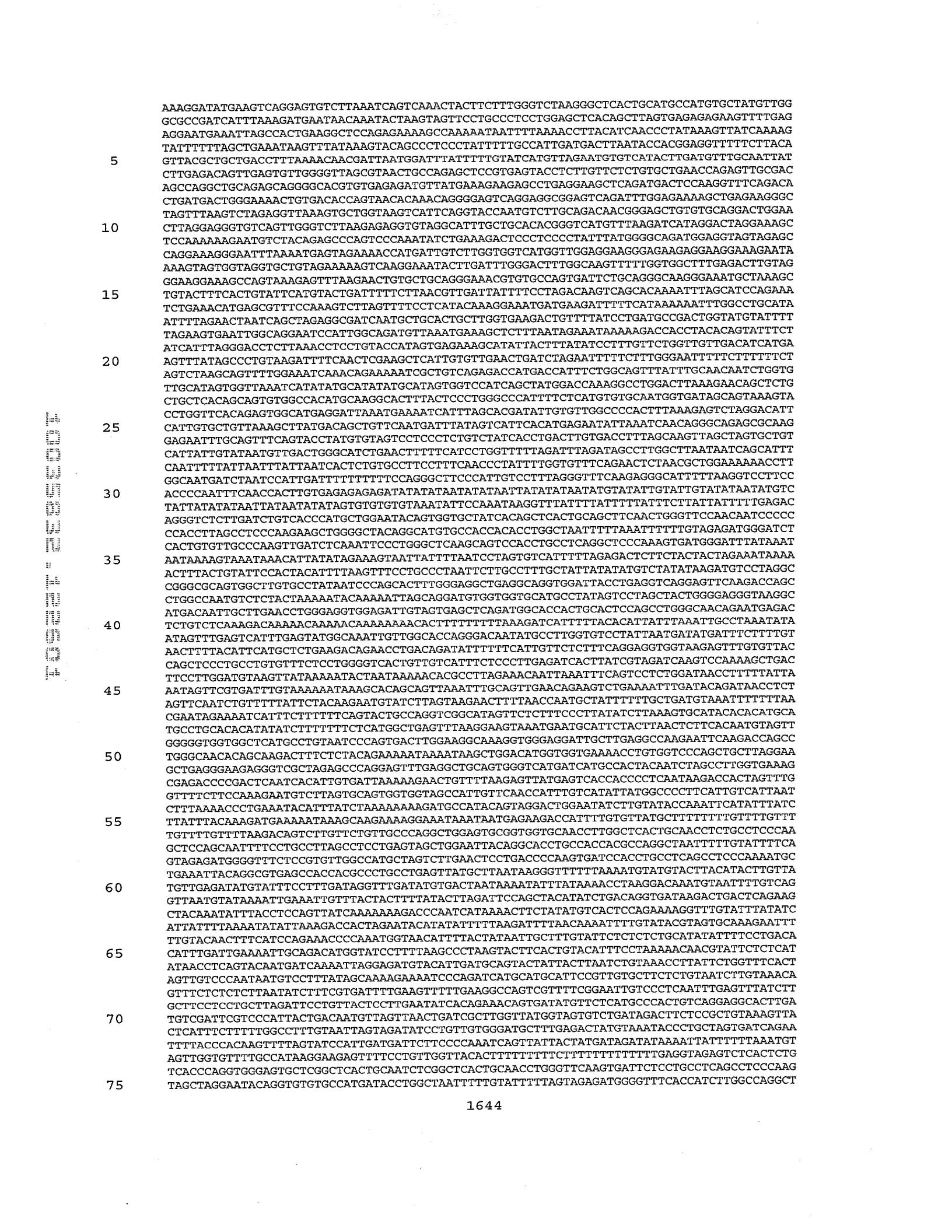


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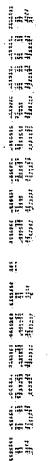


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Inventor: Willingham, Aarron T.
Inventor: Gingeras, Thomas R.
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Sequence Number: 1643

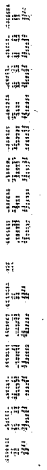
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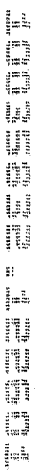
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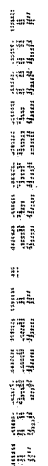
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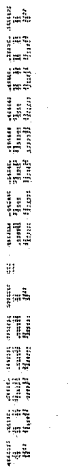
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HUMAN SEQUENCE - mRNA

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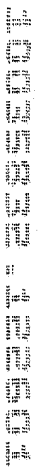
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HUMAN SEQUENCE - CODING
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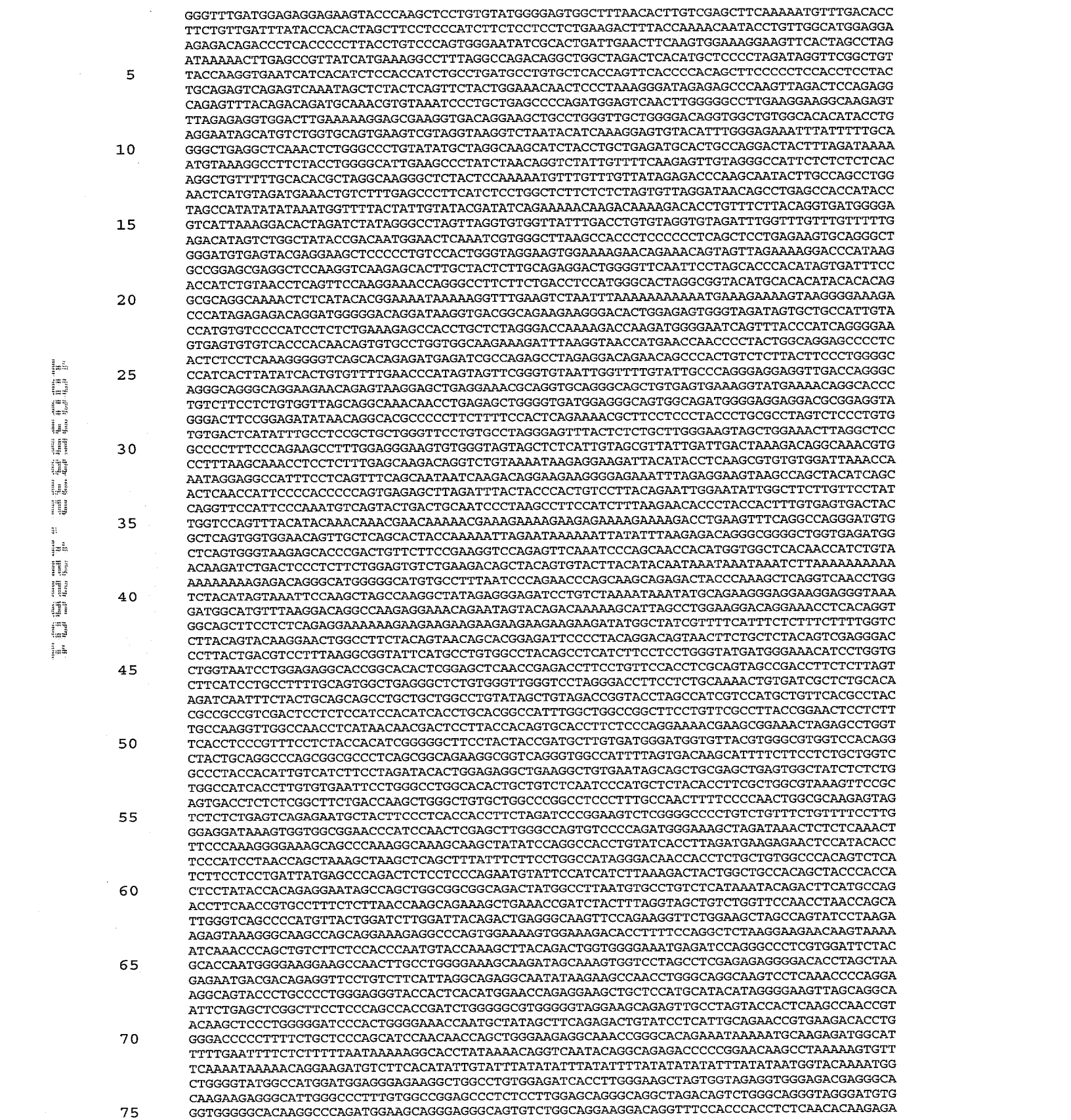
Table 79
MOUSE NOMENCLATURE
ICSGNM Blr1
Celera mCG10708

HUMAN NOMENCLATURE
HGNC BLR1
Celera hCG37947

MOUSE SEQUENCE - GENOMIC
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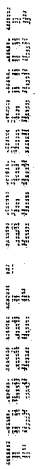
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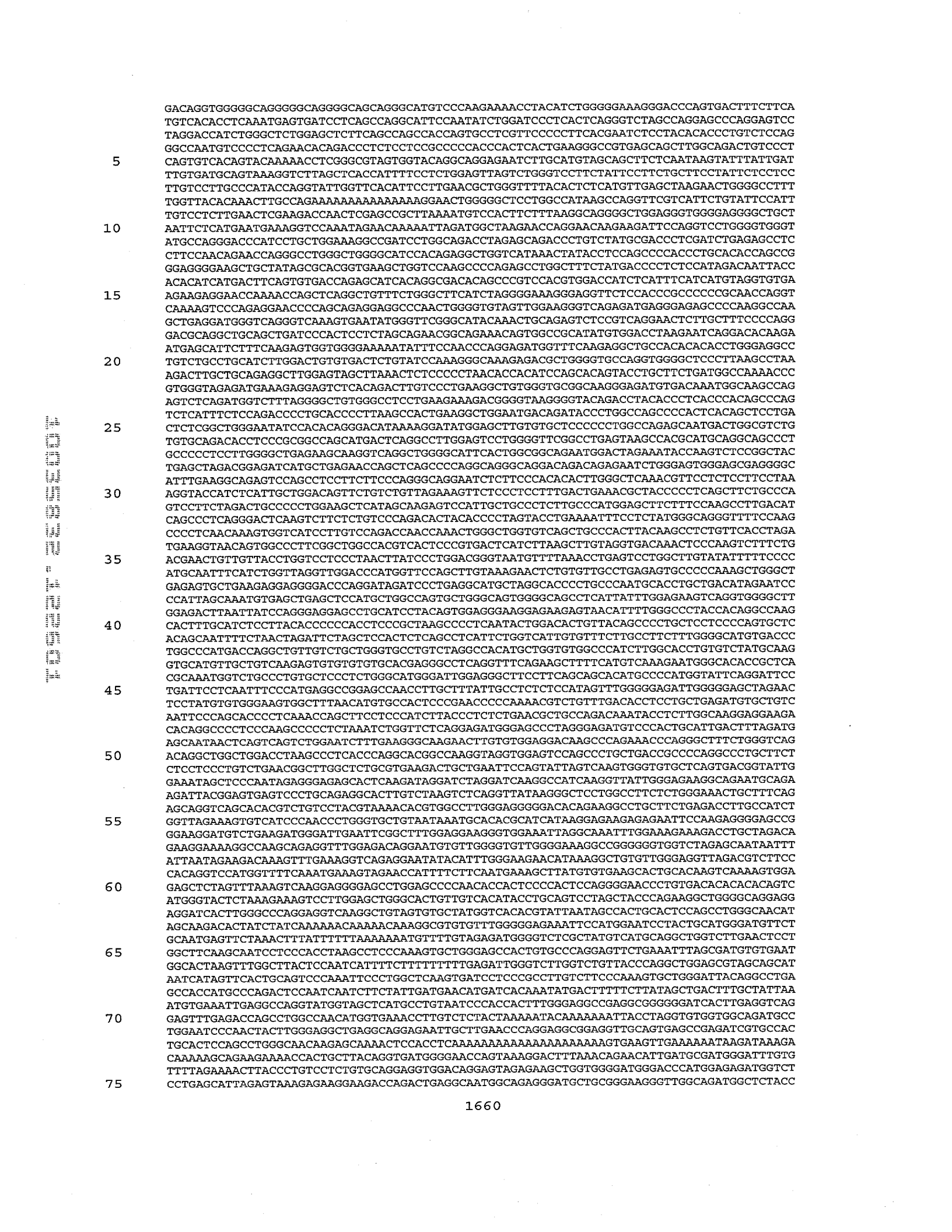
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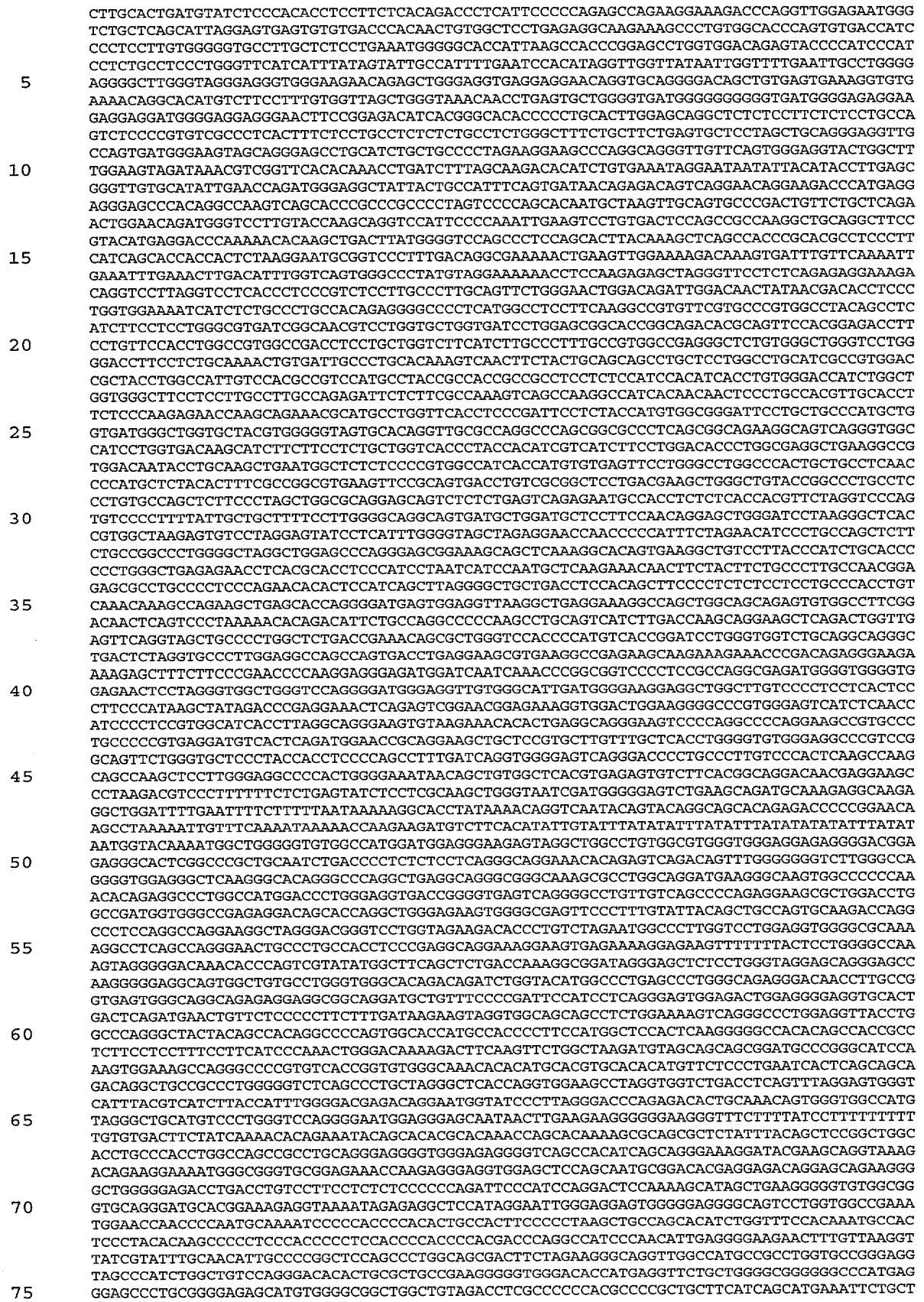


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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 80

MOUSE NOMENCLATURE

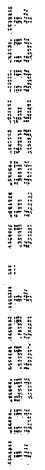
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HUMAN NOMENCLATURE

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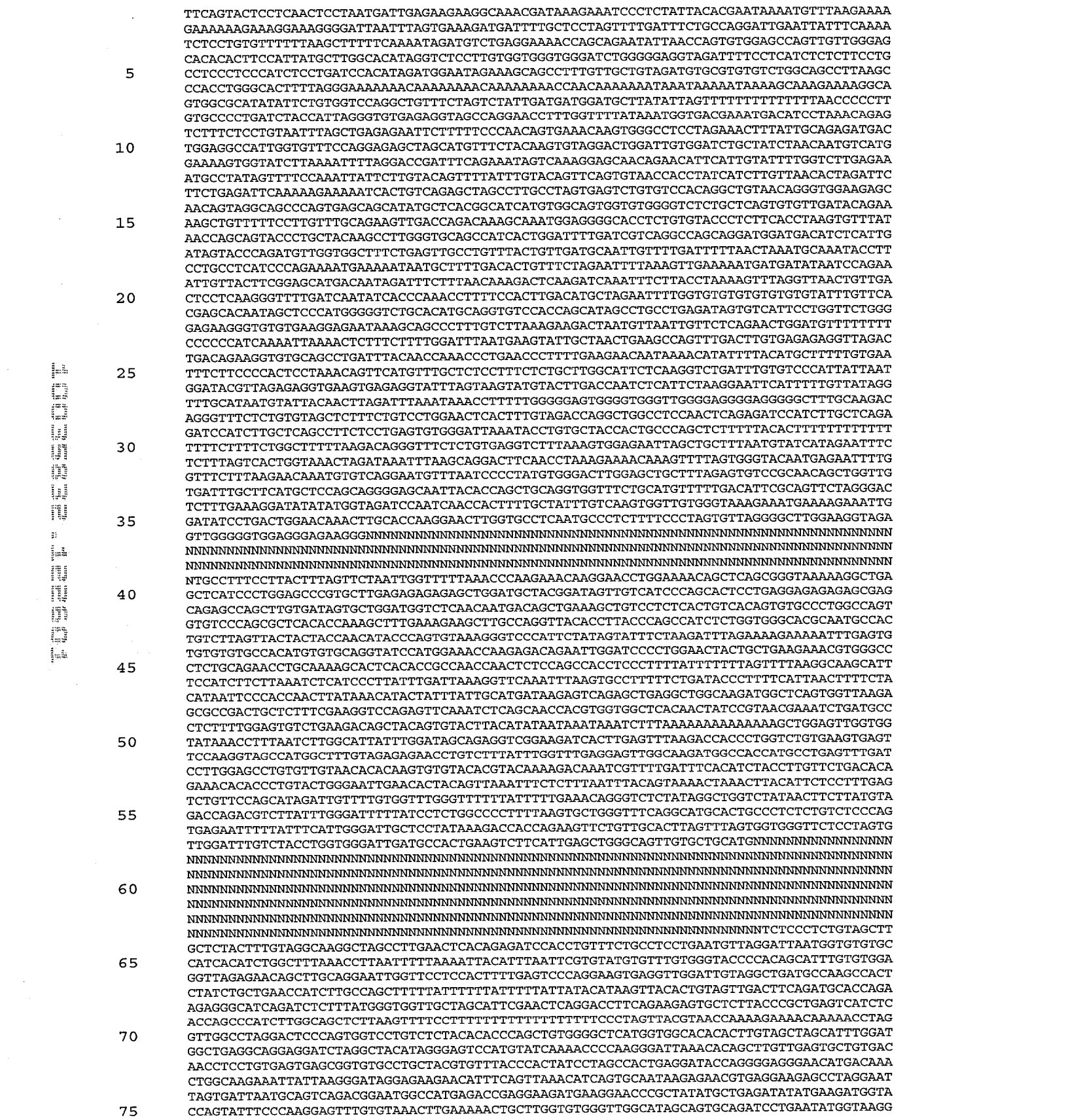
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Sequence Listing - 10/552,048

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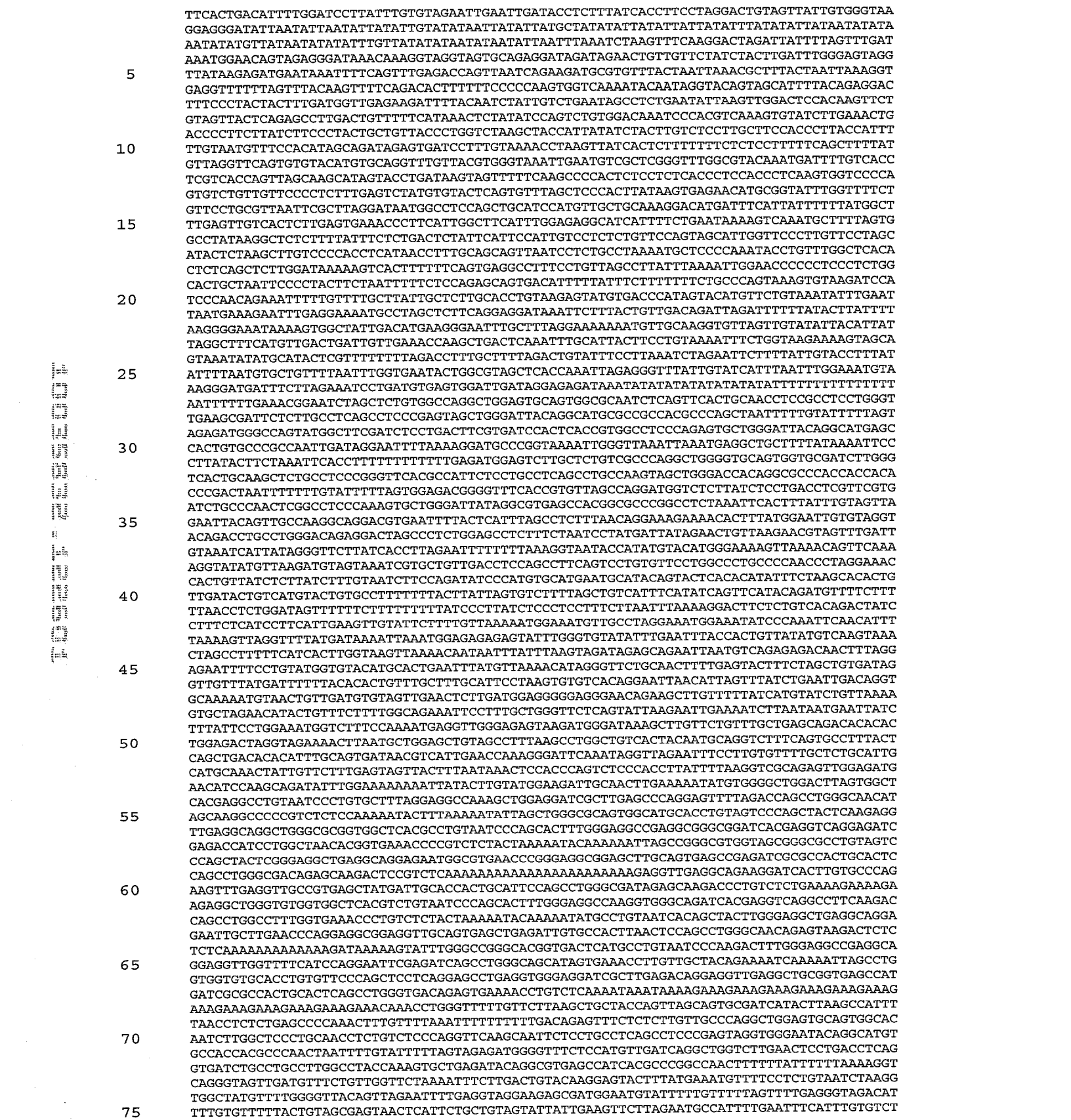


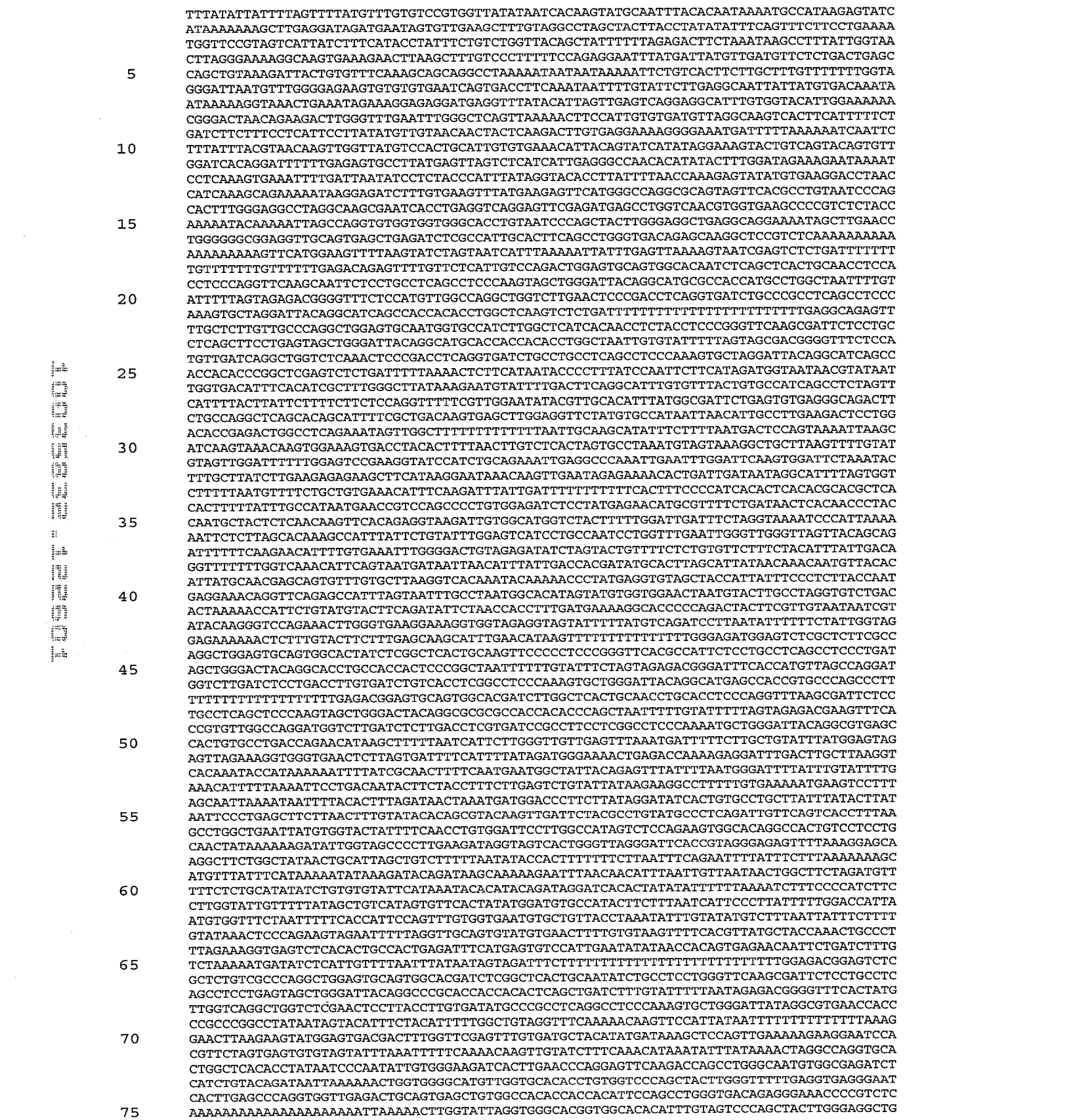
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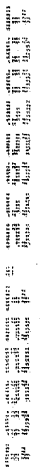
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 81

MOUSE NOMENCLATURE

ICSGNM Mcm3ap

Celera mCG3107

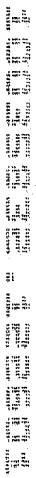
HUMAN NOMENCLATURE

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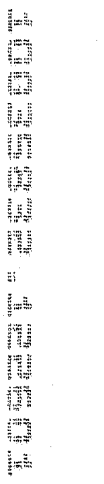
Celera hCG401250

MOUSE SEQUENCE - GENOMIC

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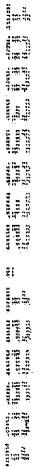
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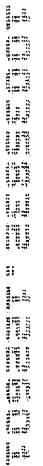
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Replacement Sheet

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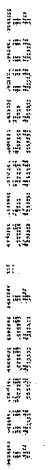
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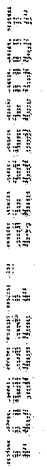
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HUMAN SEQUENCE - GENOMIC

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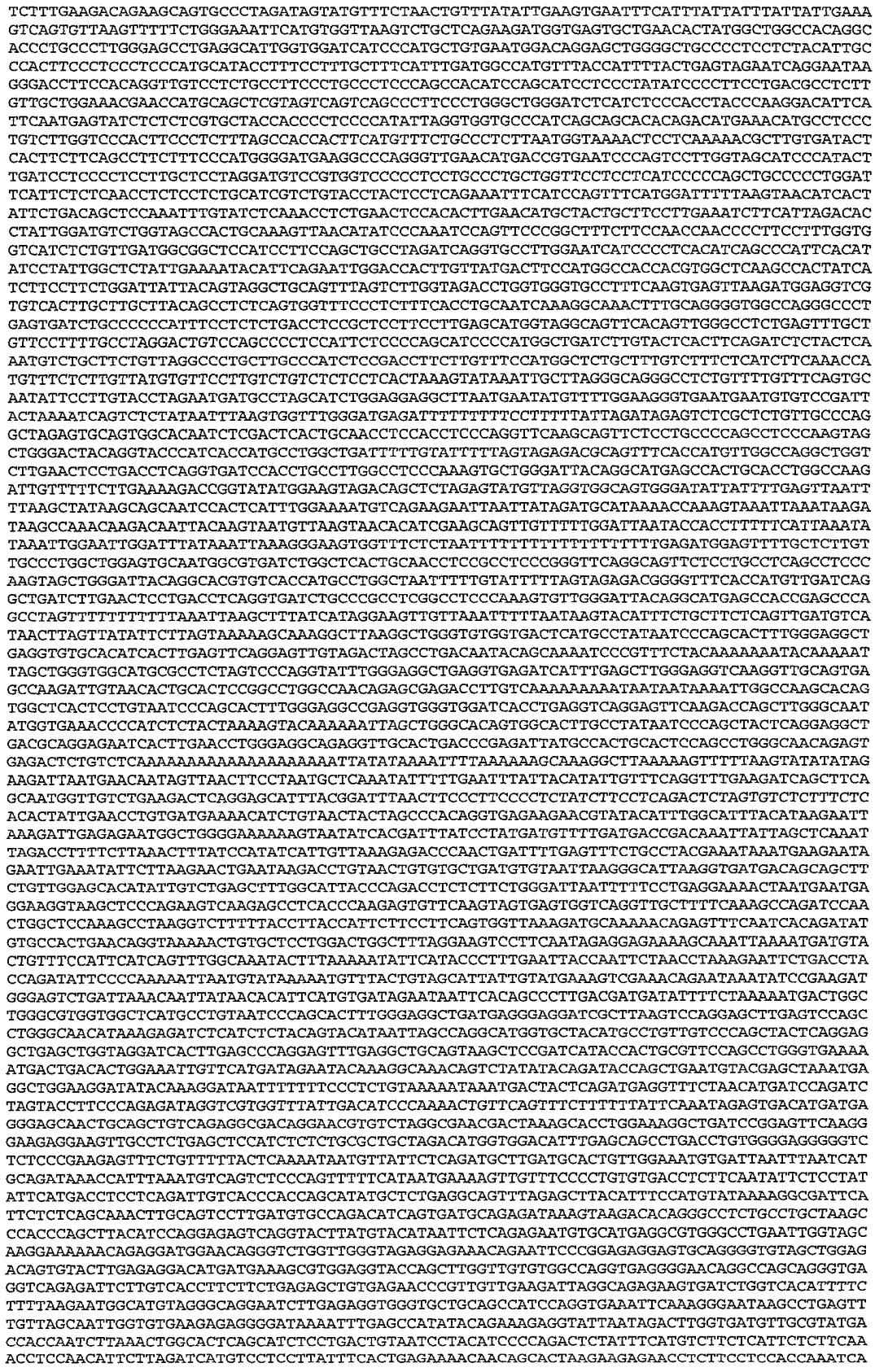


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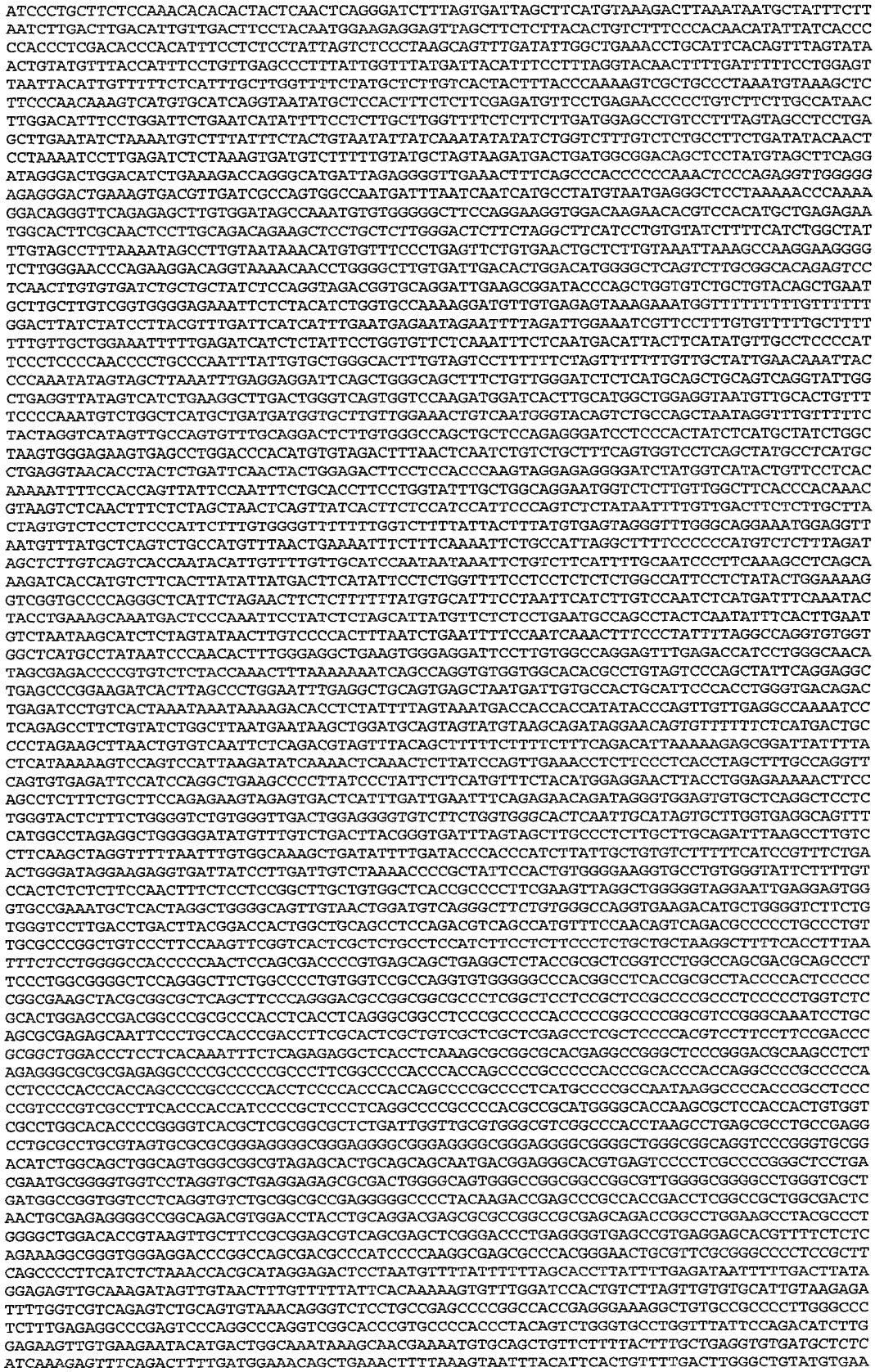
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Translation - Sequence Listing



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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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US 09/538,838 Sequence Listing

Table 82

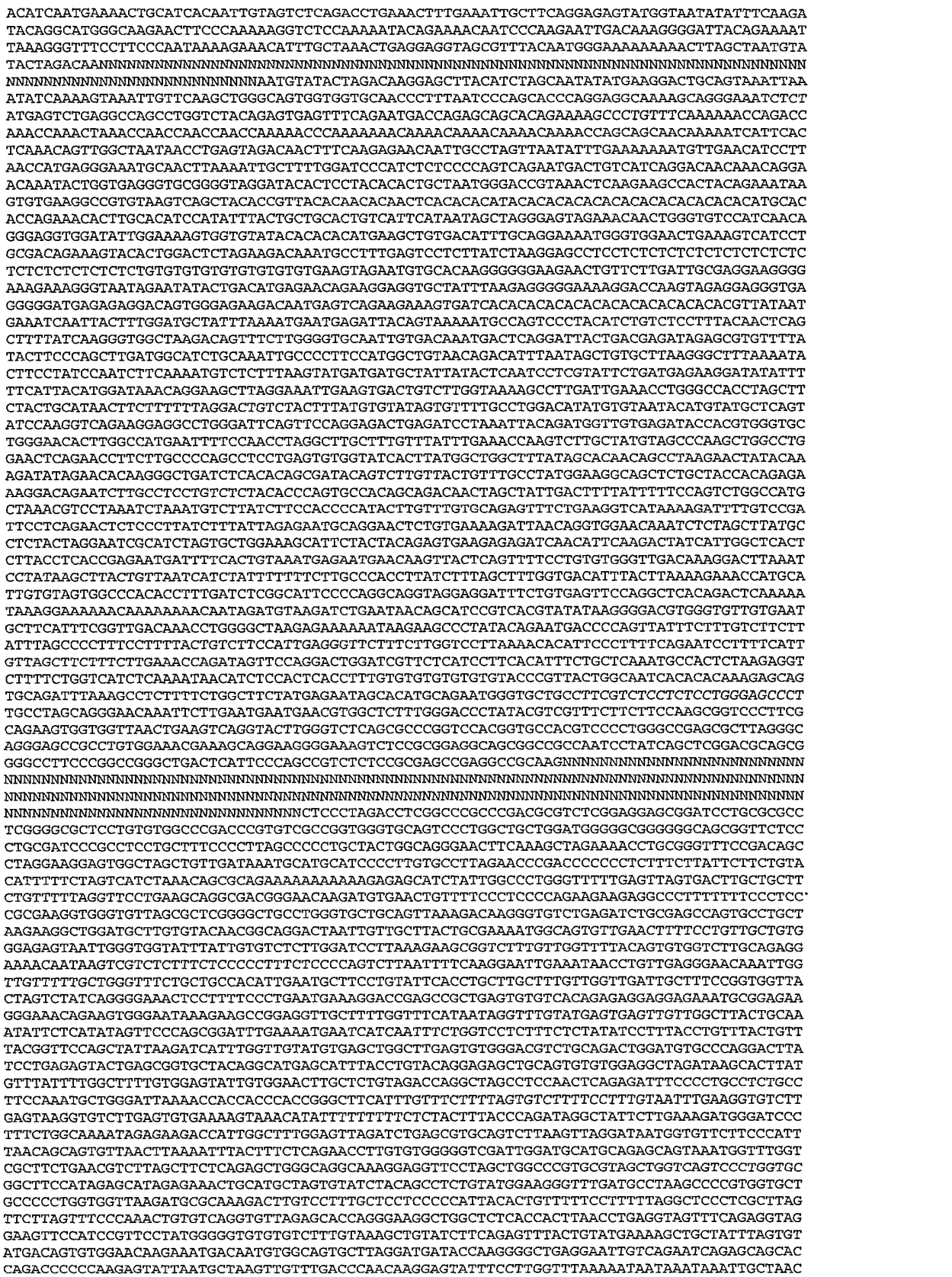
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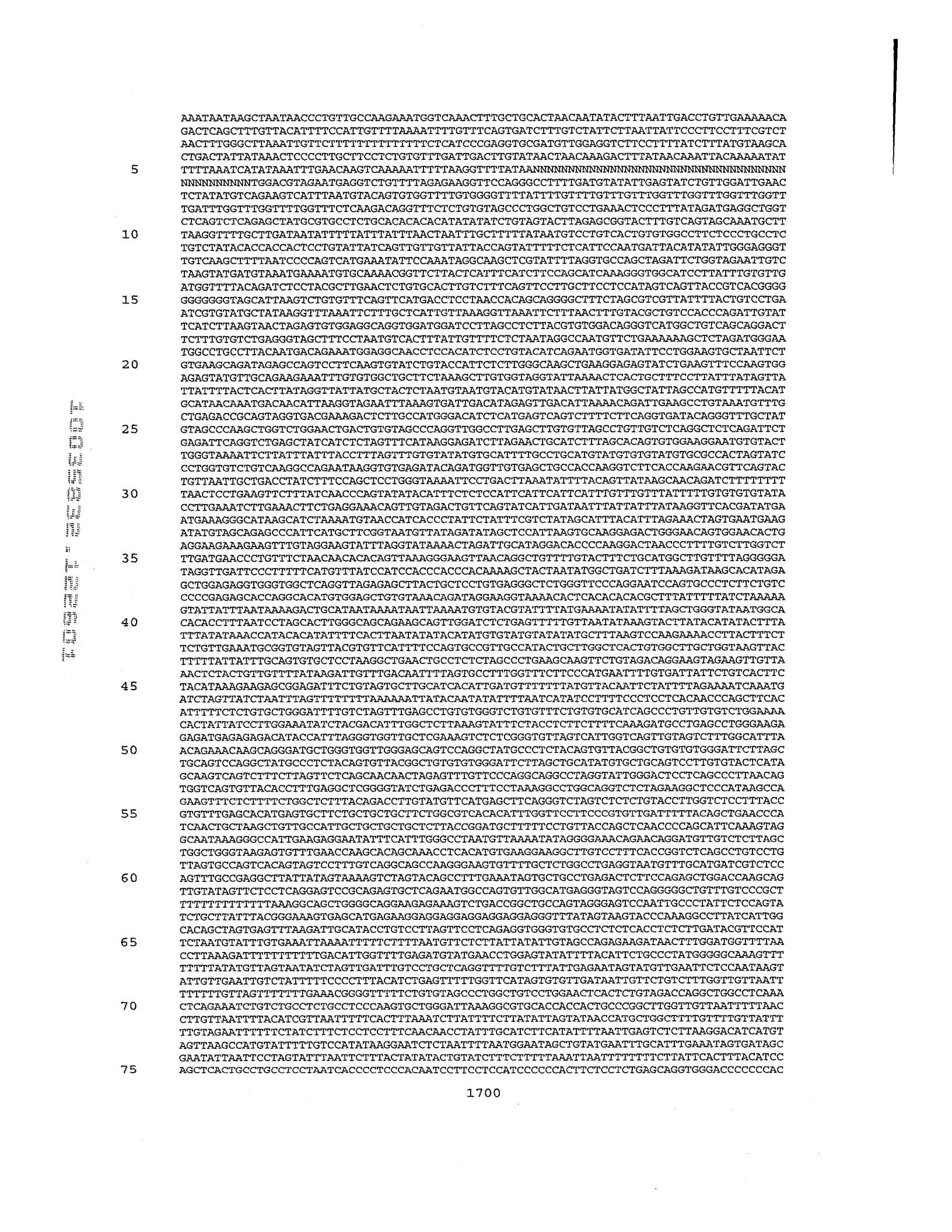
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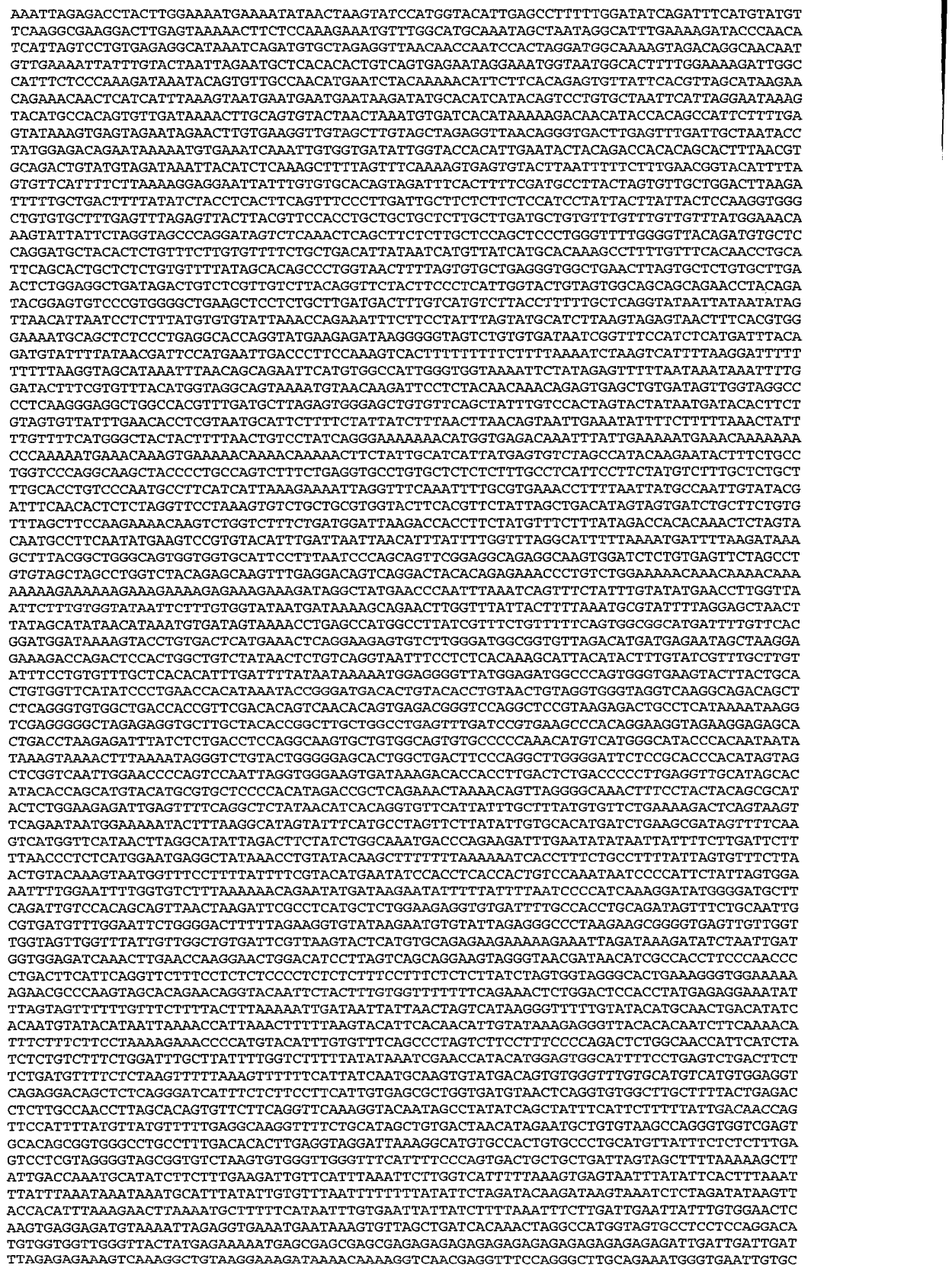


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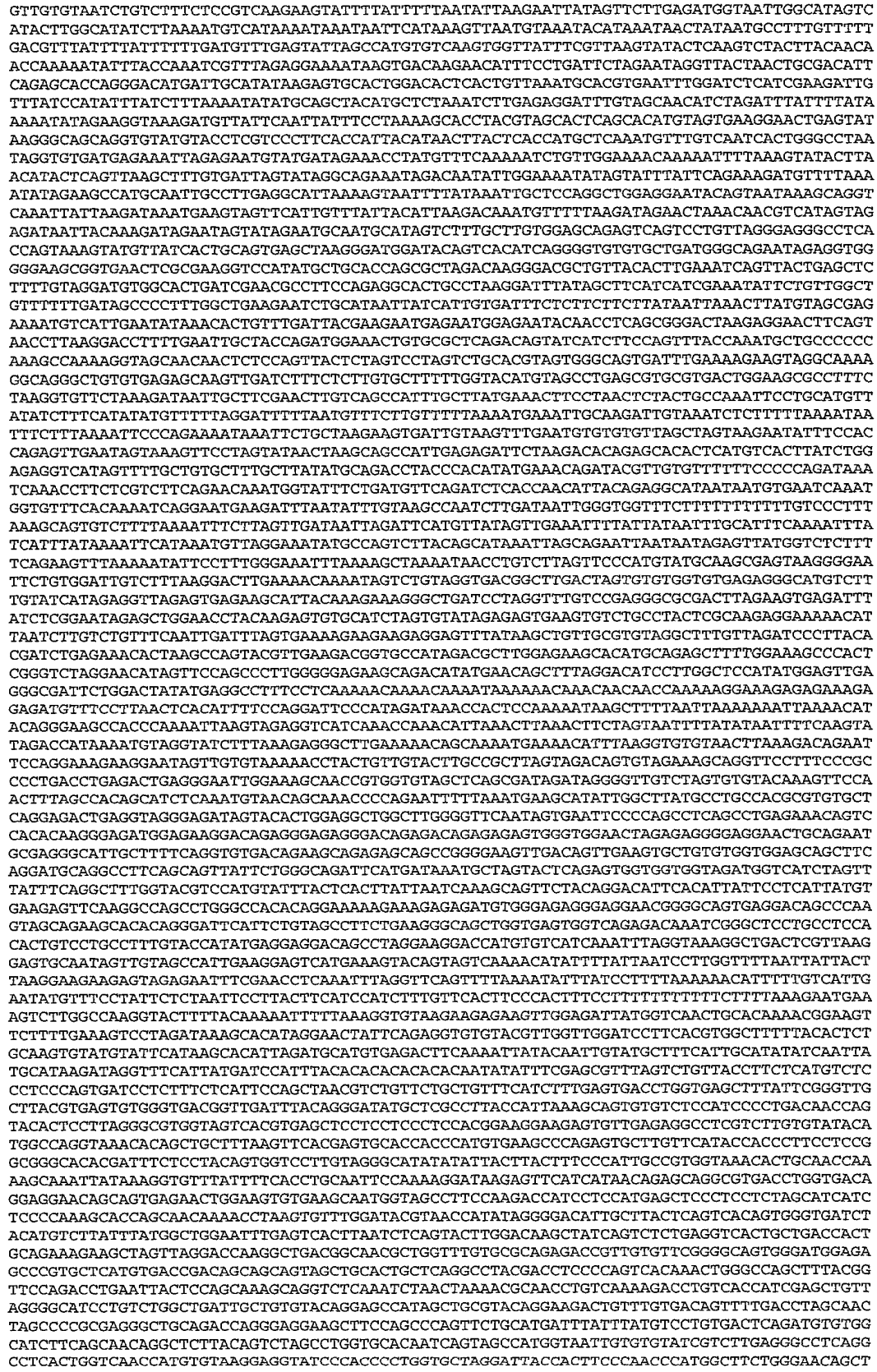
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MOUSE SEQUENCE - mRNA
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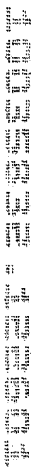
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MOUSE SEQUENCE - CODING
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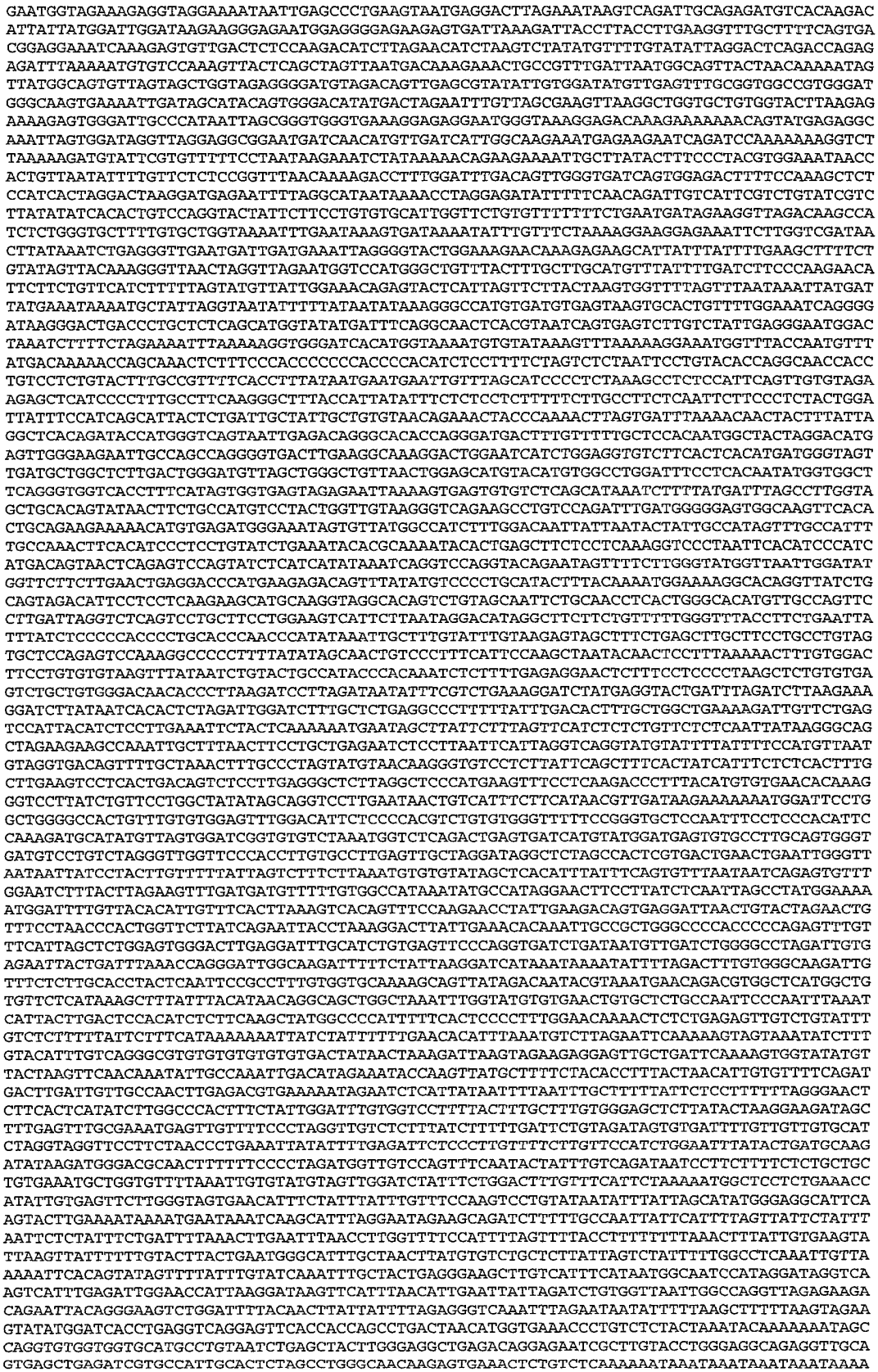
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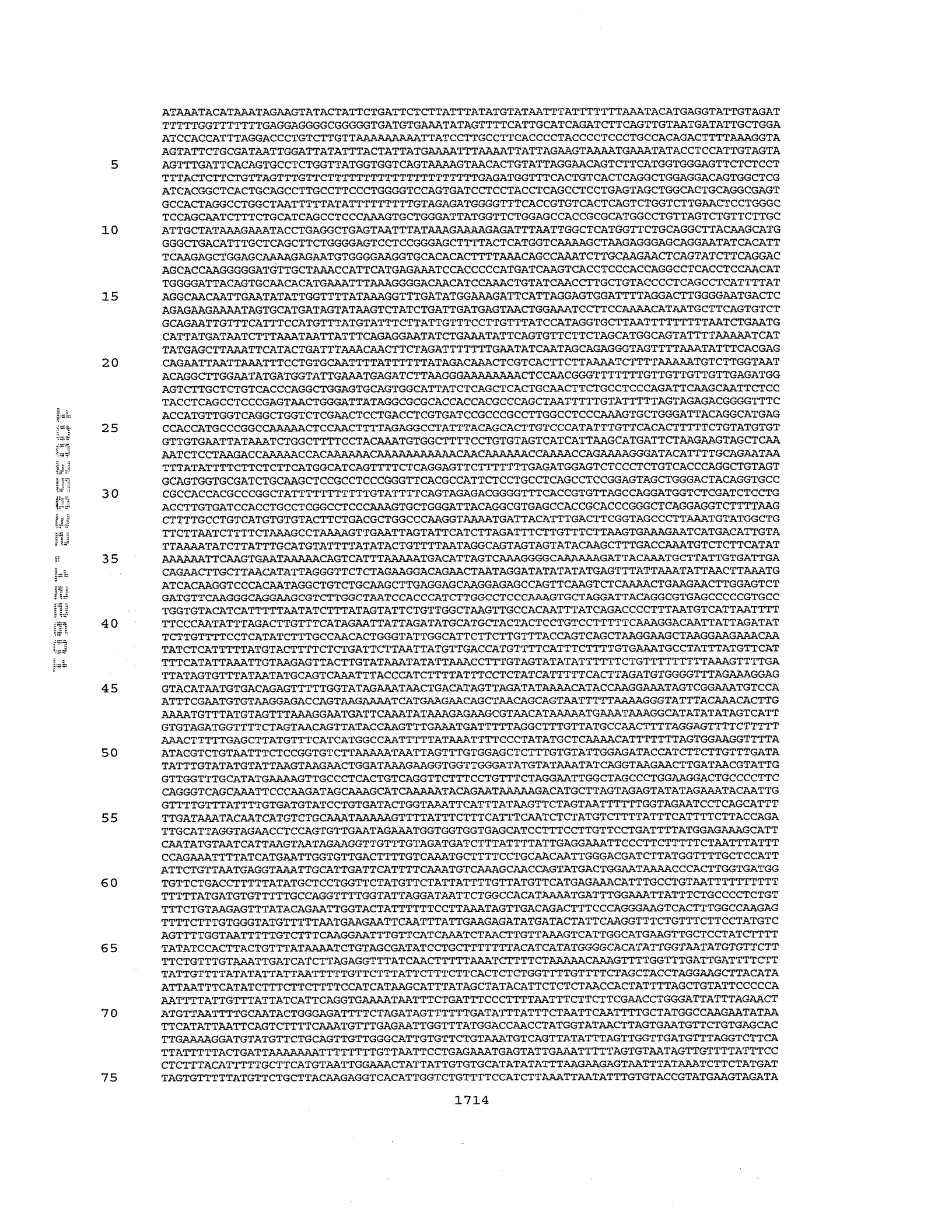
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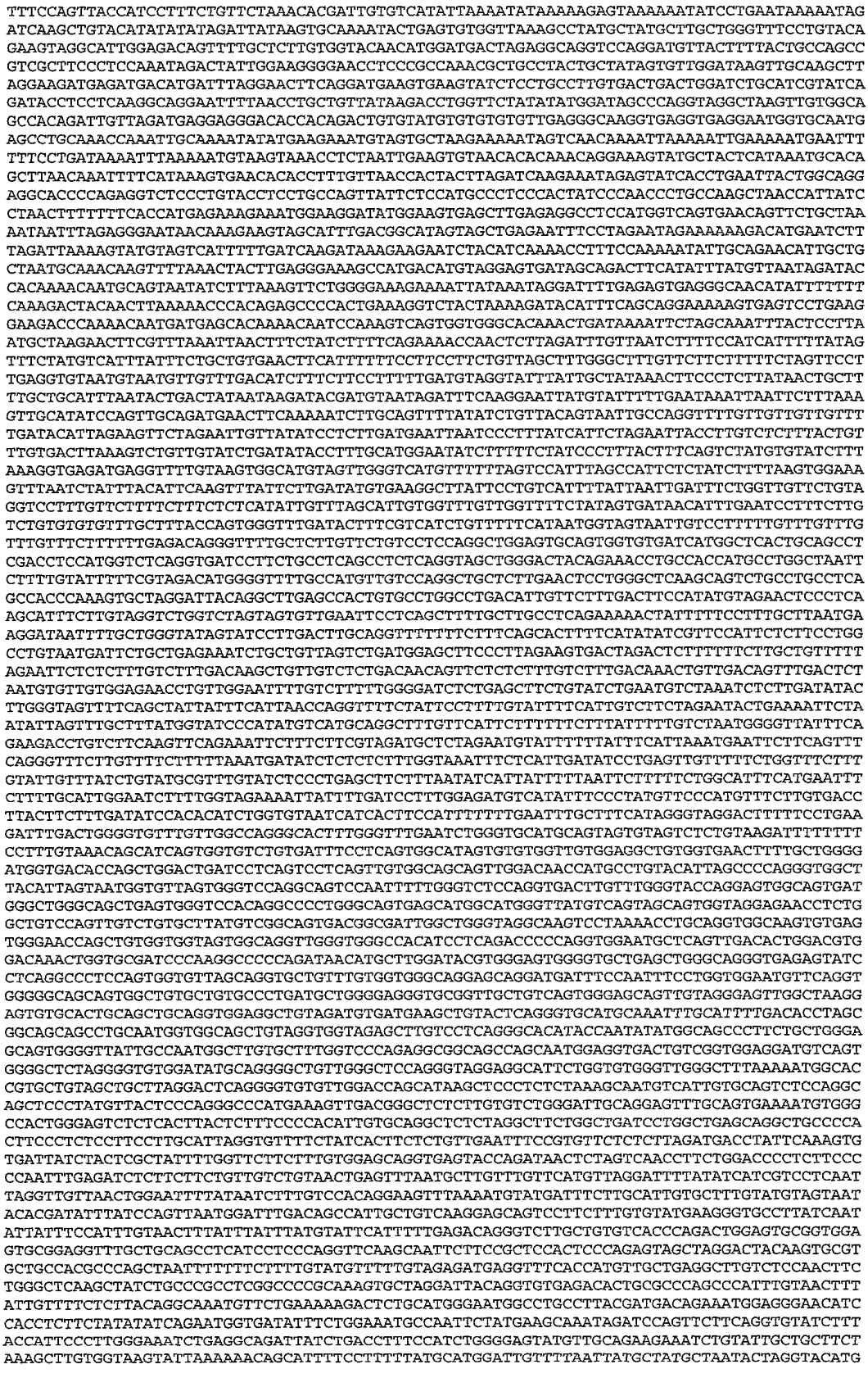
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Replacement Sheet - 12/25/2006

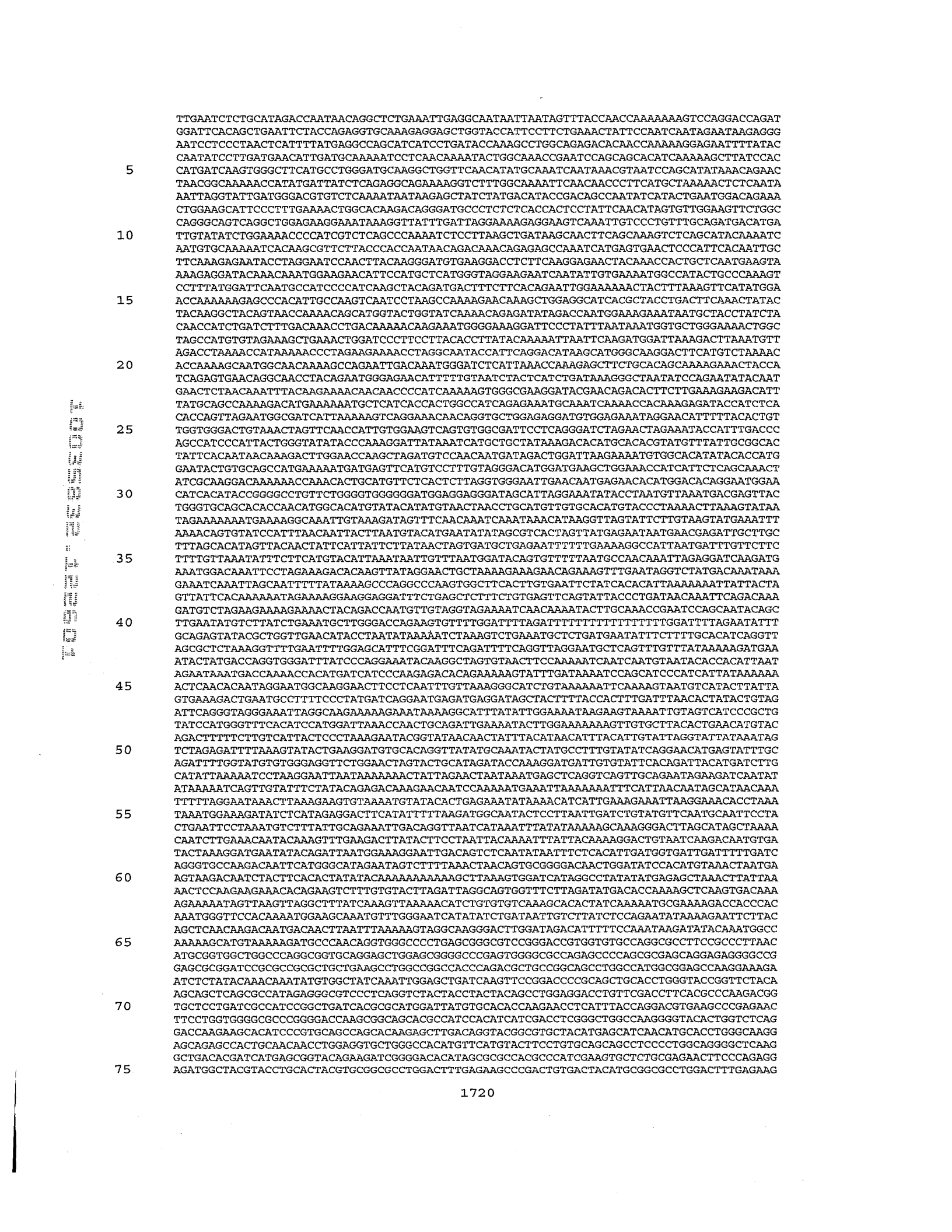


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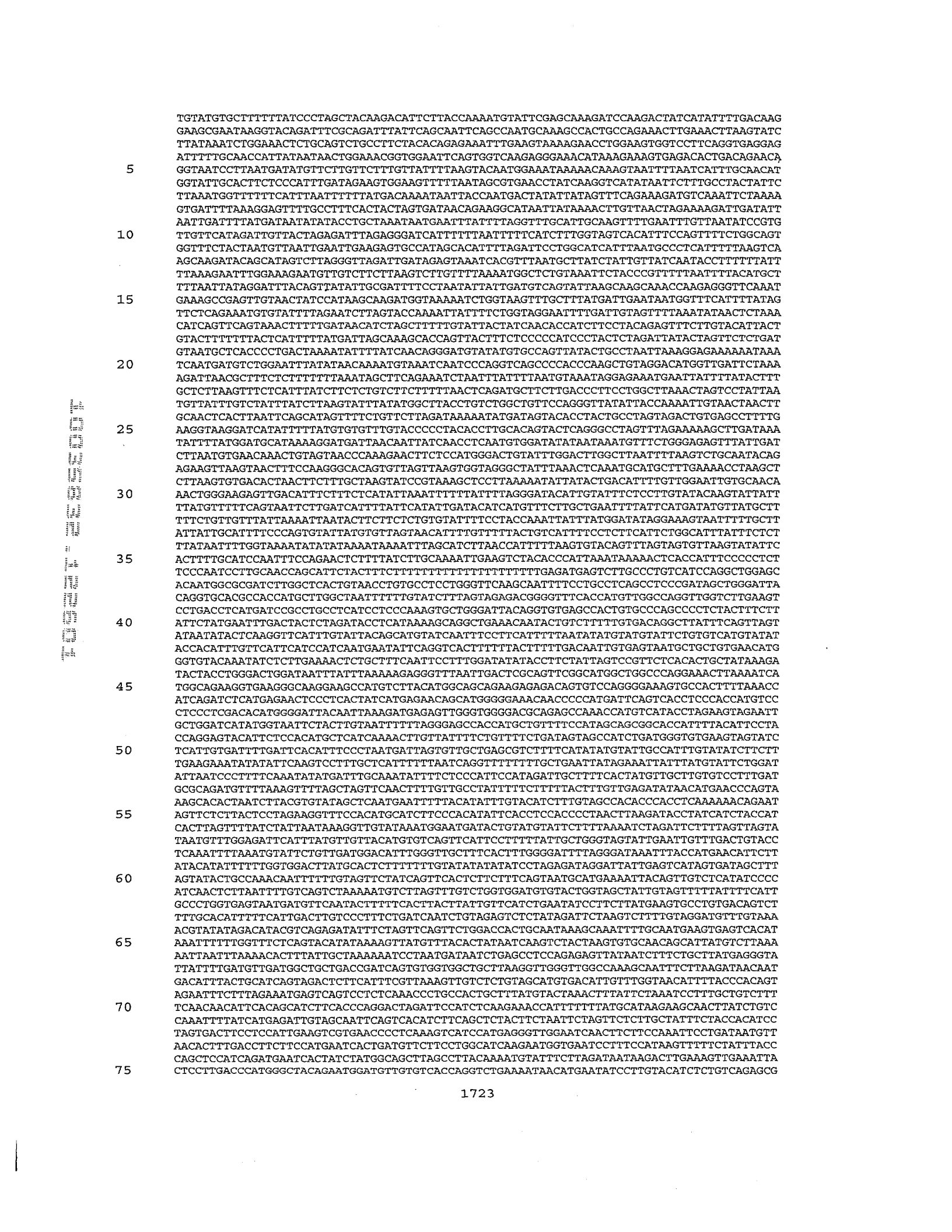
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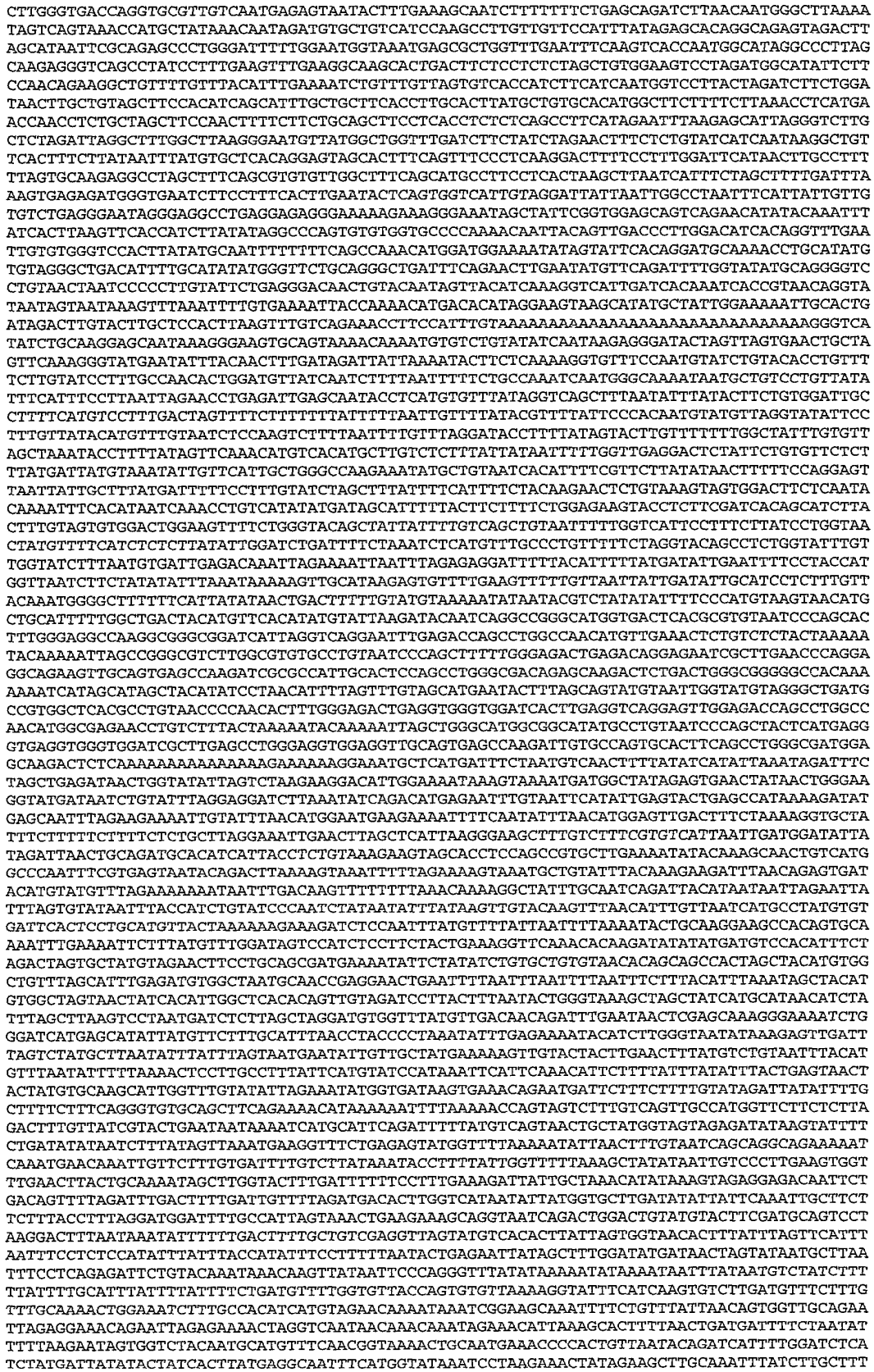
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Translation - 08/06/2004 10:56:00



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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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Application Serial No. 10/552,248
Amendment dated April 30, 2008

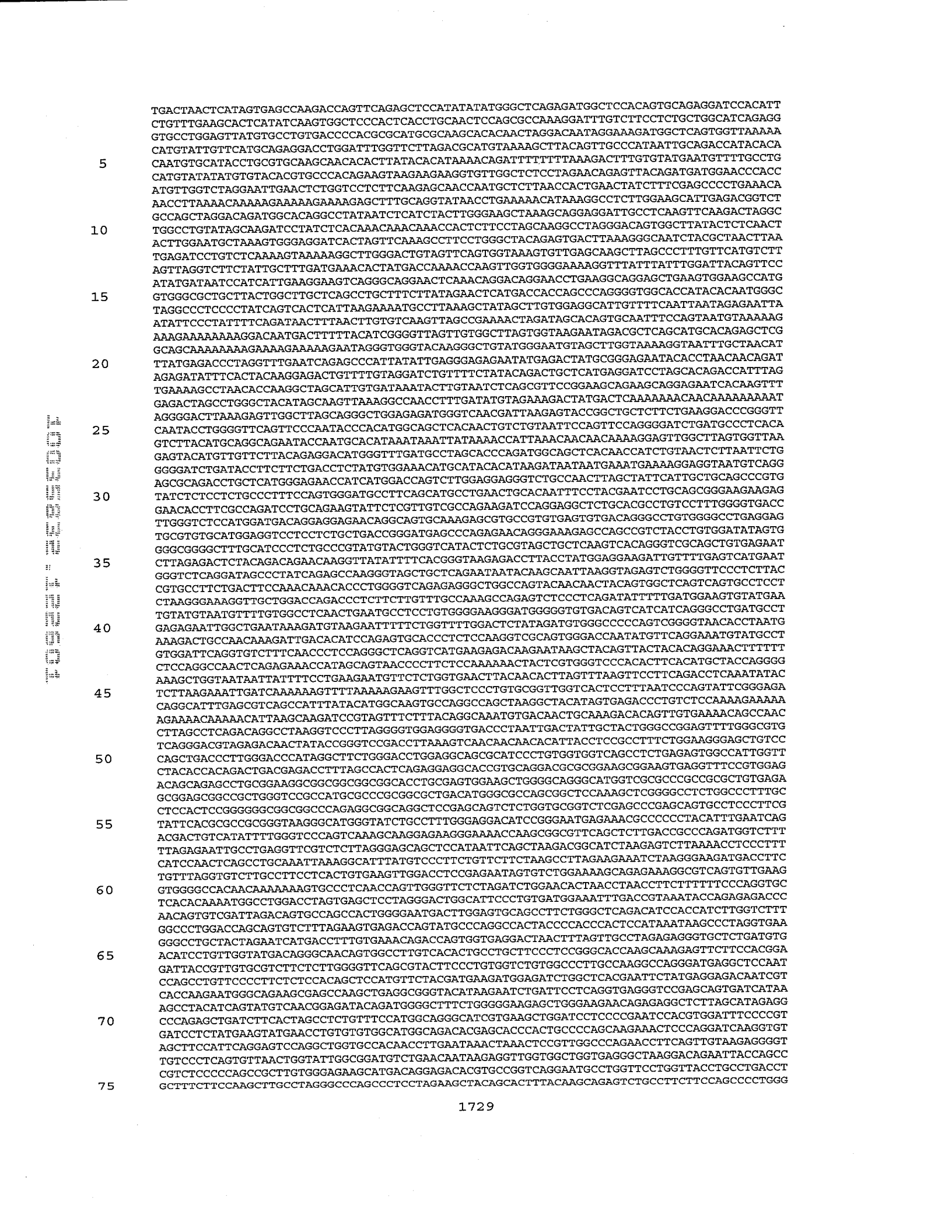
Table 83

MOUSE NOMENCLATURE
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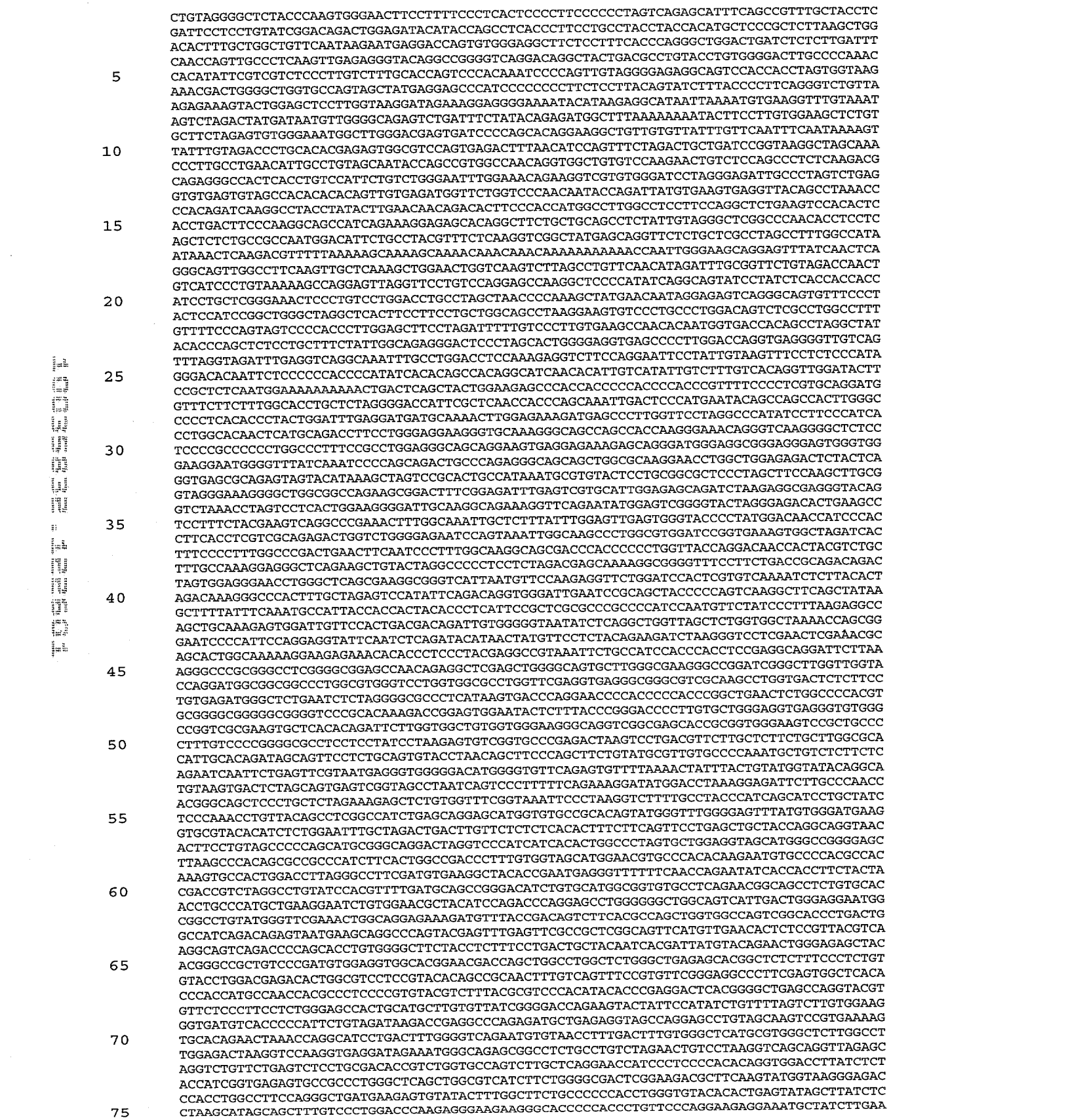
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - CODING

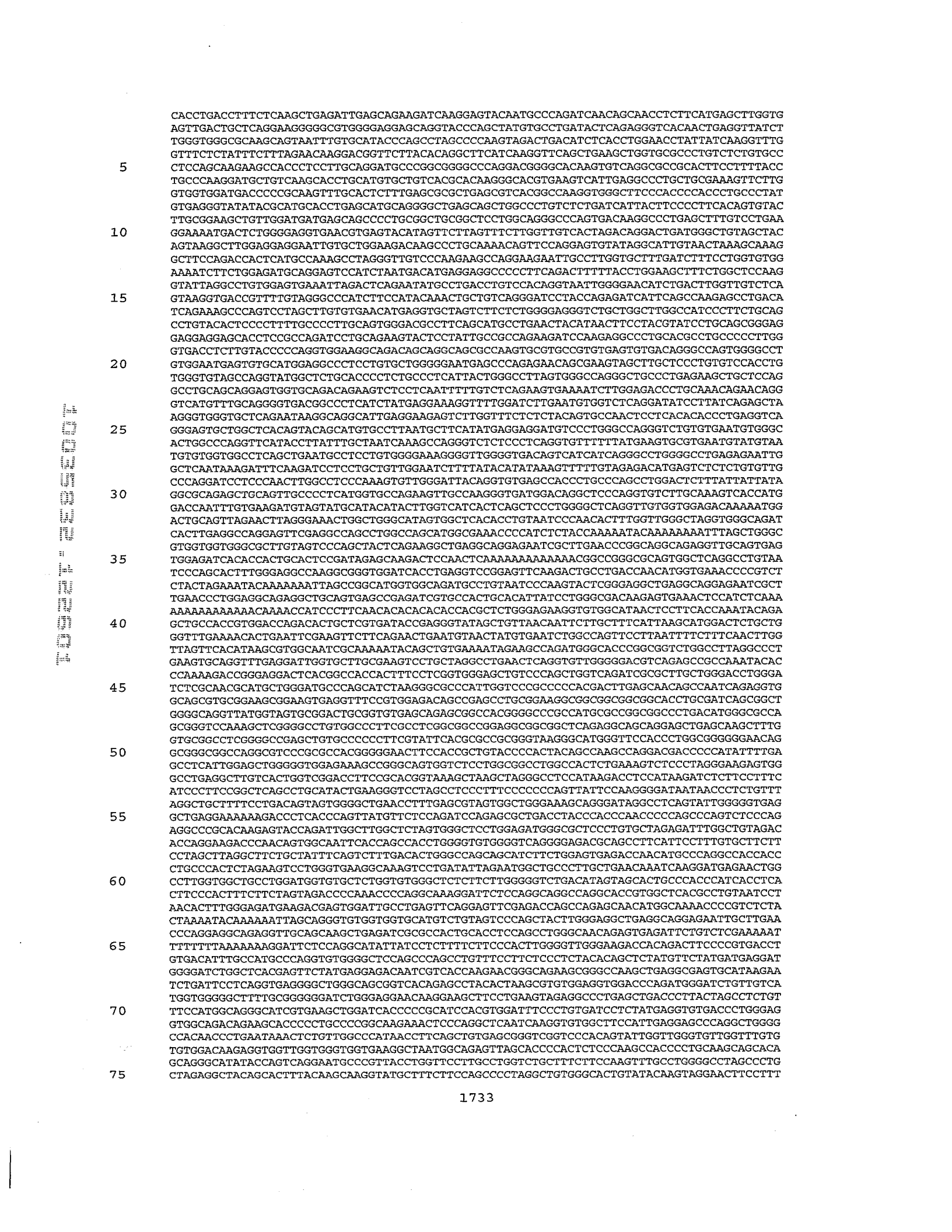
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HUMAN SEQUENCE - GENOMIC

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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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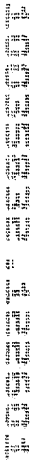
Table 84

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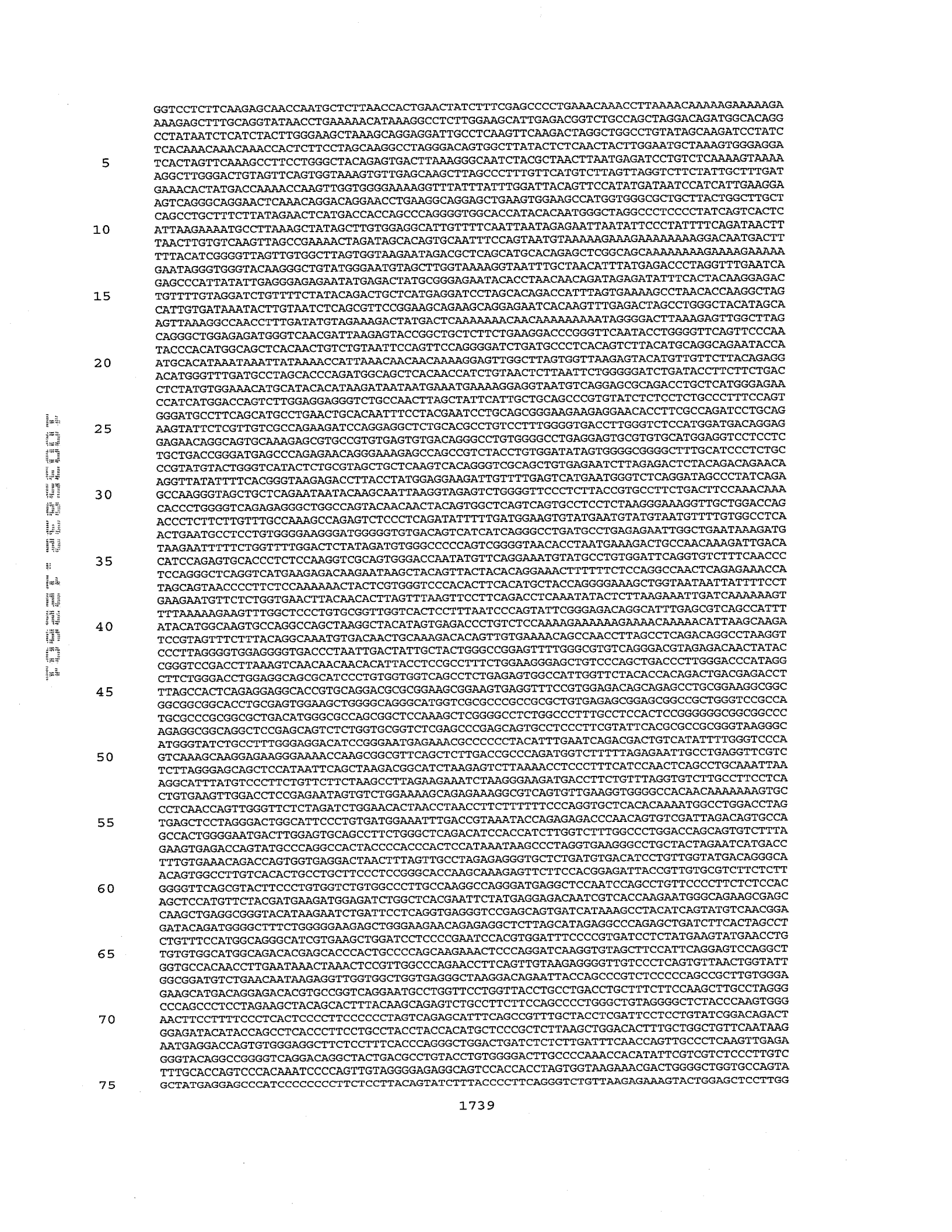
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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

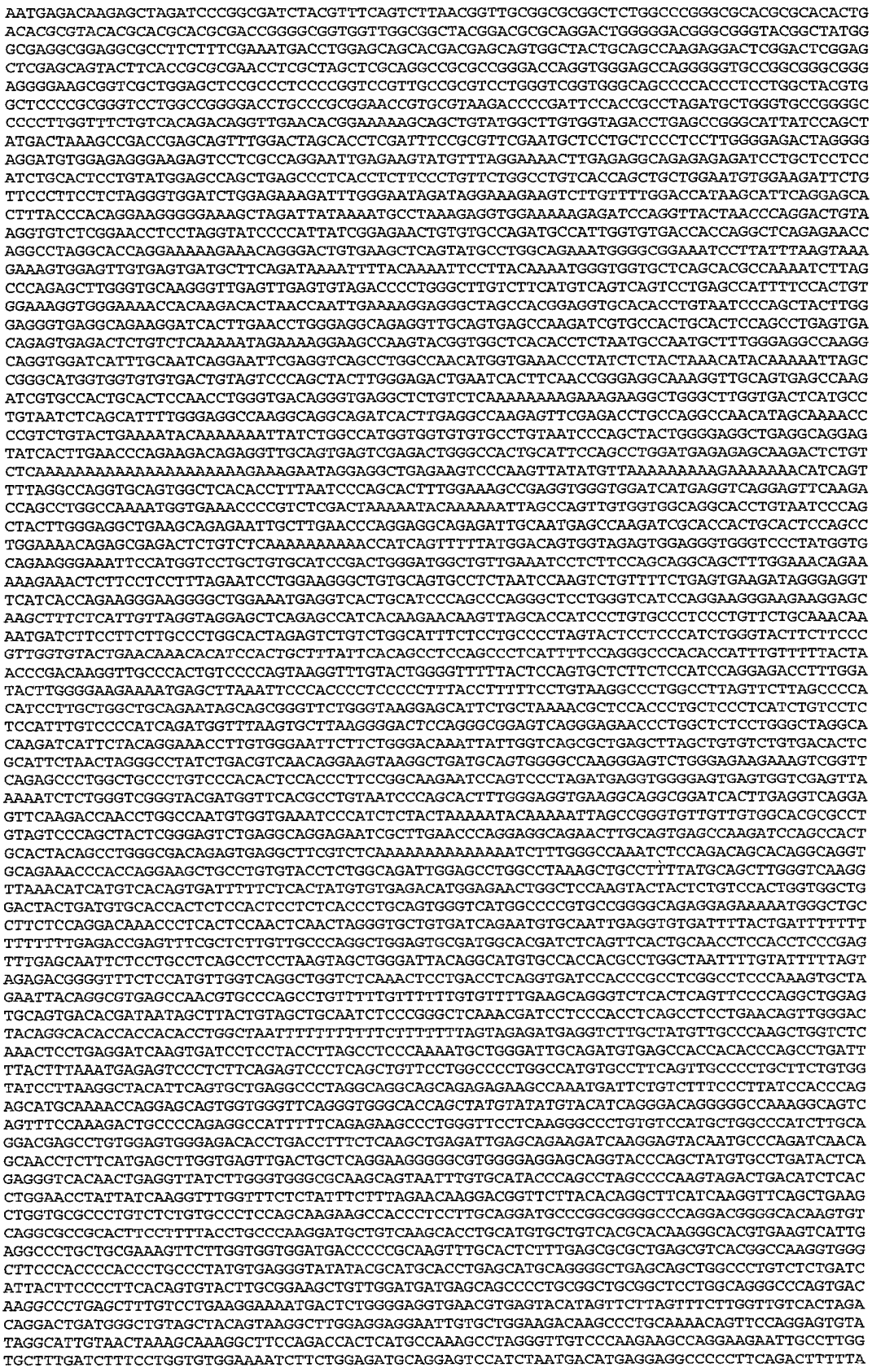
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HUMAN SEQUENCE - GENOMIC

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HUMAN SEQUENCE - mRNA

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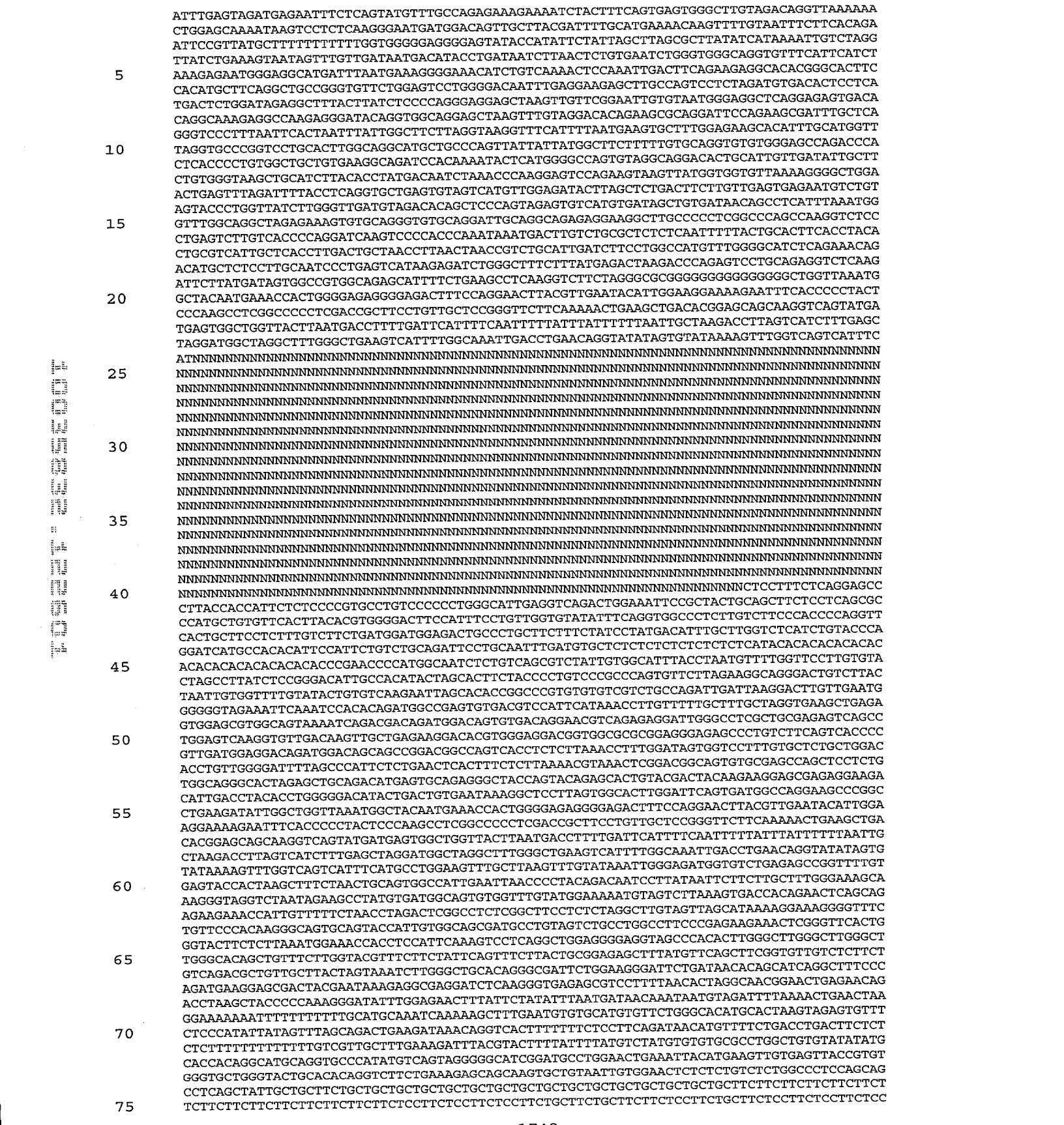
Table 85

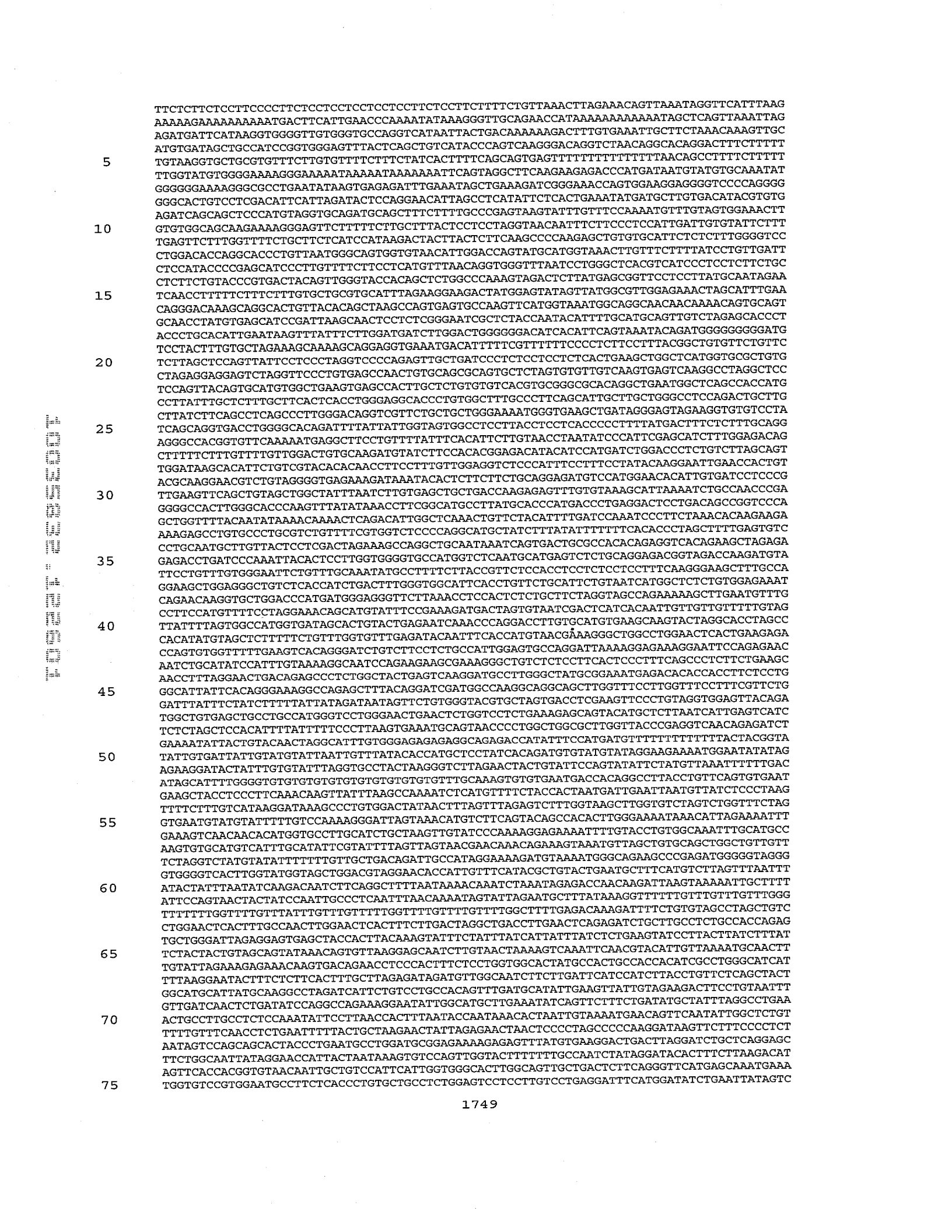
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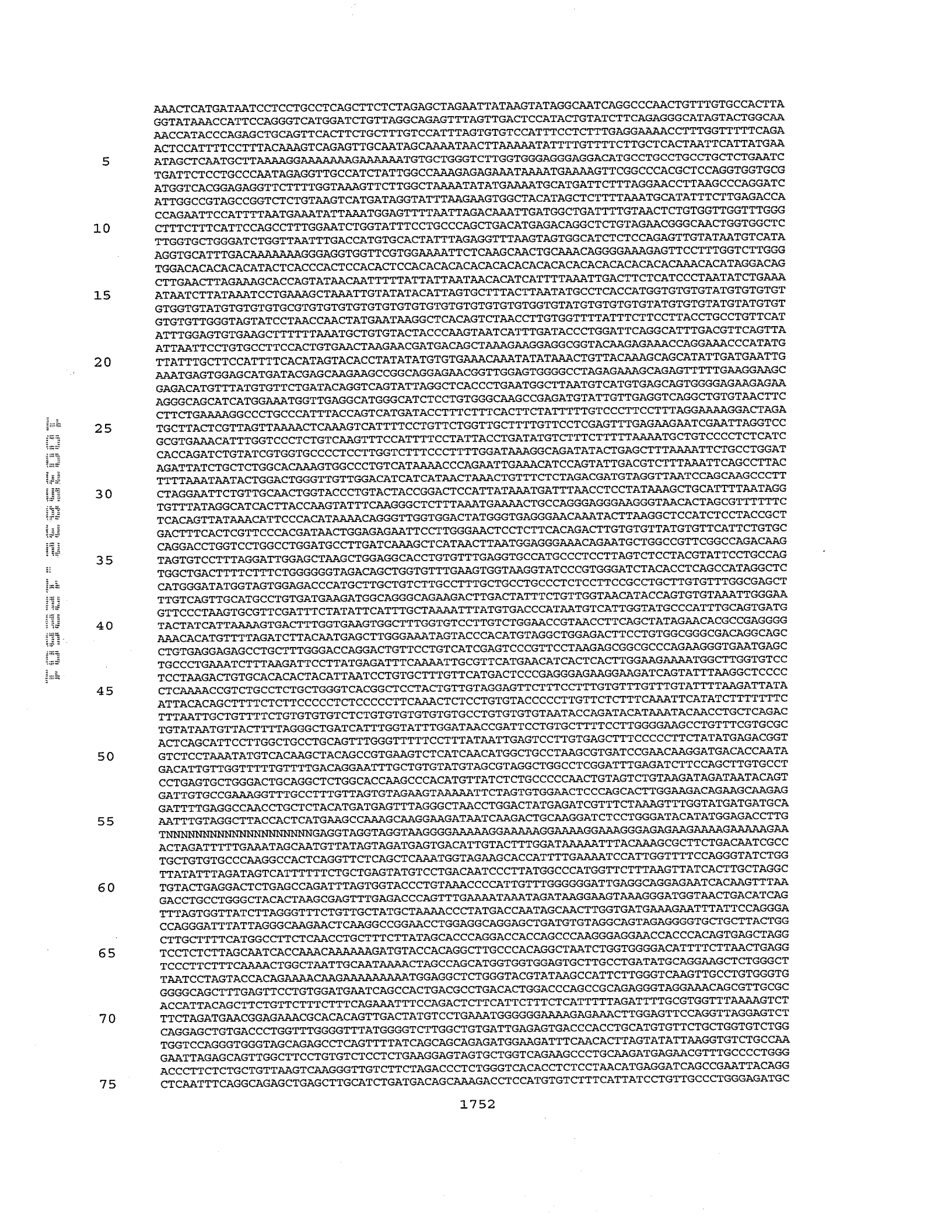


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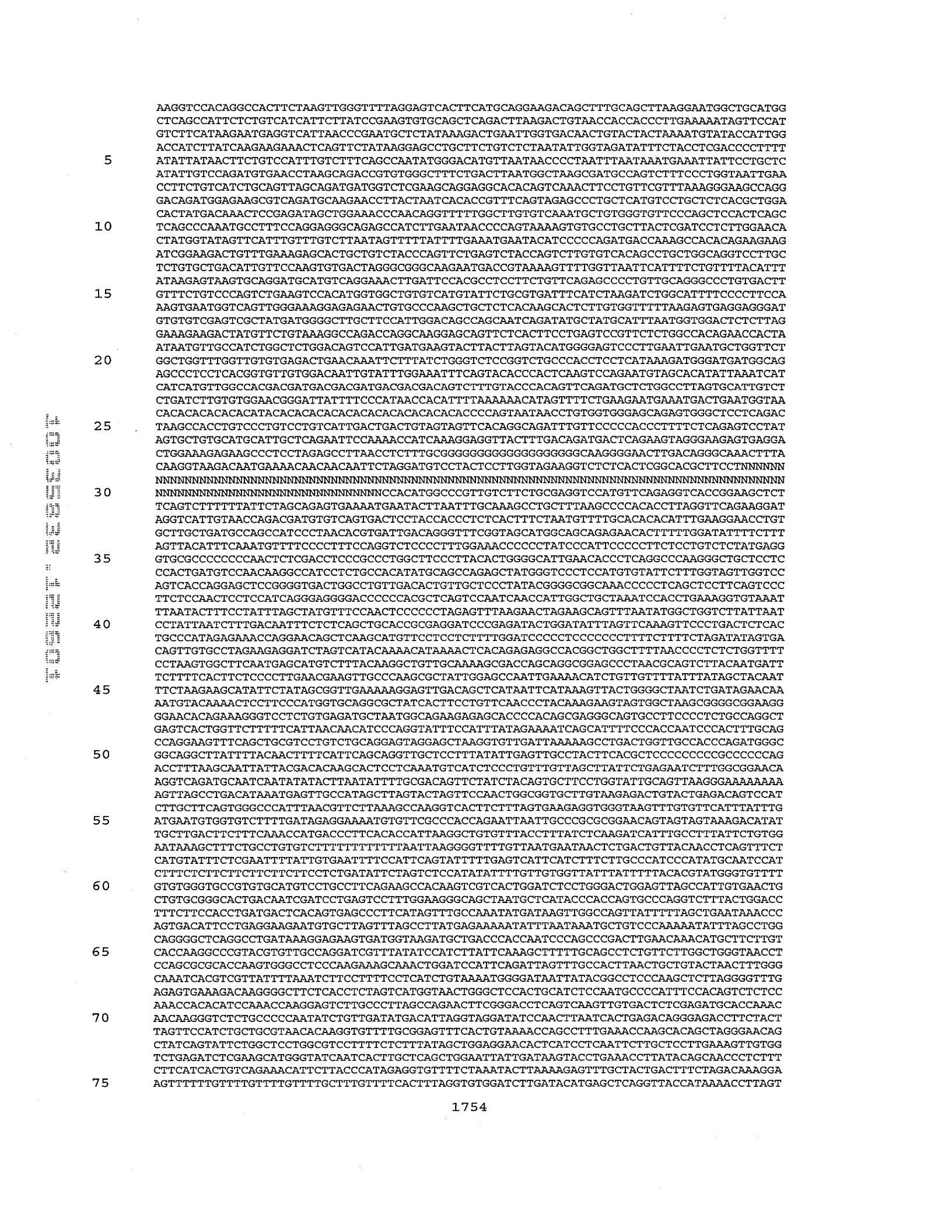
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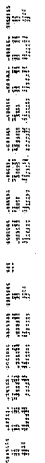


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FIGURE 3 SEQUENCE LISTING

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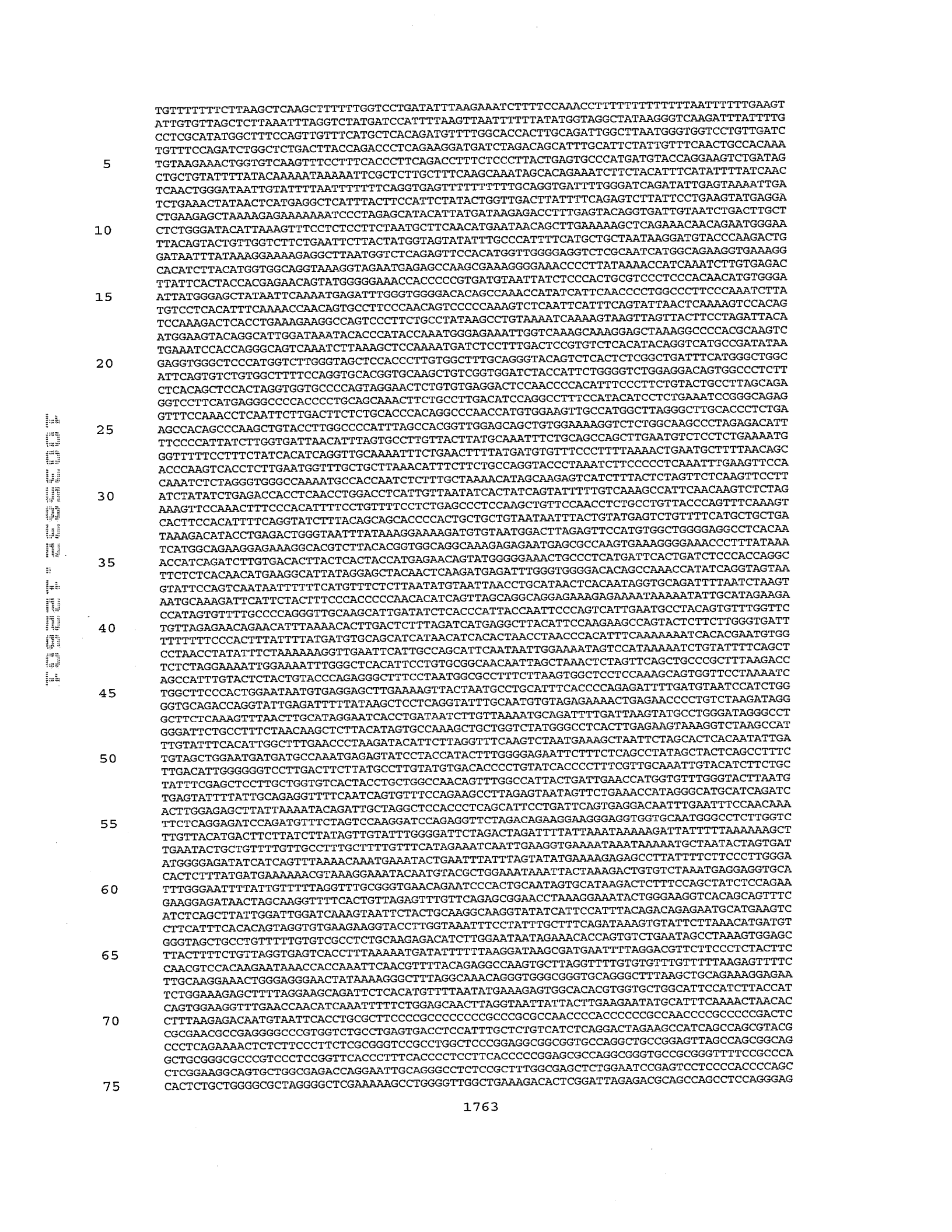
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MOUSE SEQUENCE - mRNA
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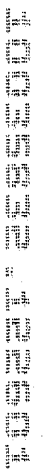
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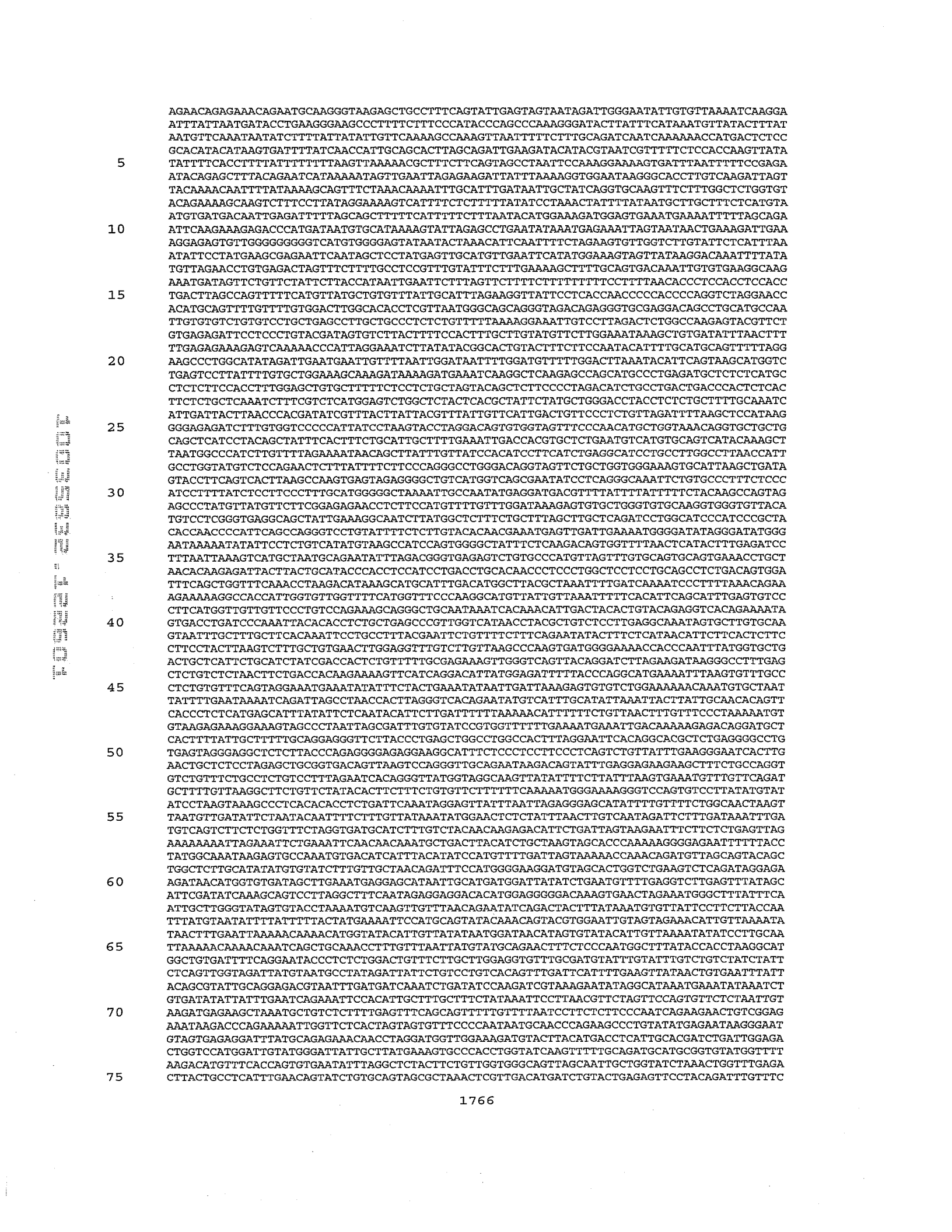


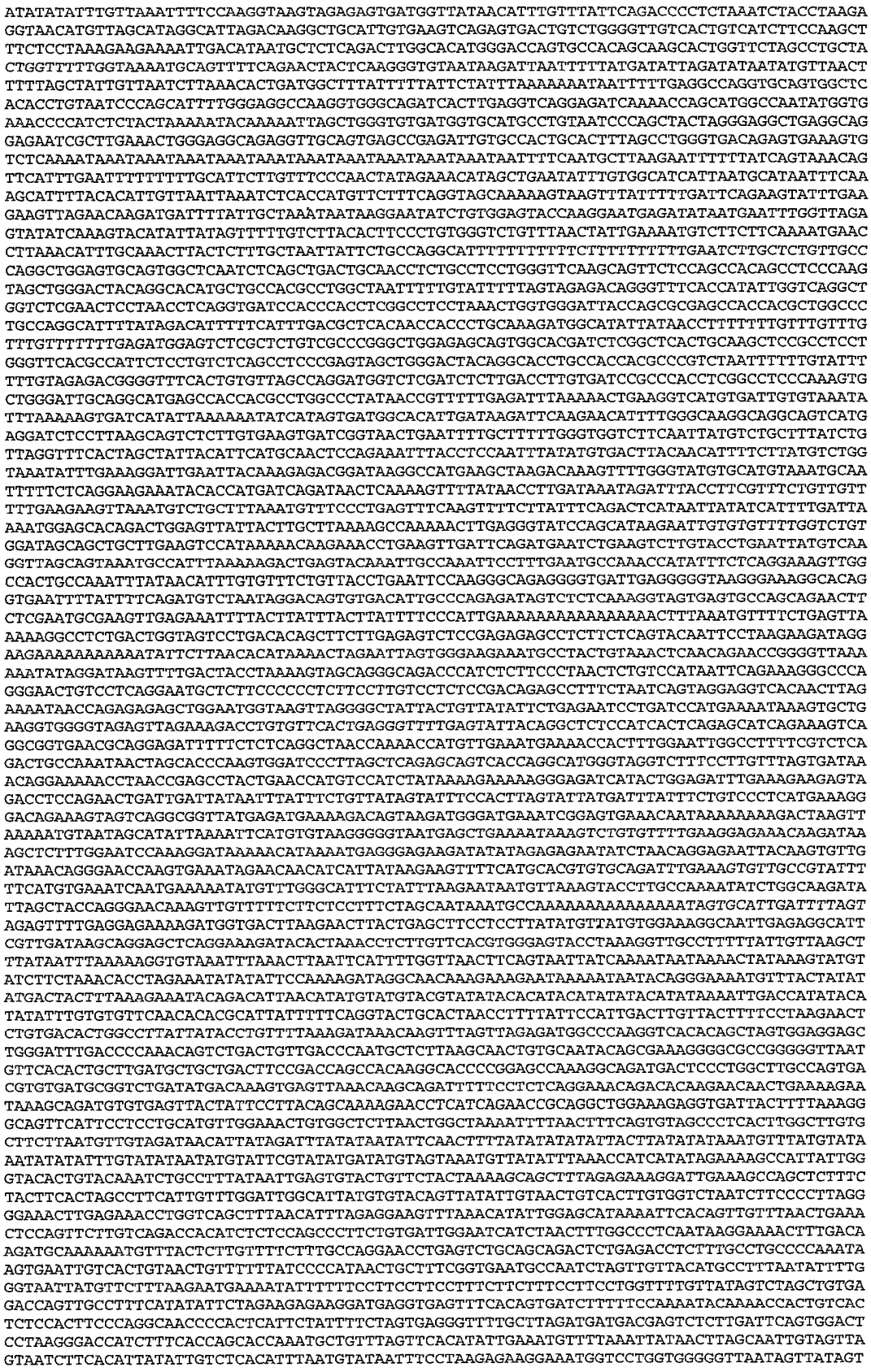
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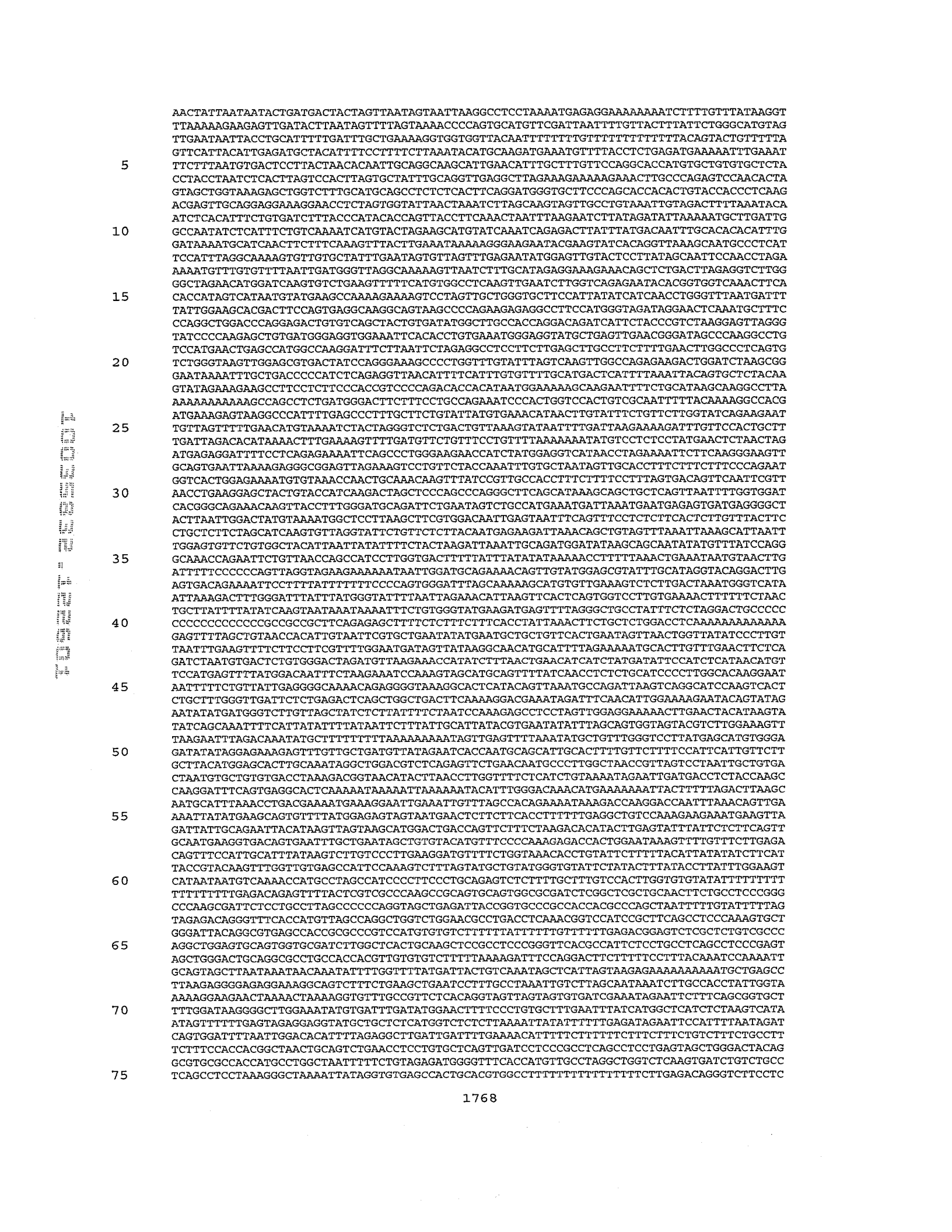
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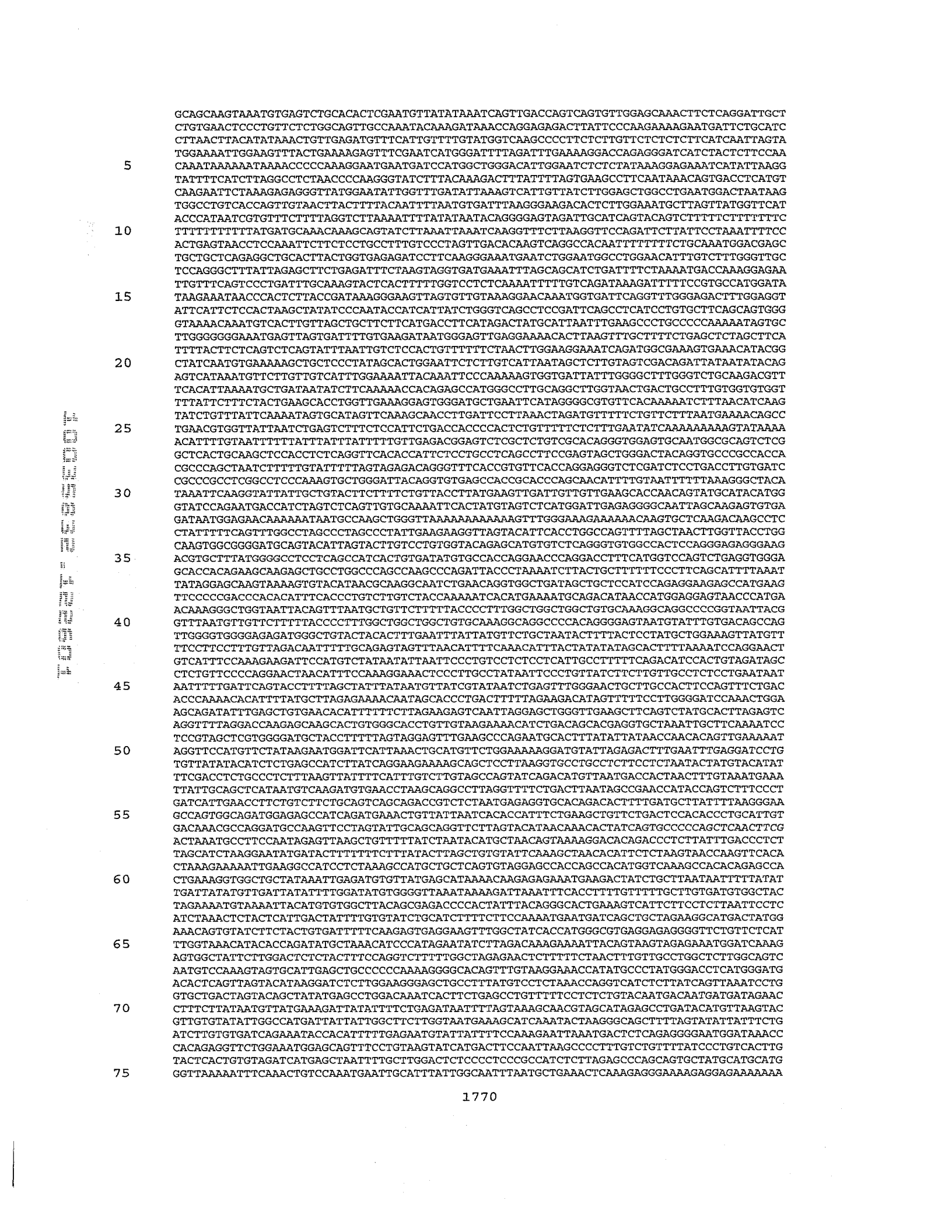
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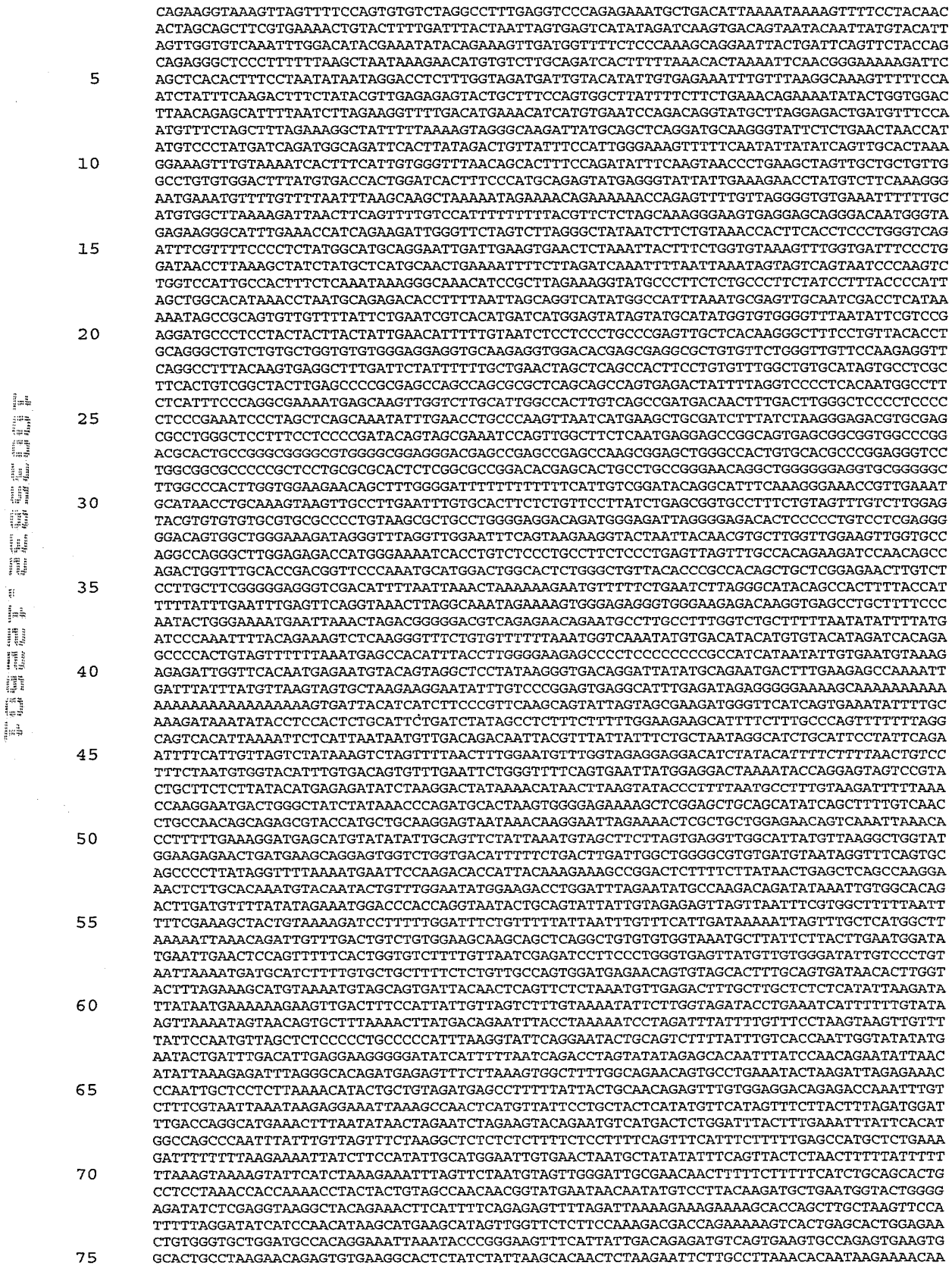
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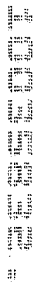
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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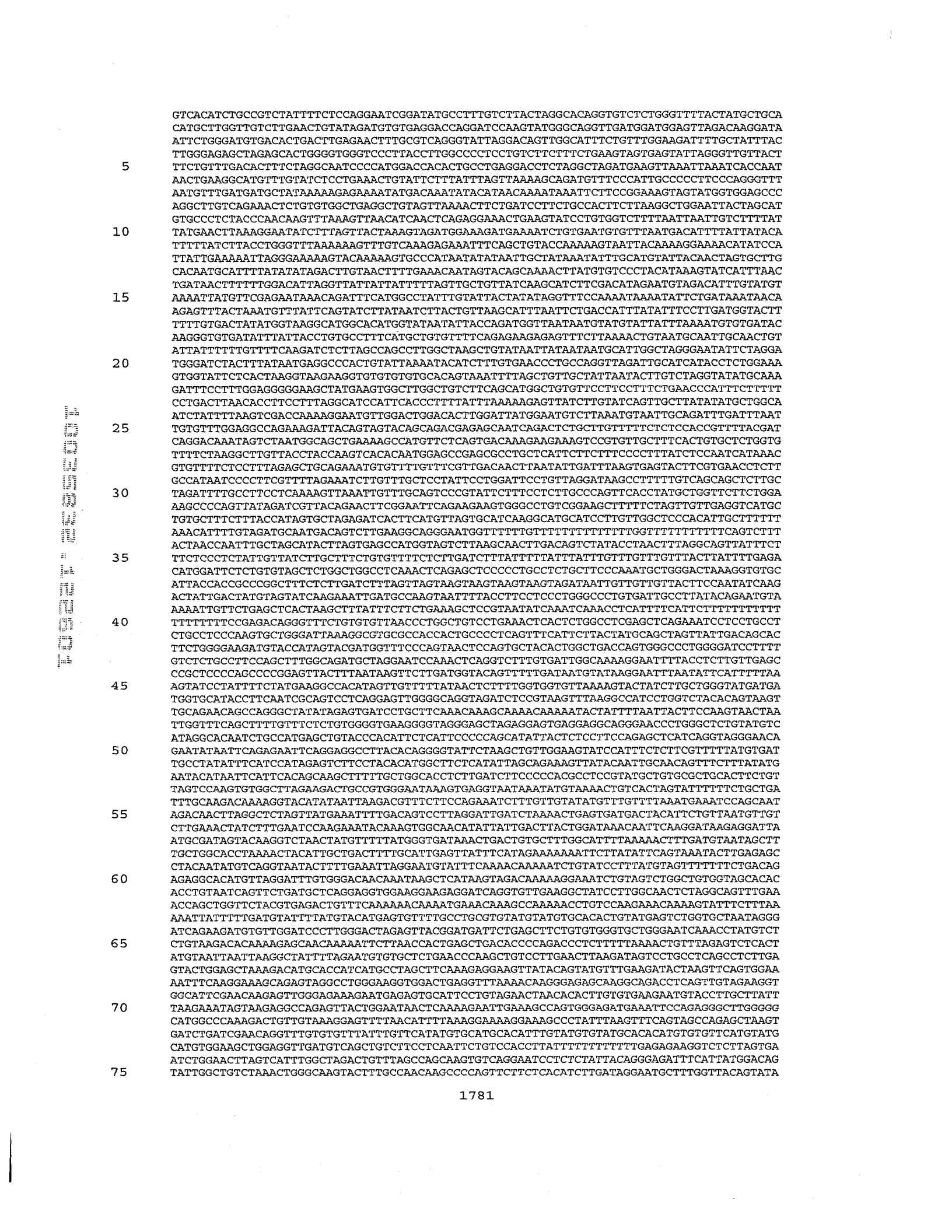
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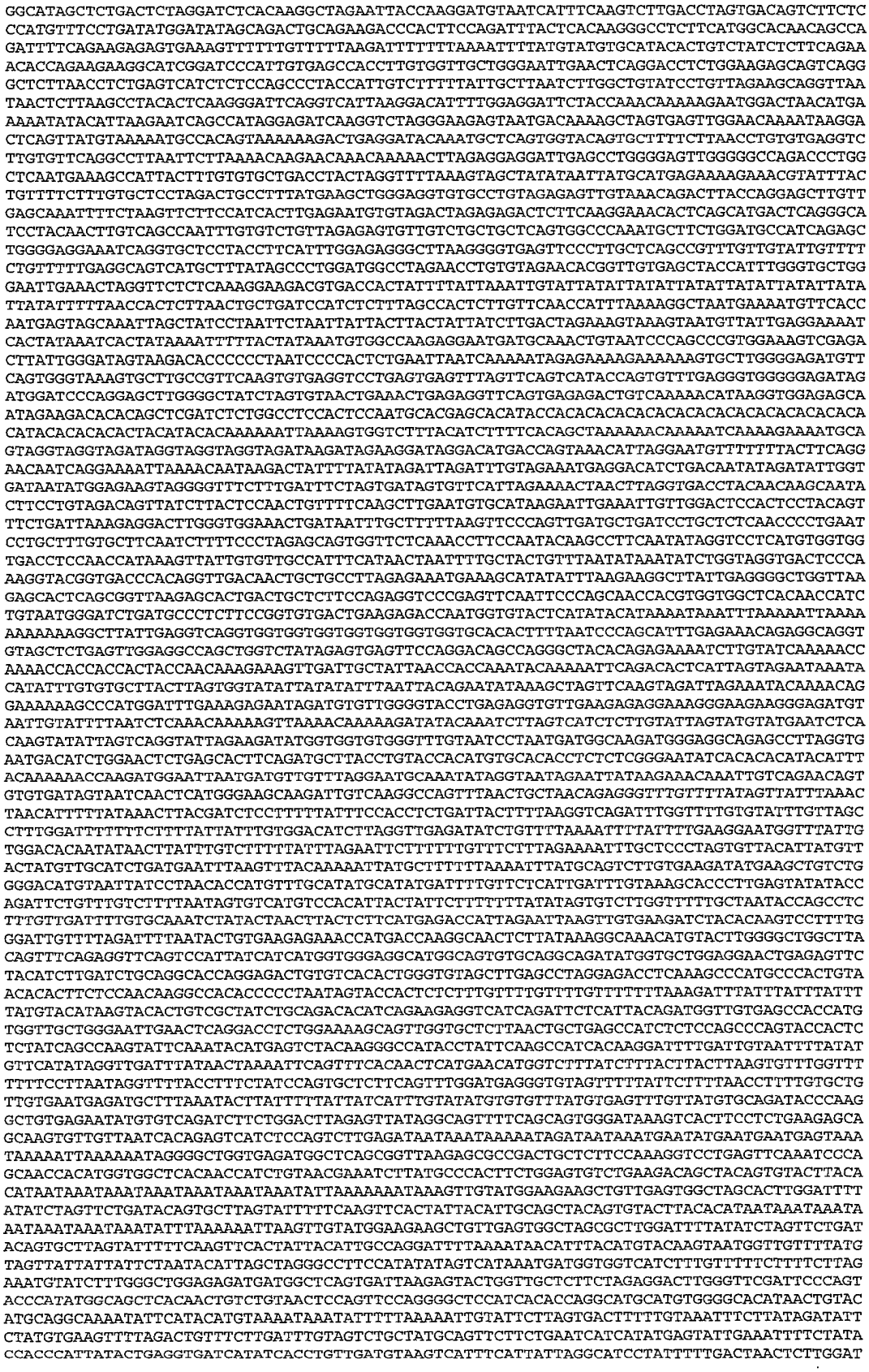
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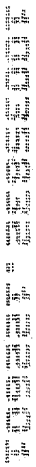
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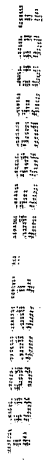
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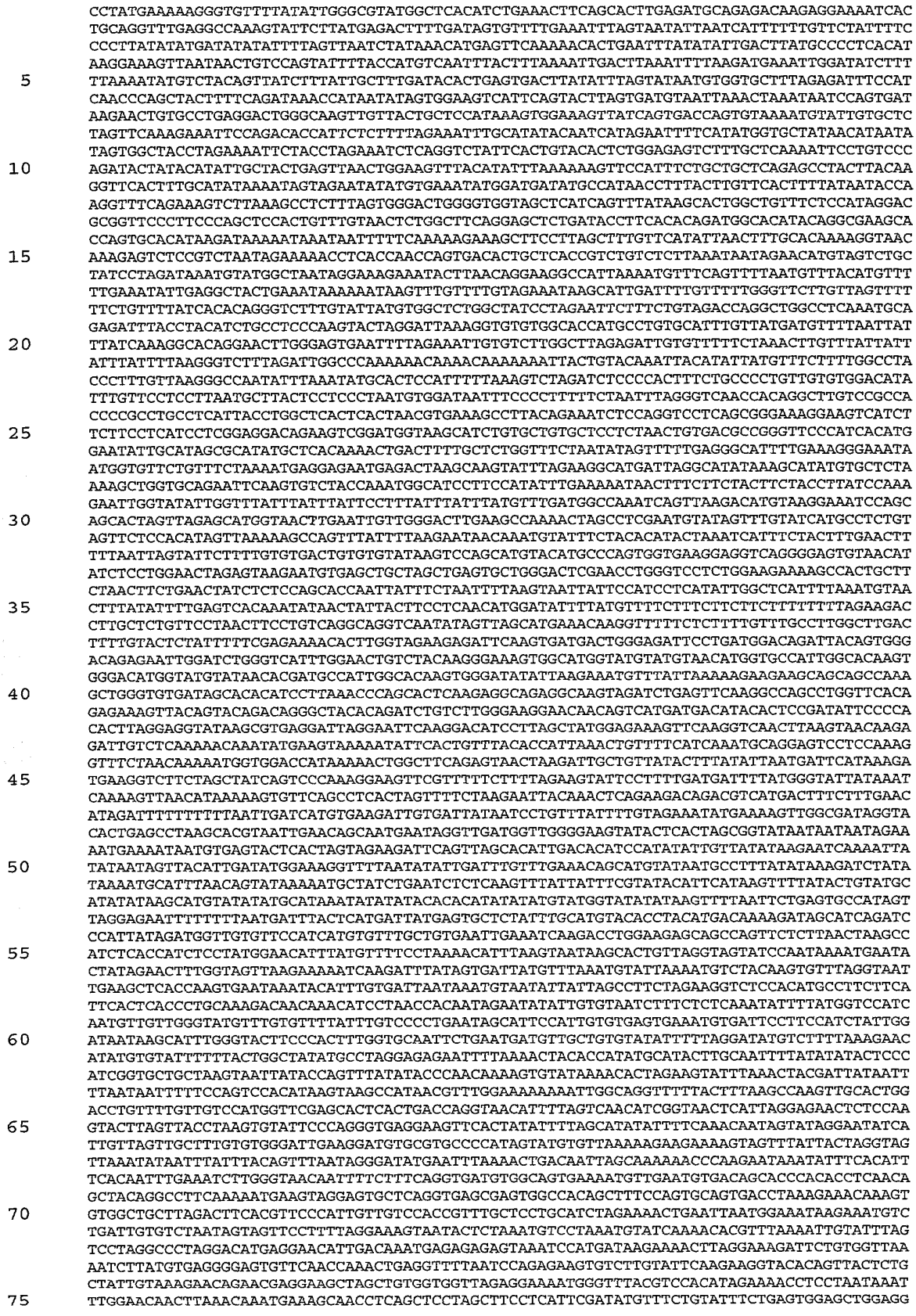
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Replacement Sheet



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MOUSE SEQUENCE - mRNA
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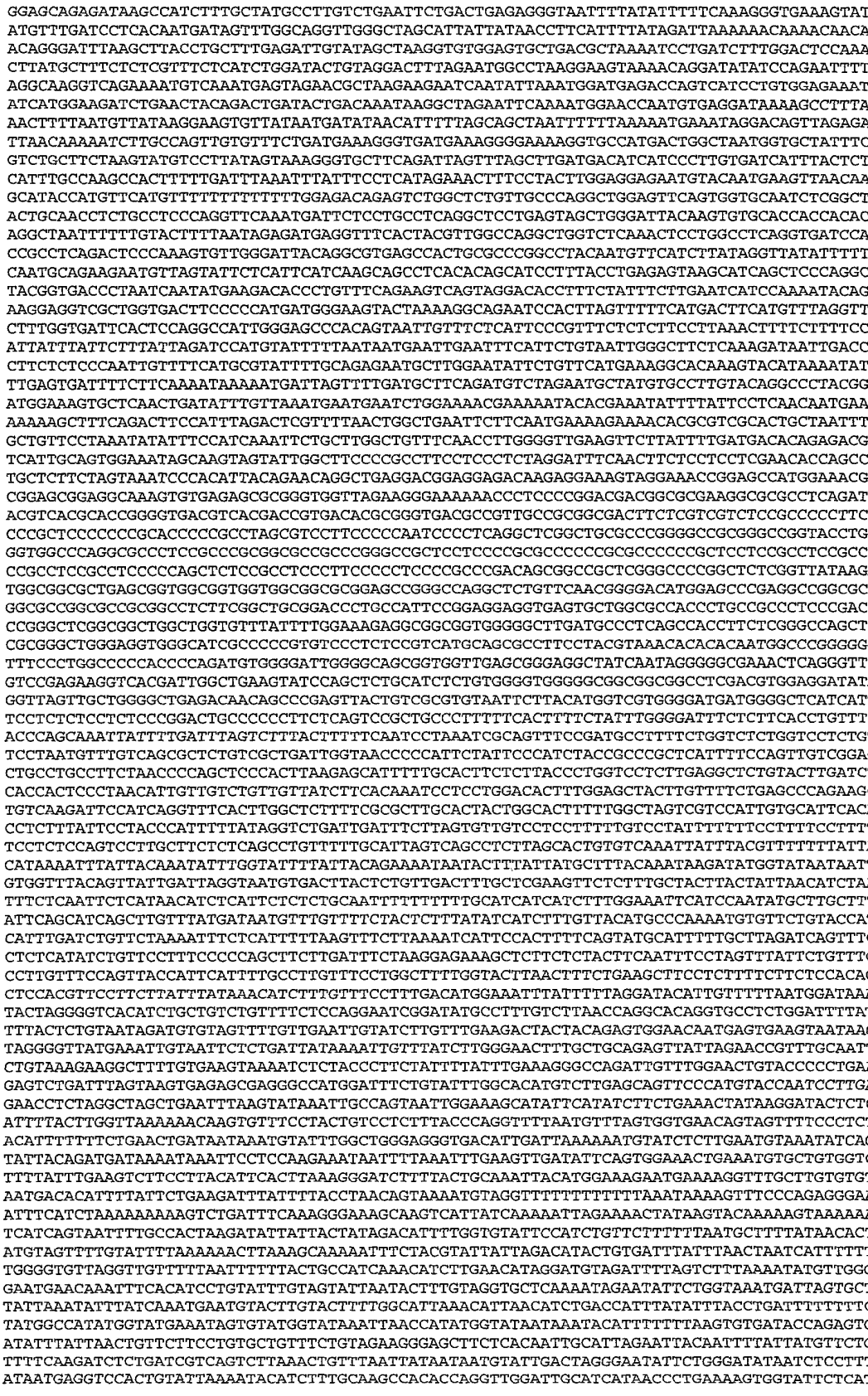
MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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FIGURE 35 SEQUENCE

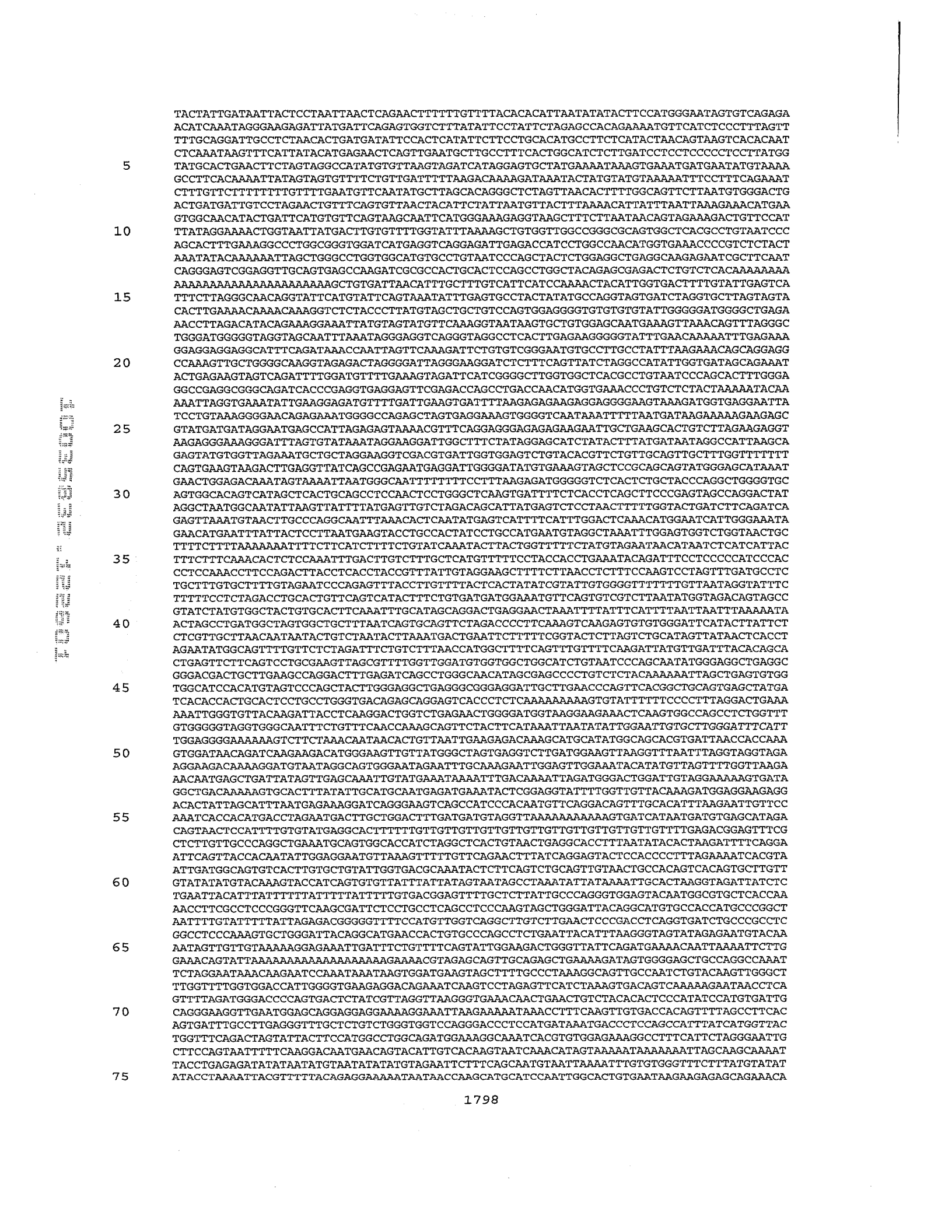
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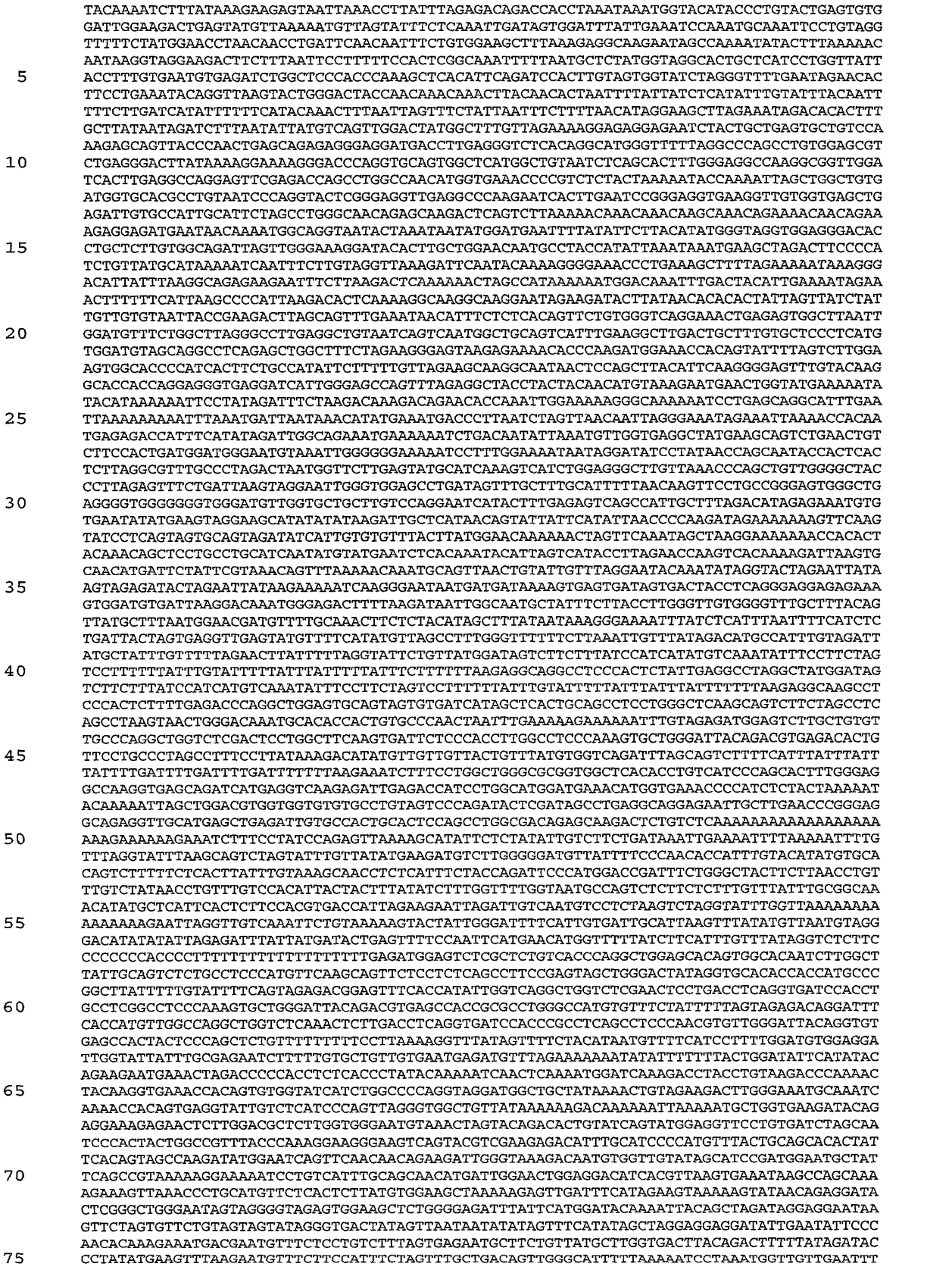


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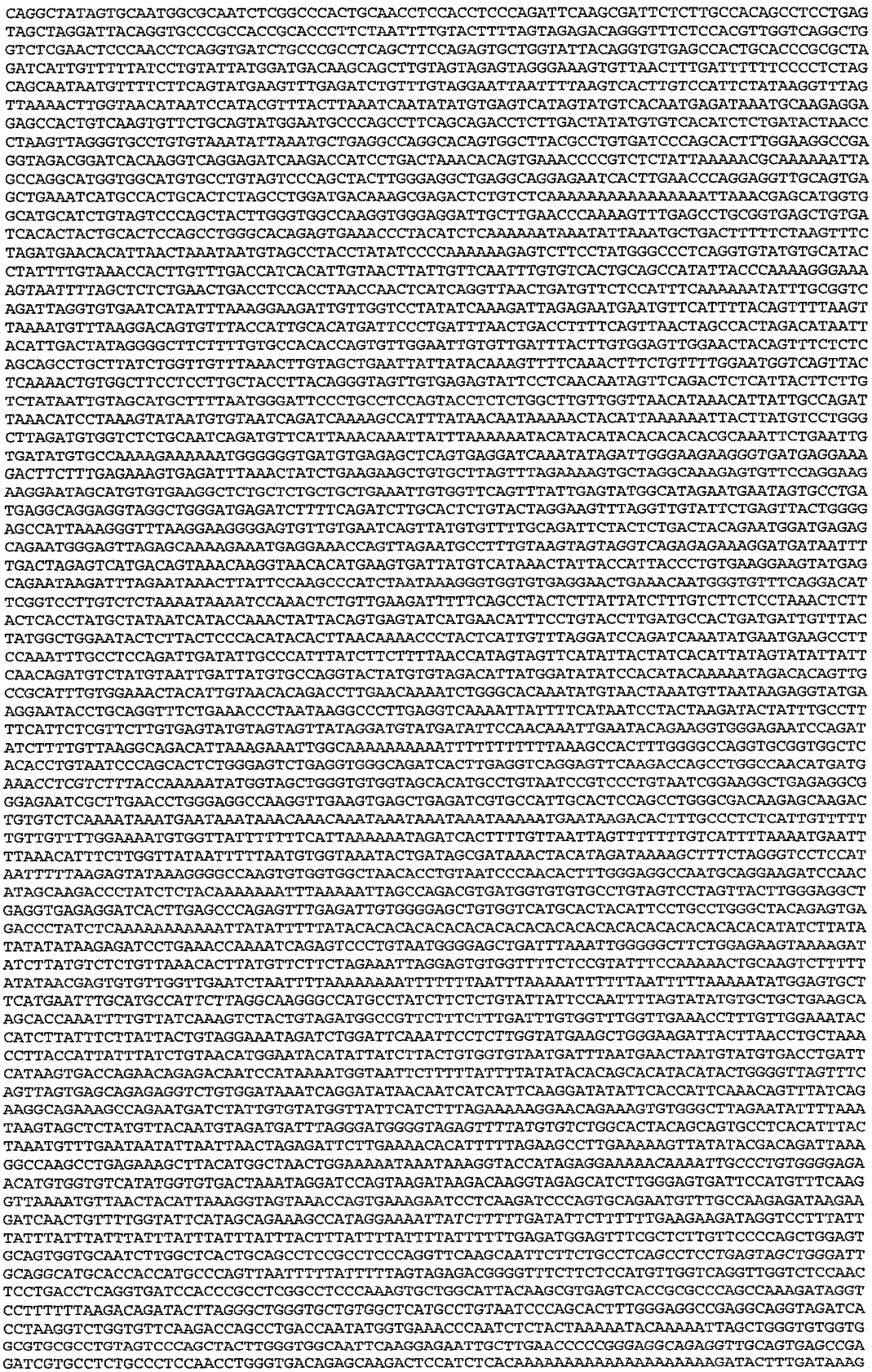


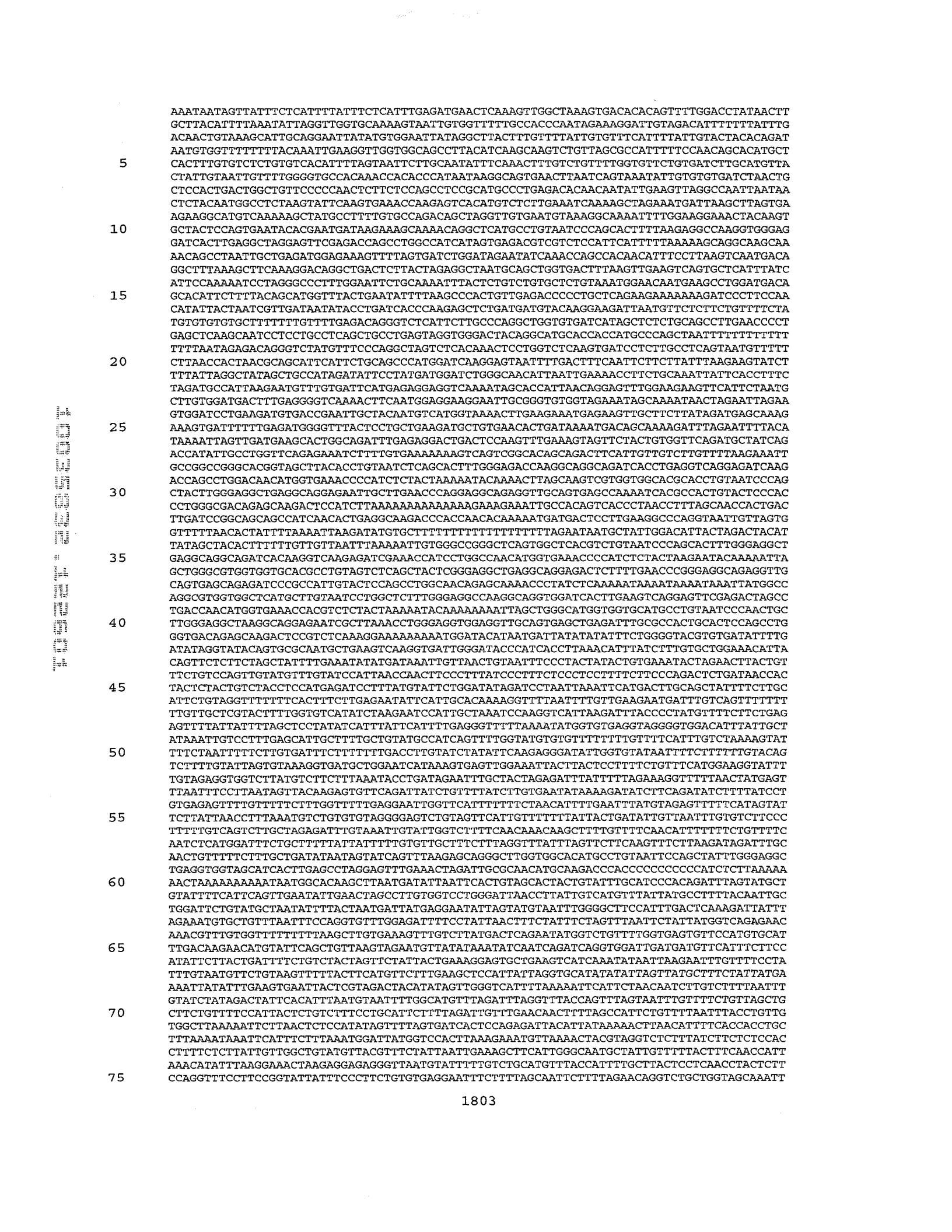
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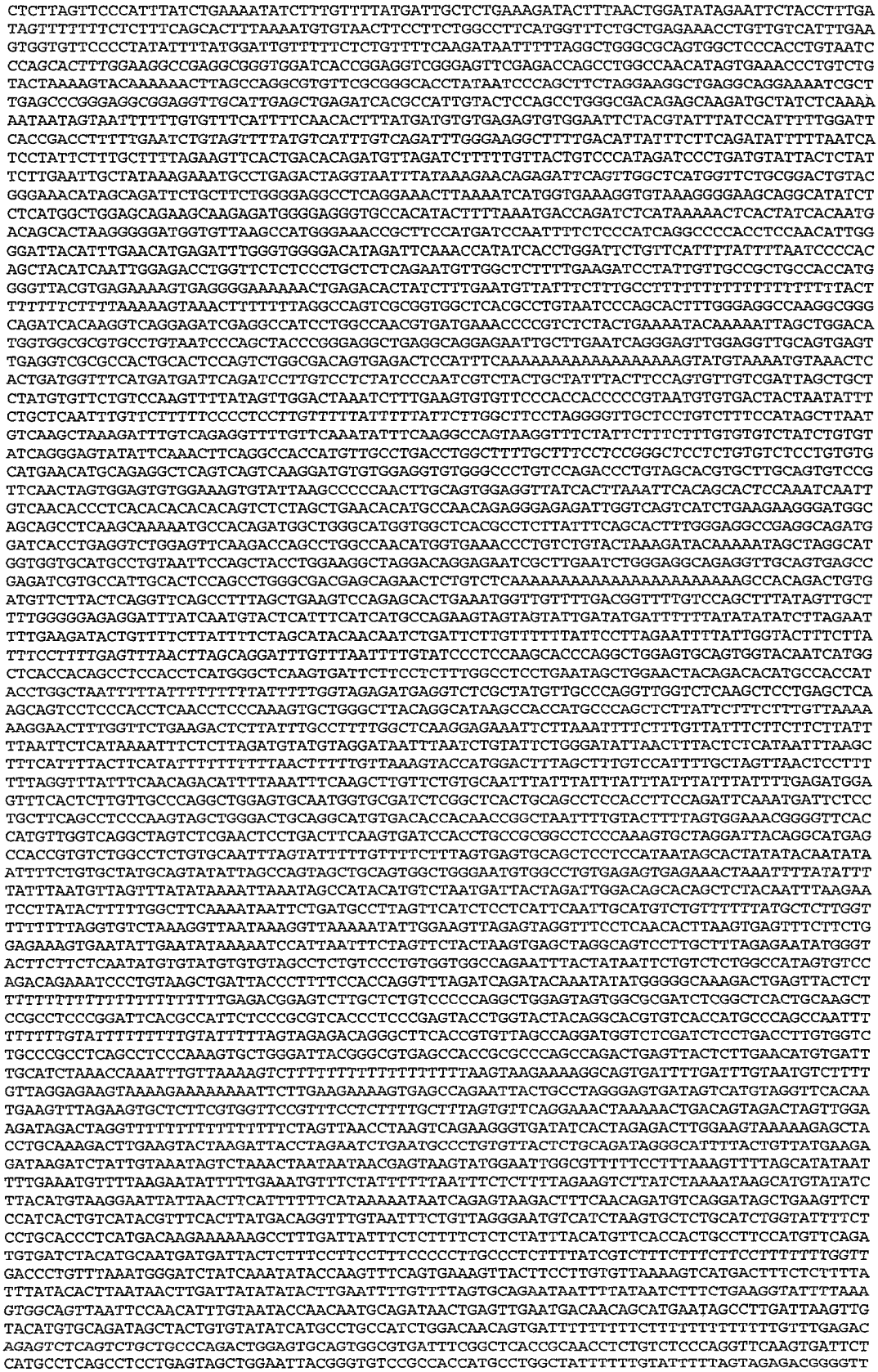
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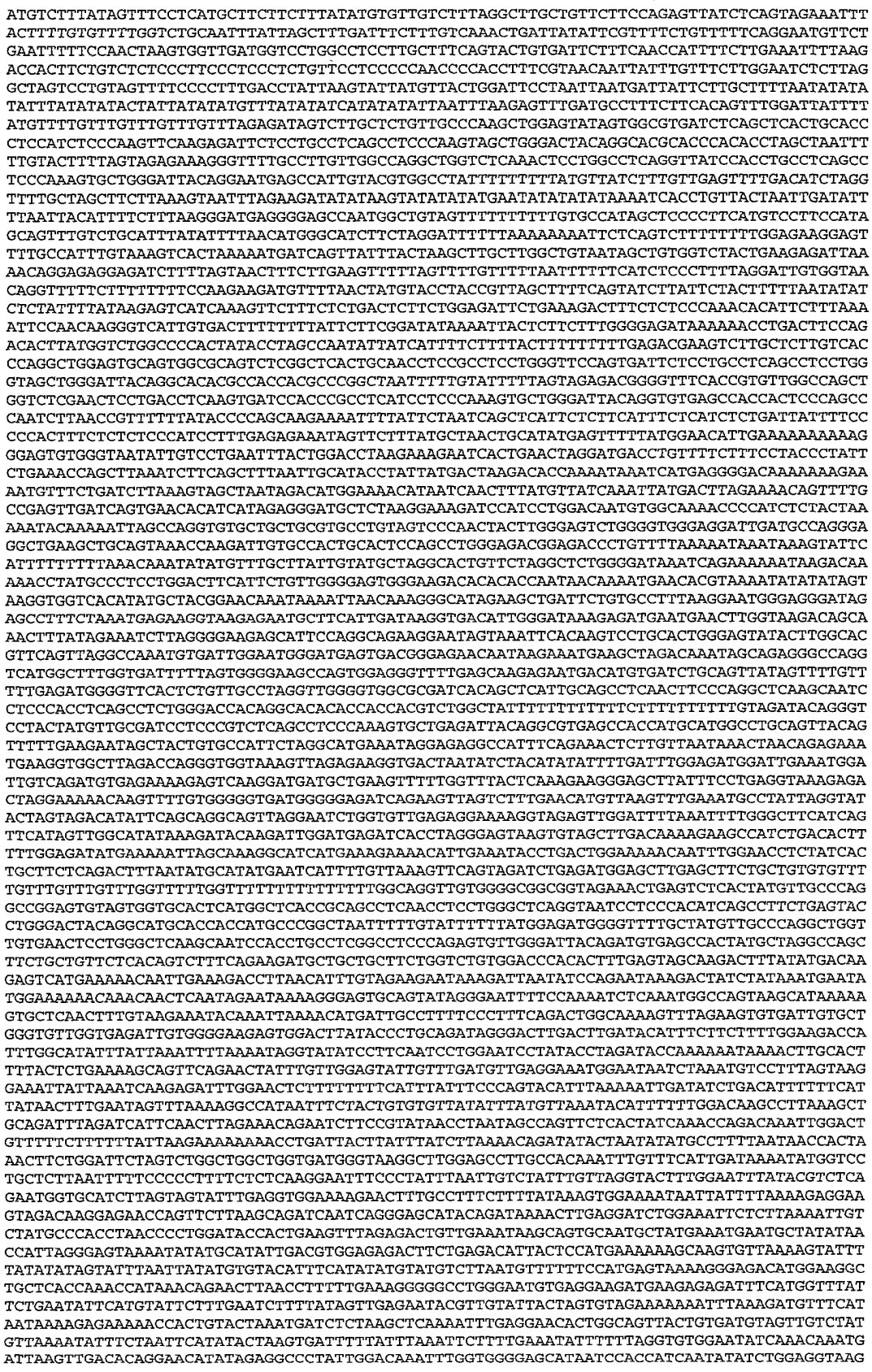
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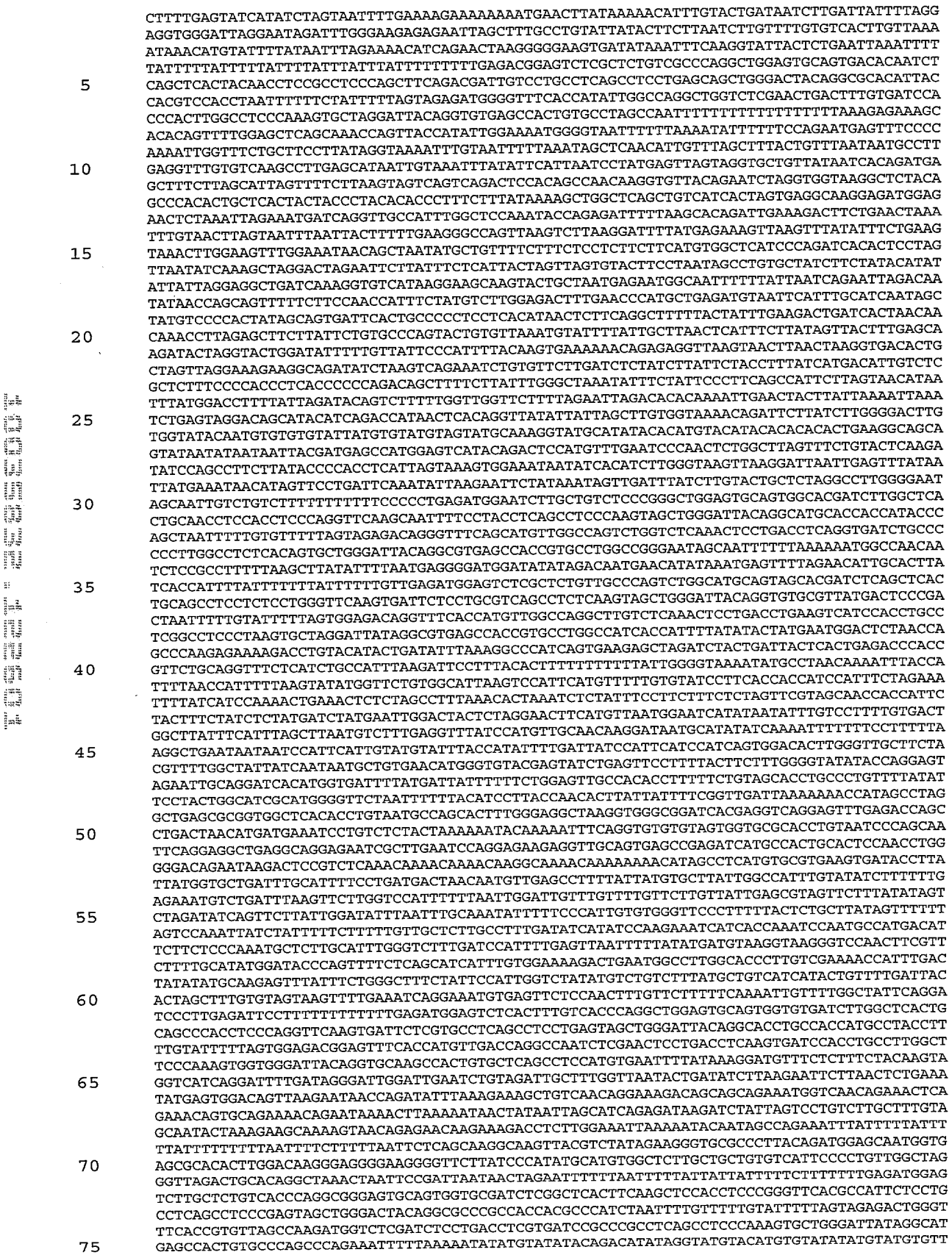


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FIGURE 1 - SEQUENCE LISTING

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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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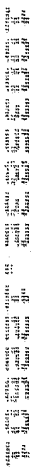
Table 87

MOUSE NOMENCLATURE
ICSGNM Tle3
Celera mCG21830

HUMAN NOMENCLATURE
HGNC TLE3
Celera hCG38796

MOUSE SEQUENCE - GENOMIC

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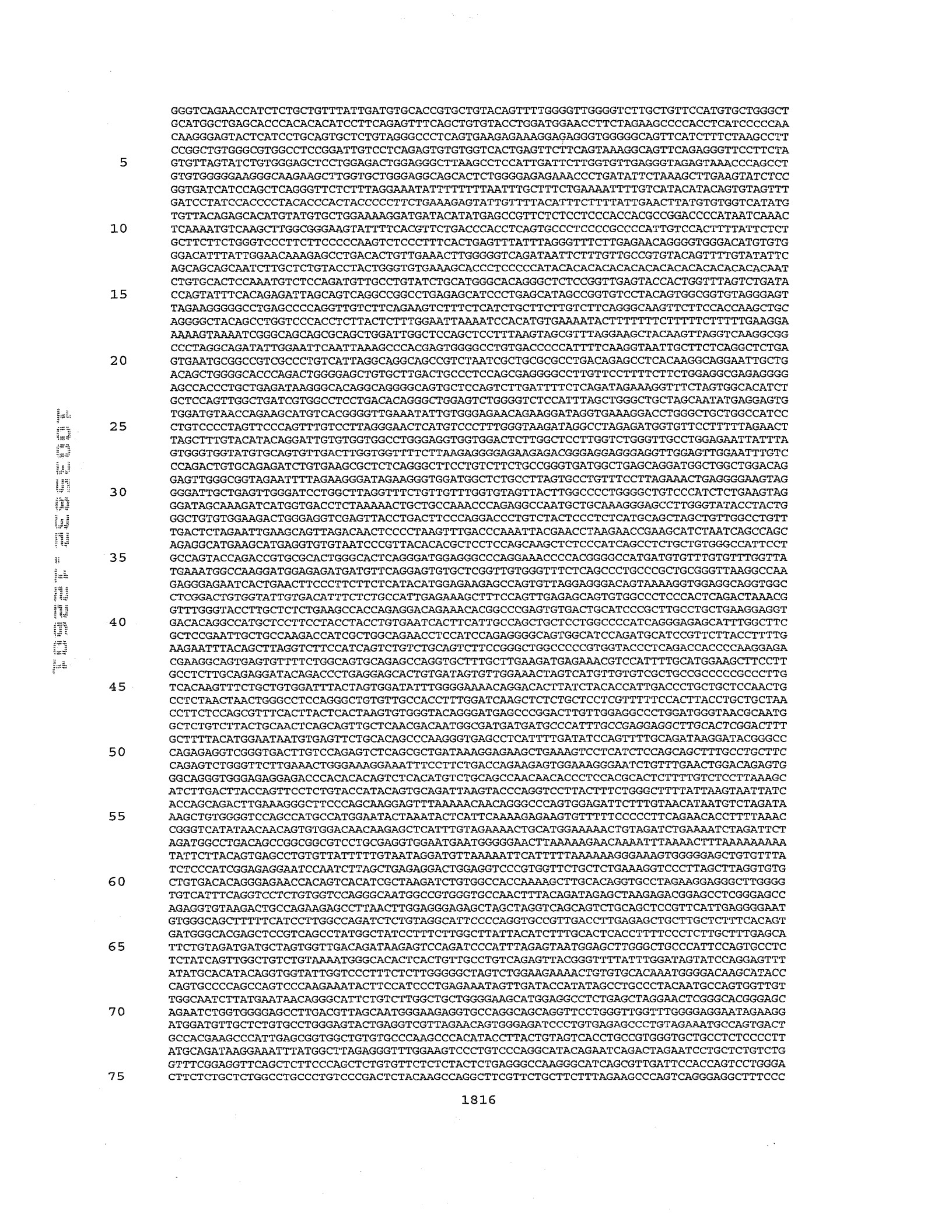


Sep 22, 2005 11:44 AM

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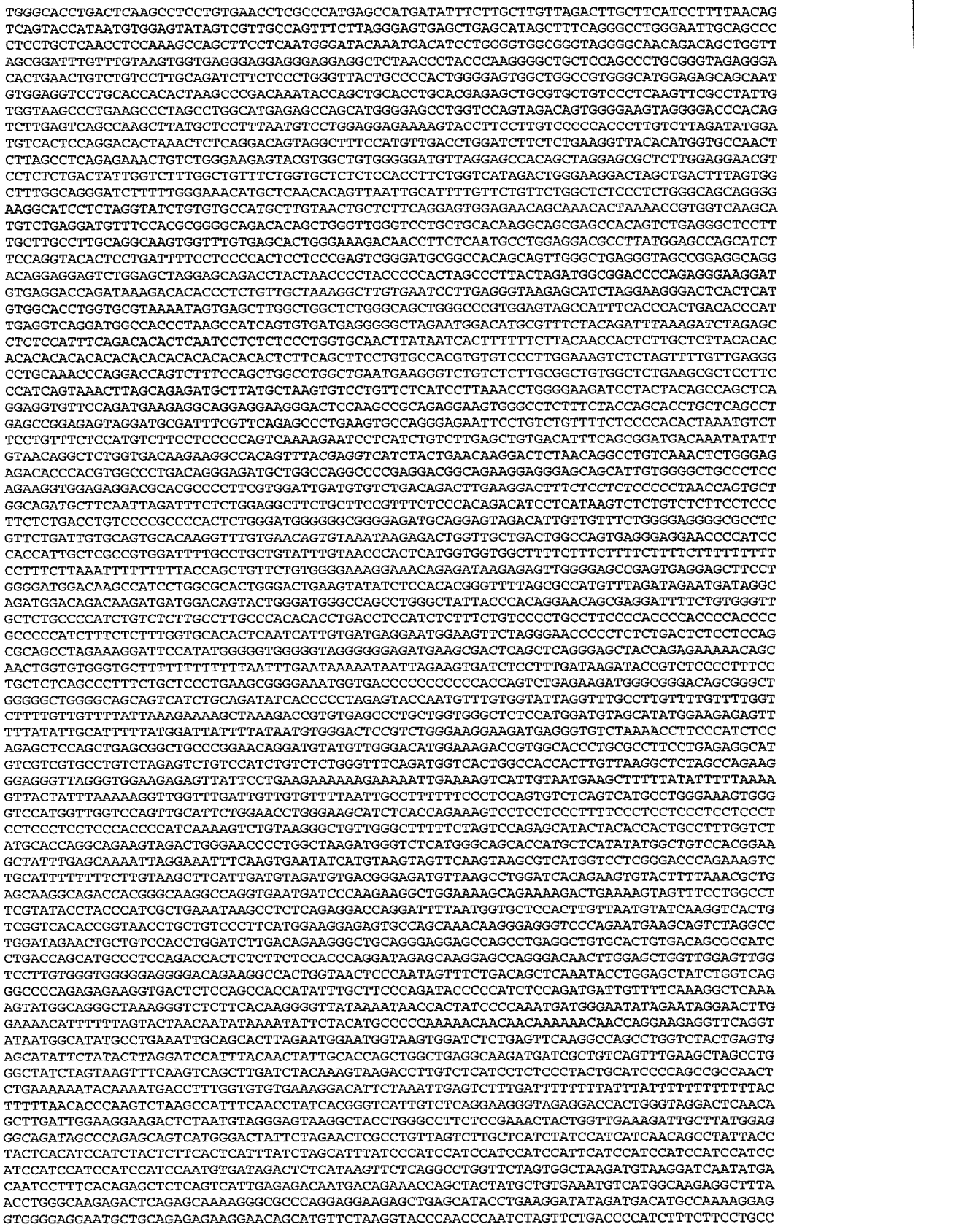
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Art Unit: 1635

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Application/Control Number: 10/552,000
Attorney Docket Number: 2004P00194WOUS

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Replacement Sheet



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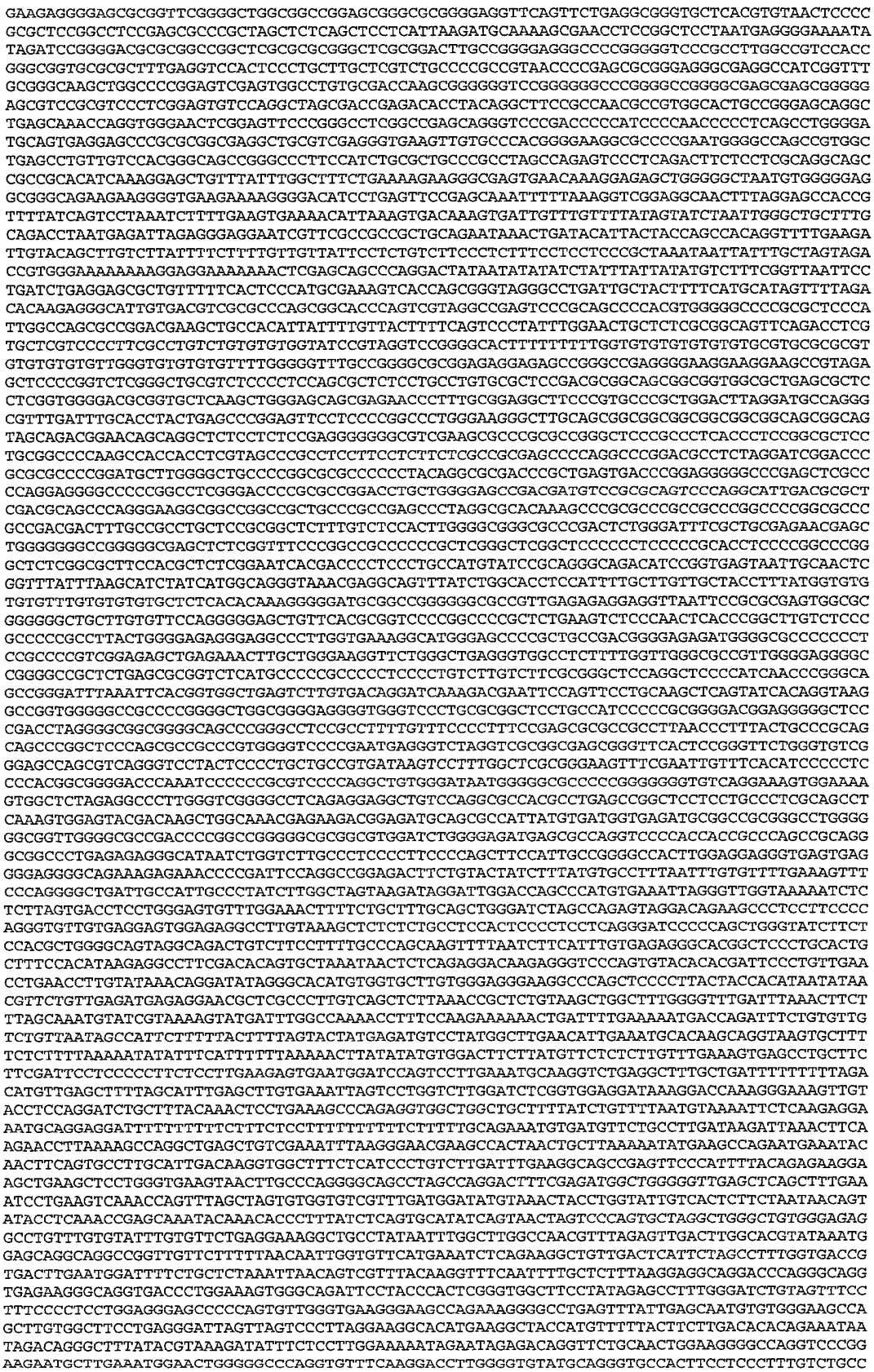
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Application: 09/944,886 Attorney Docket: 10191-2600

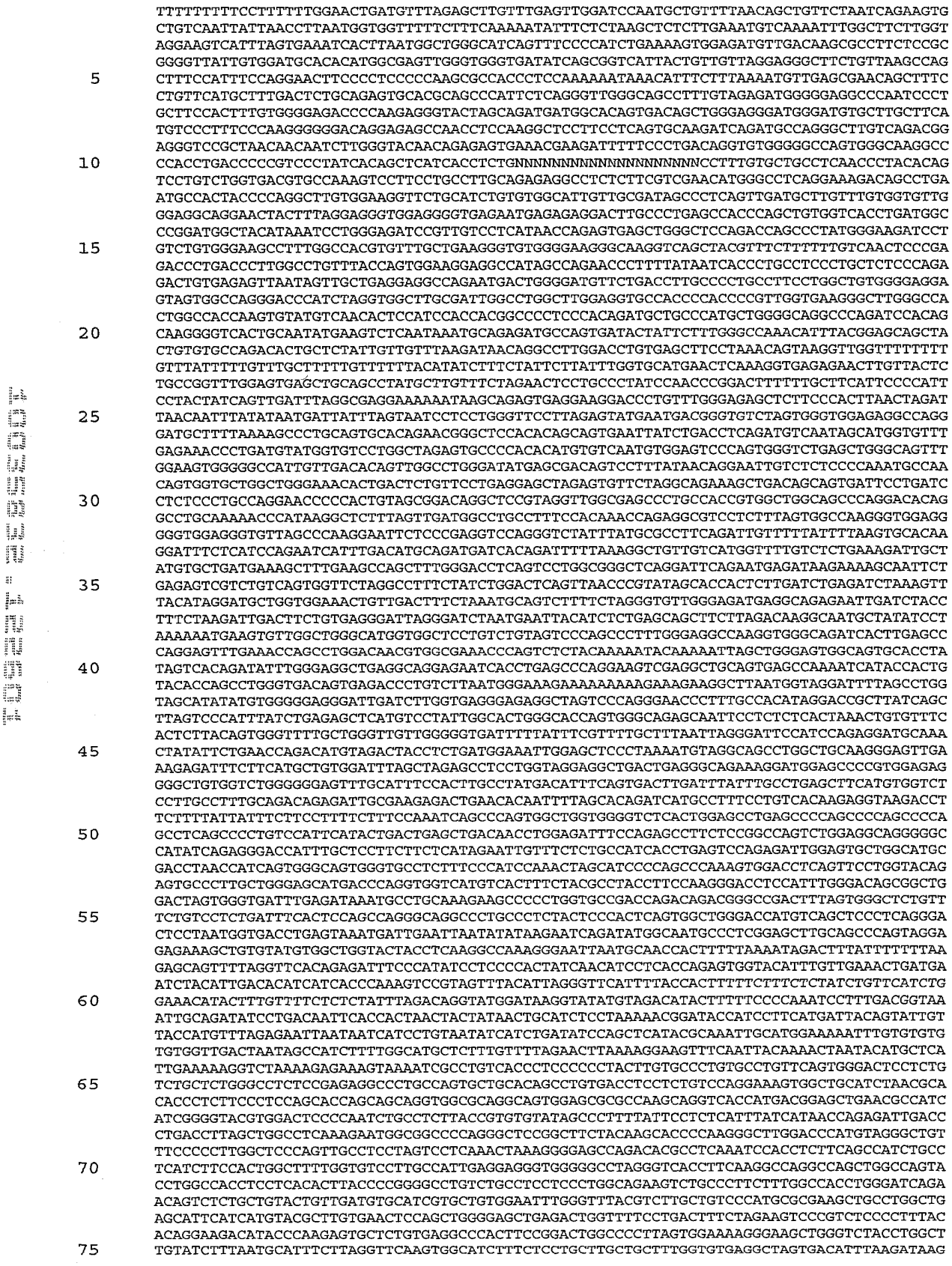
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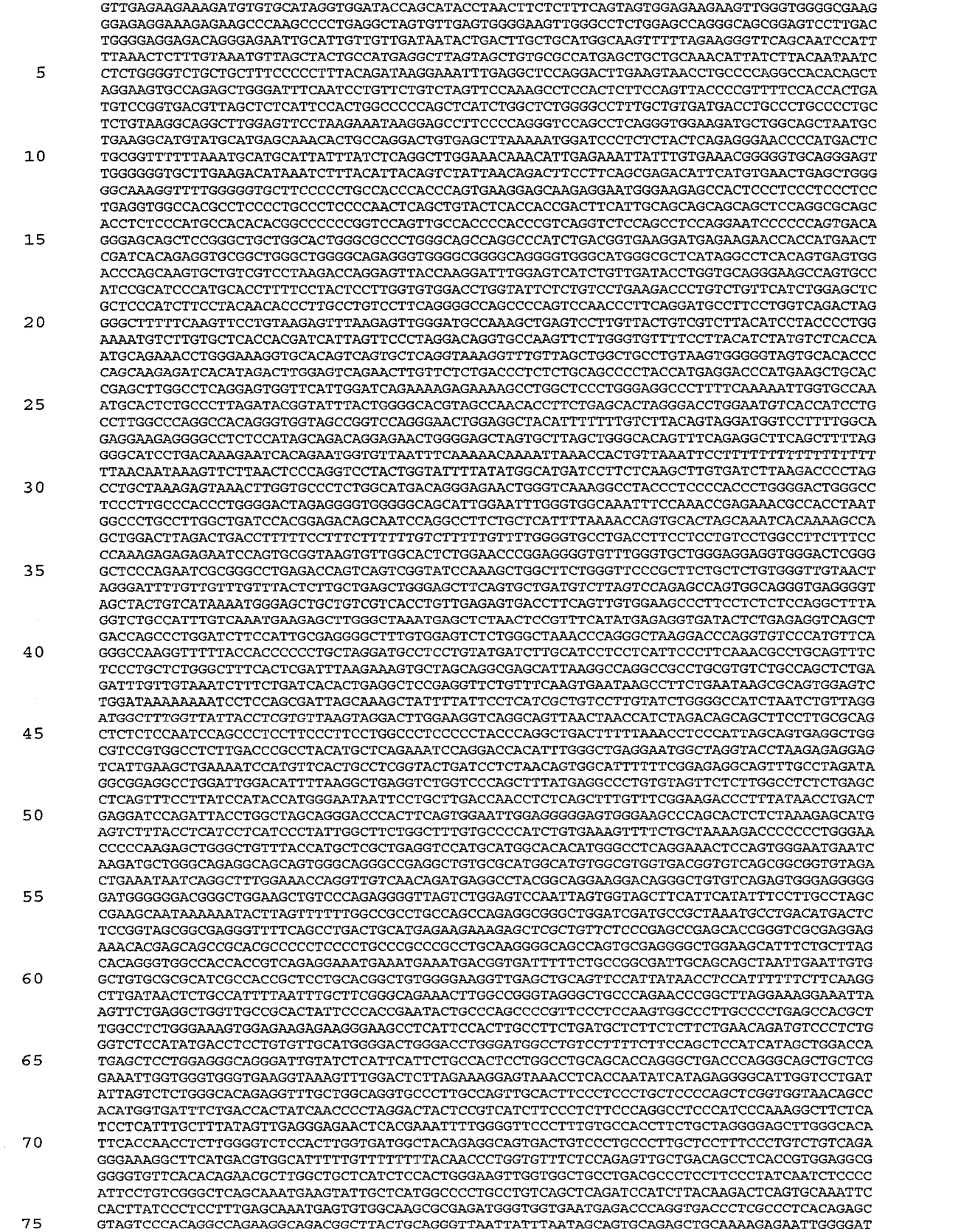
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Application/Control Number: 09/887,207
Art Unit: 1637

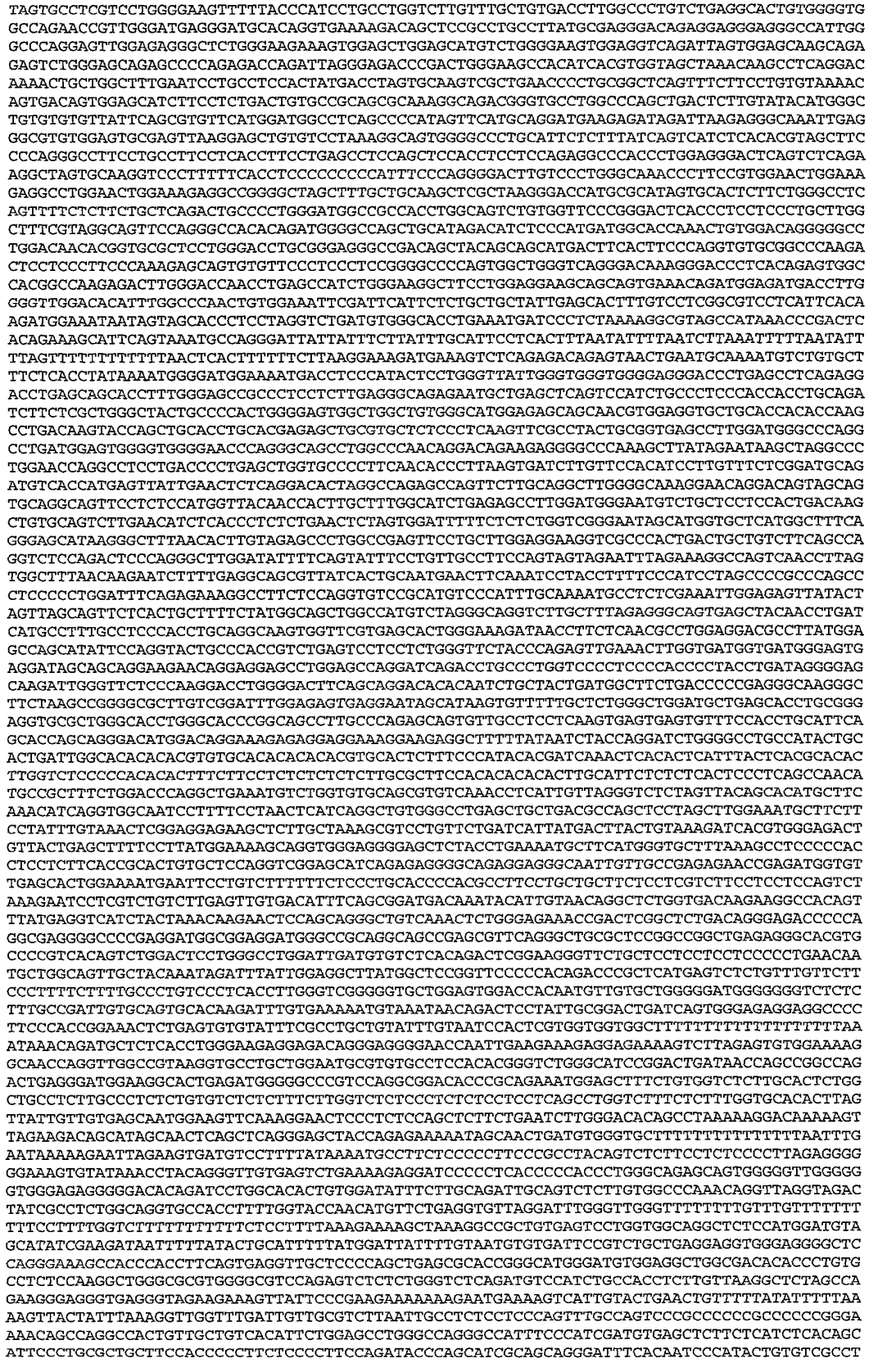
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING

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Table 88

MOUSE NOMENCLATURE

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Celera	mCG14118

HUMAN NOMENCLATURE

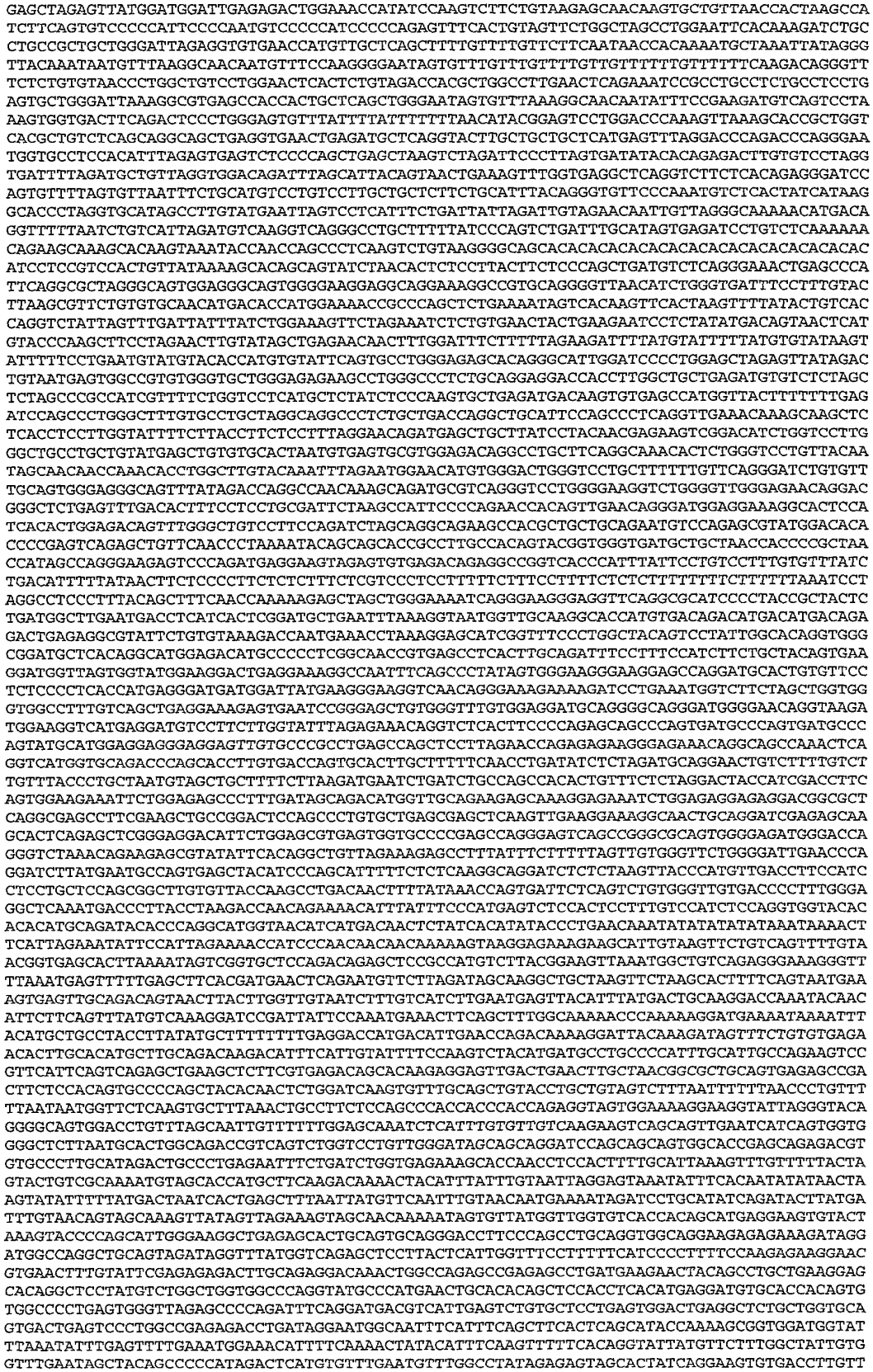
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

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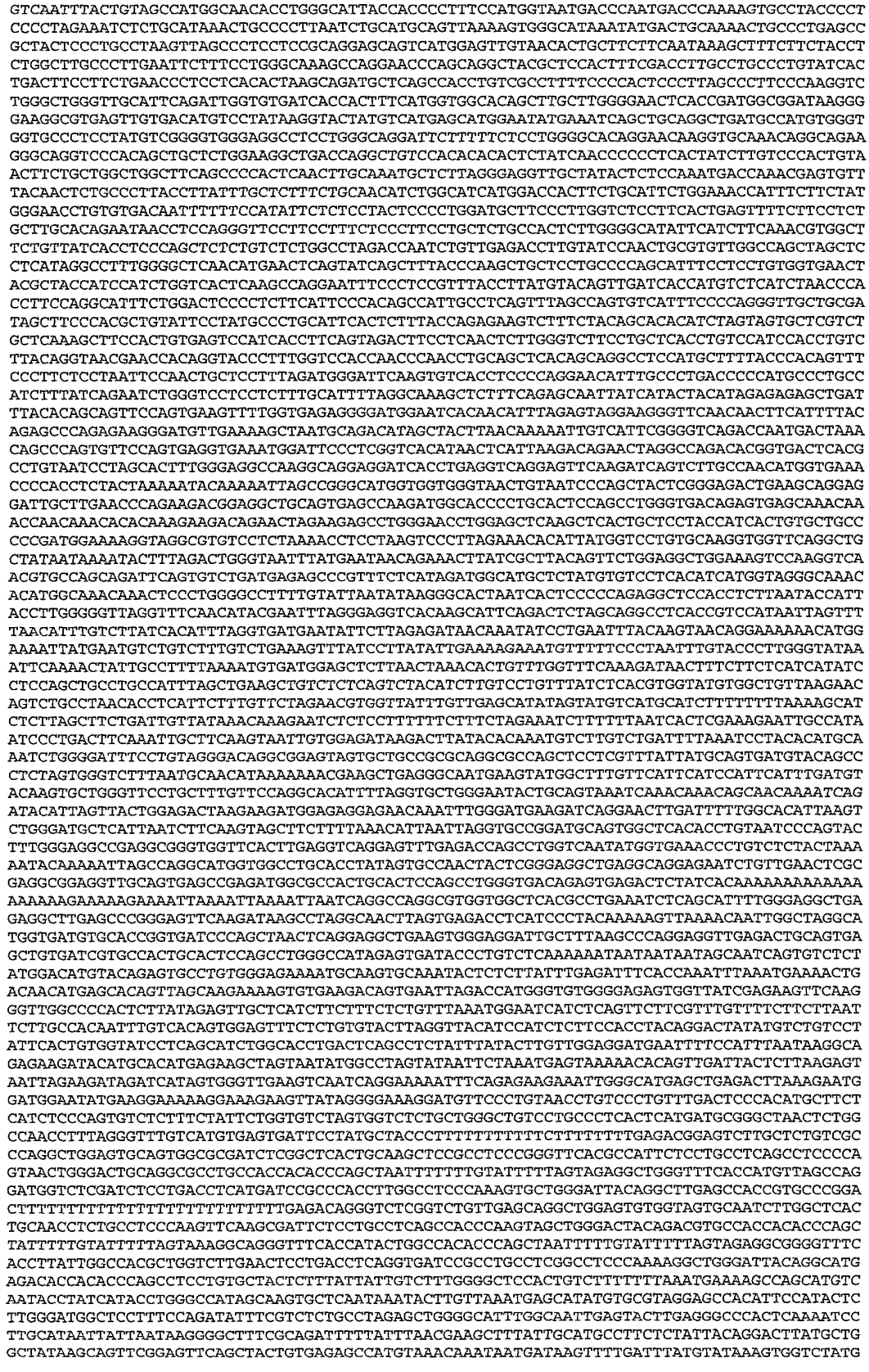
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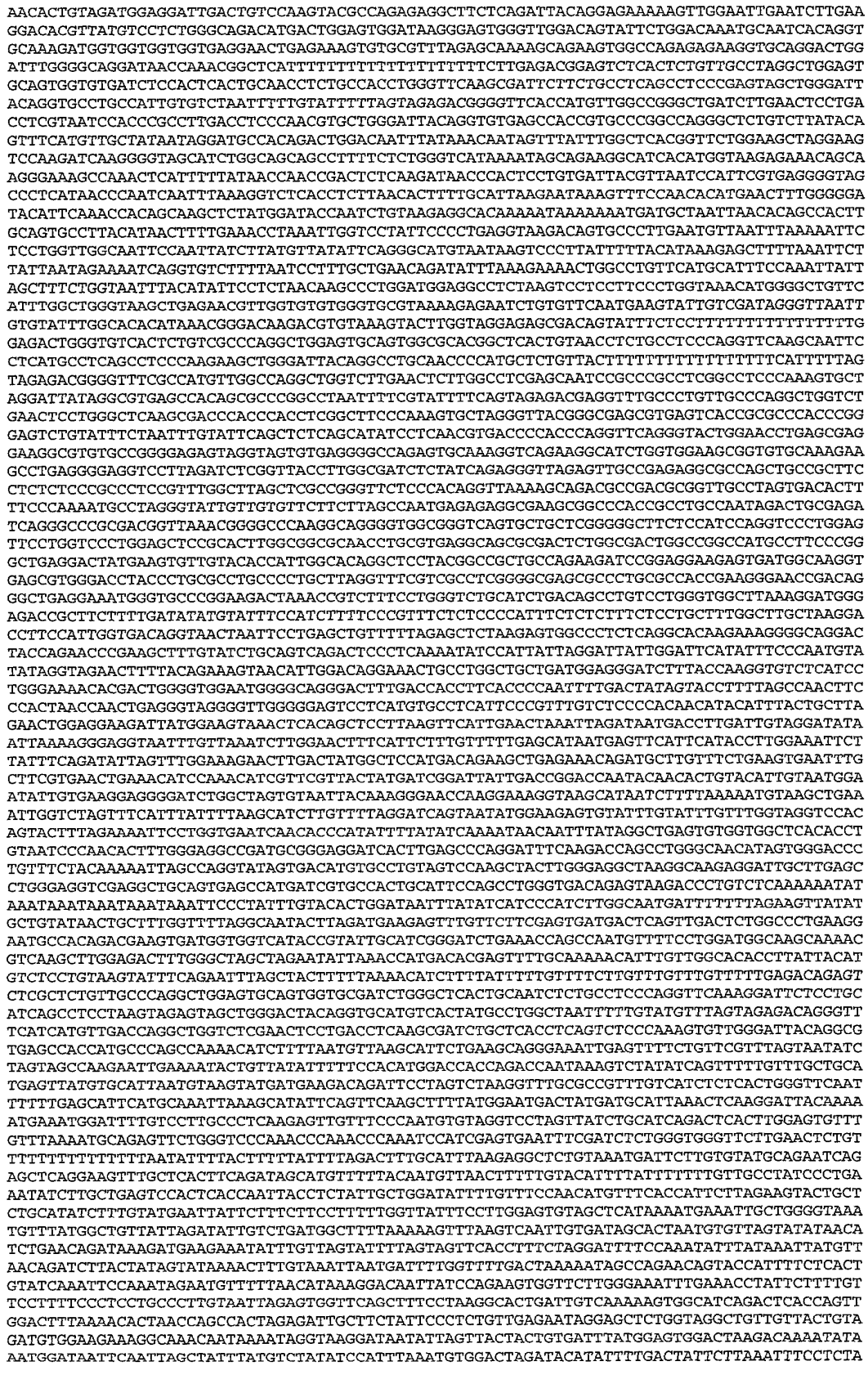
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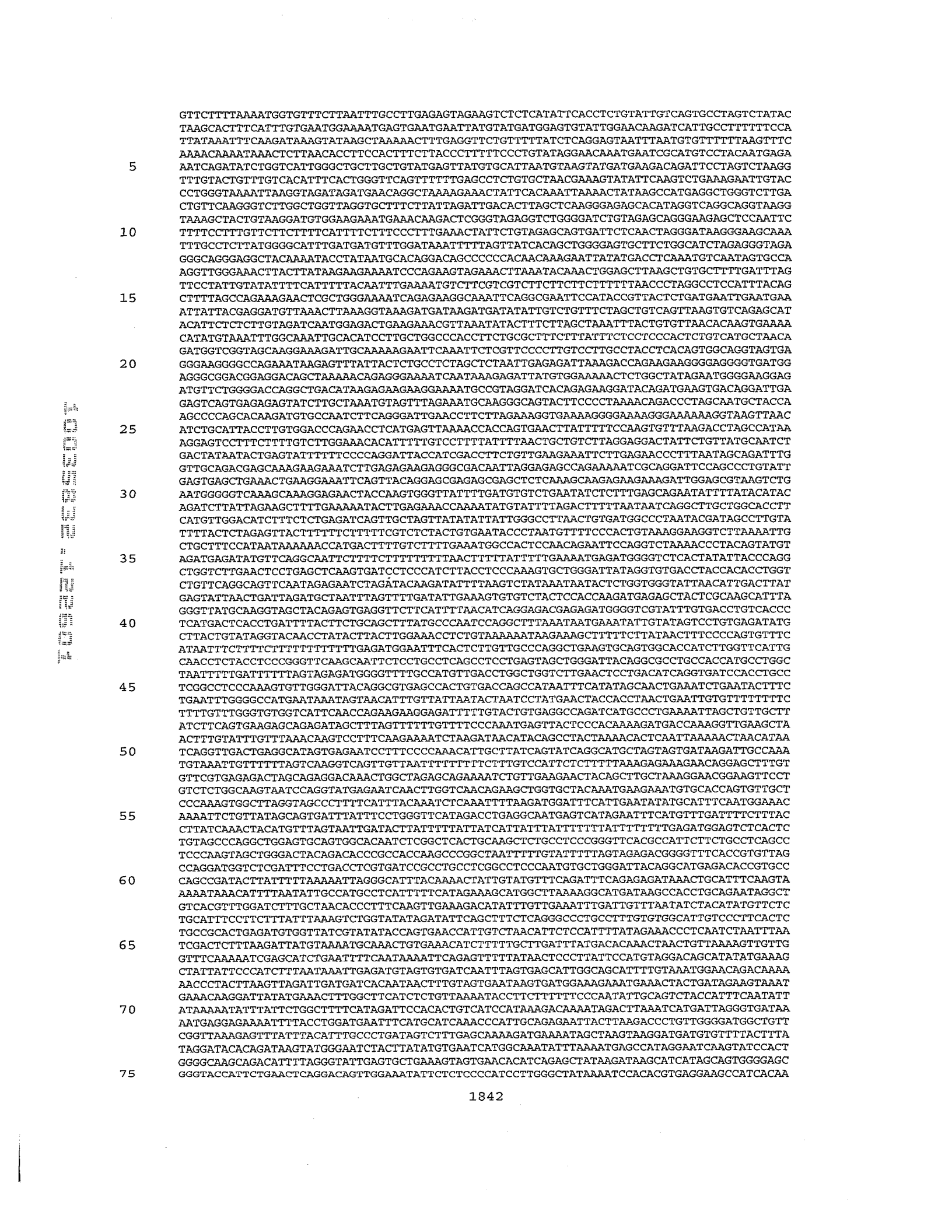
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HUMAN SEQUENCE - mRNA
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Table 89

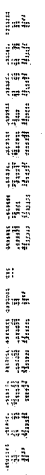
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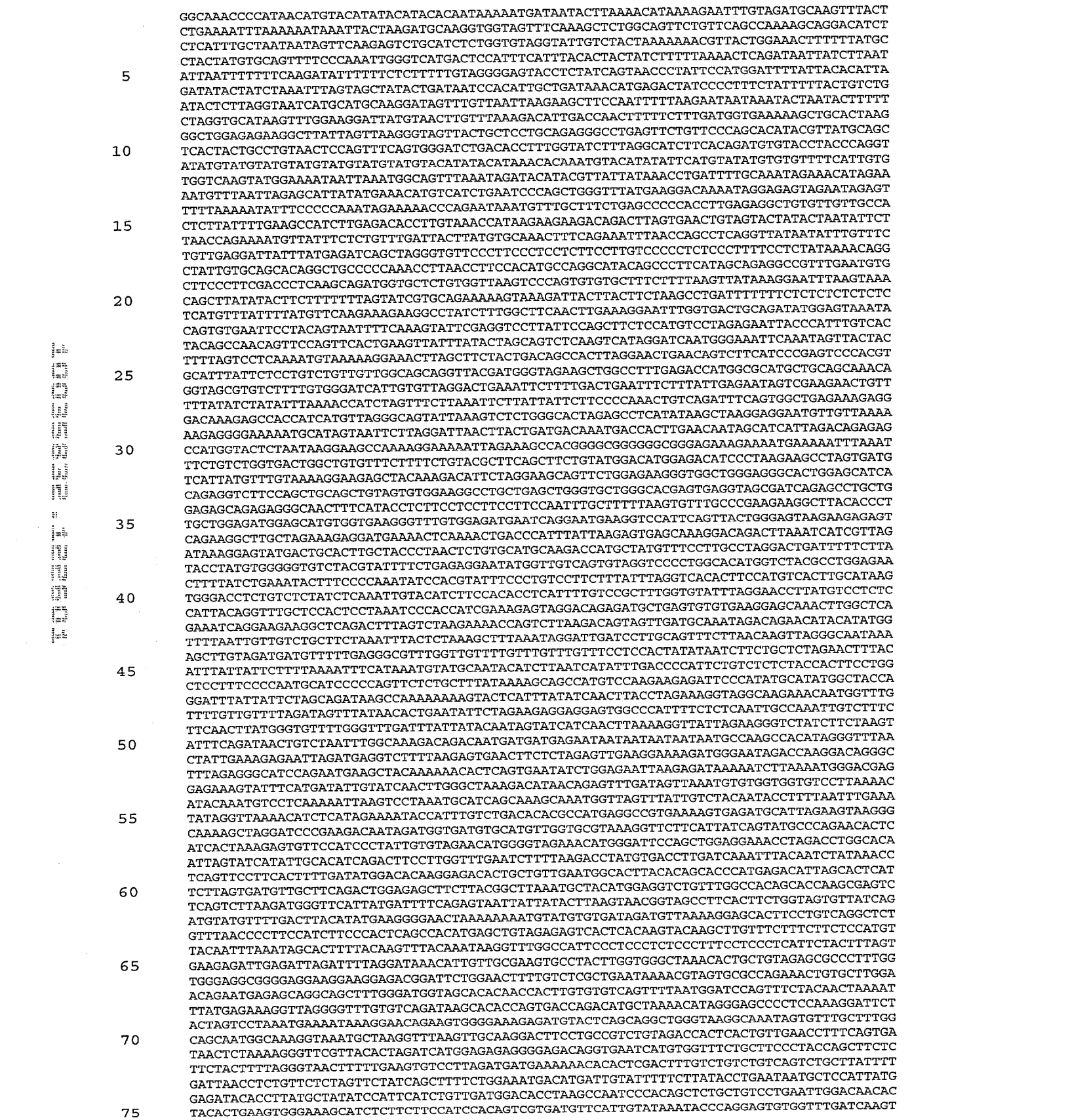
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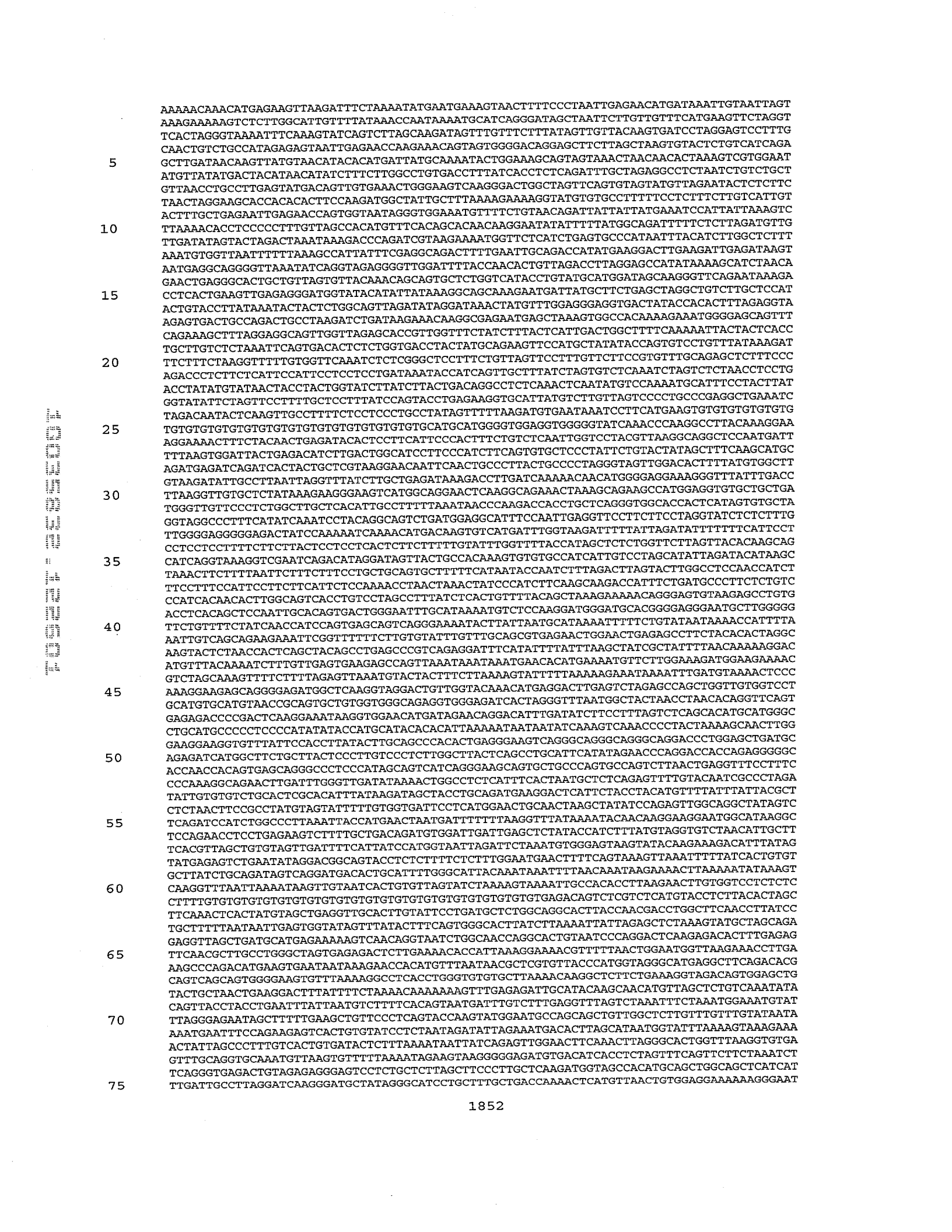
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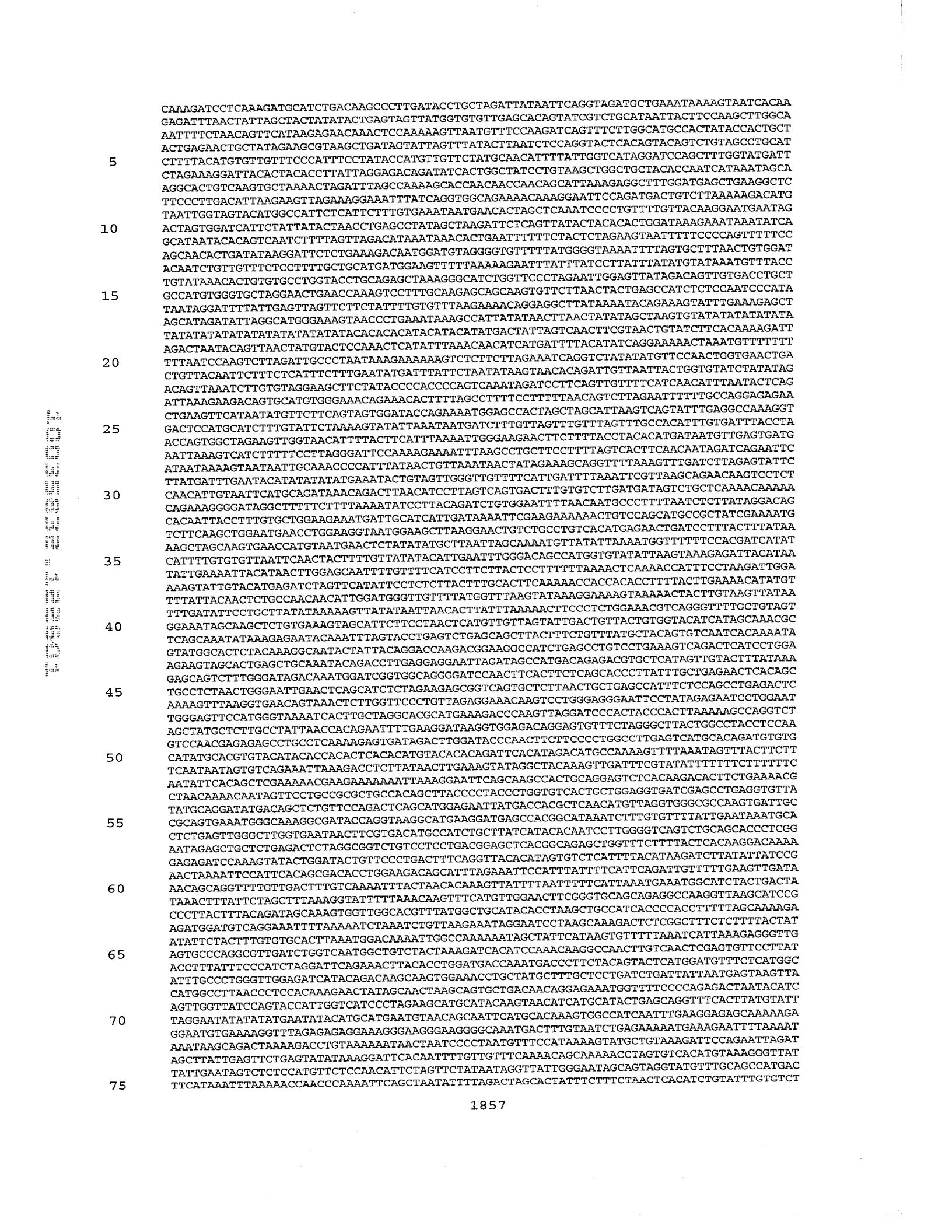
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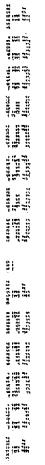
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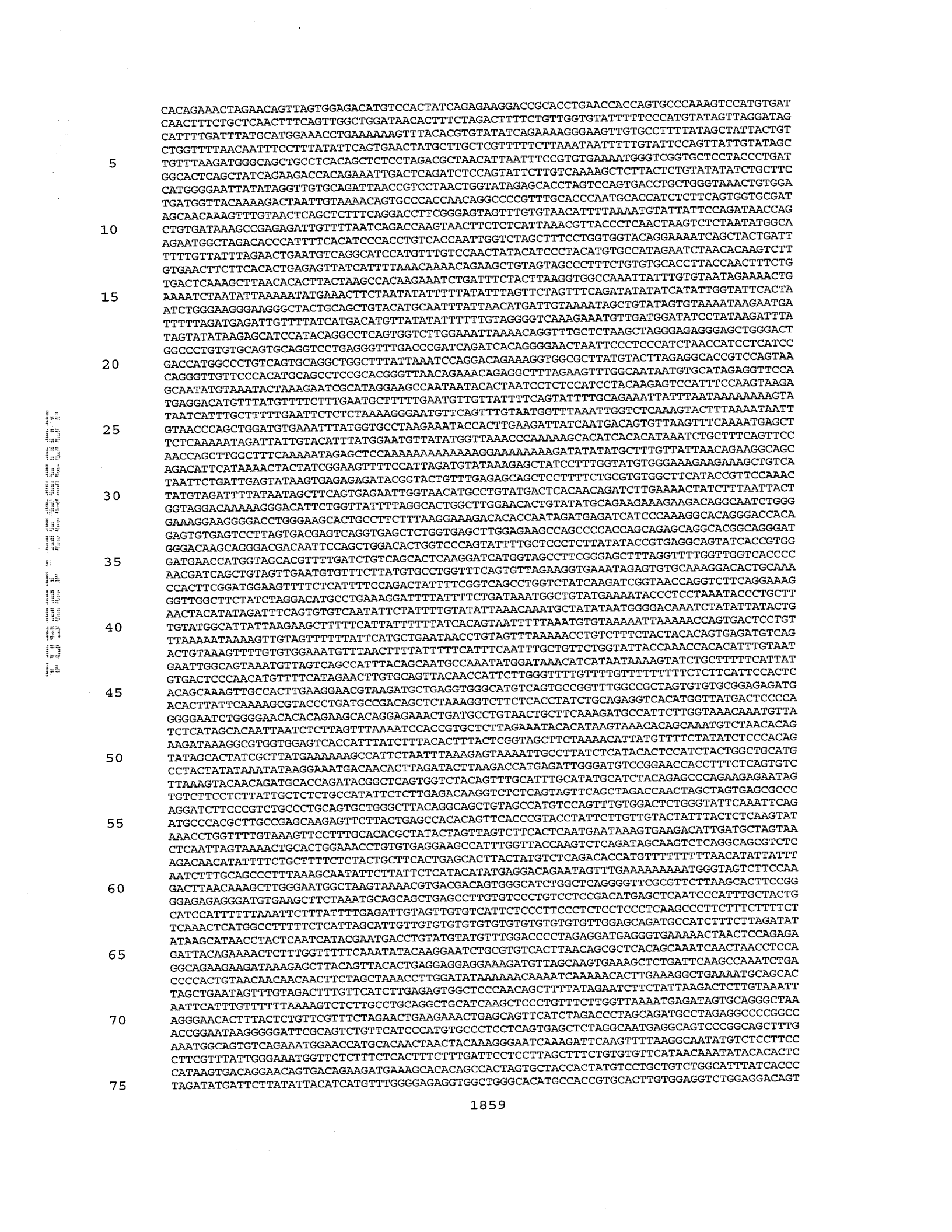
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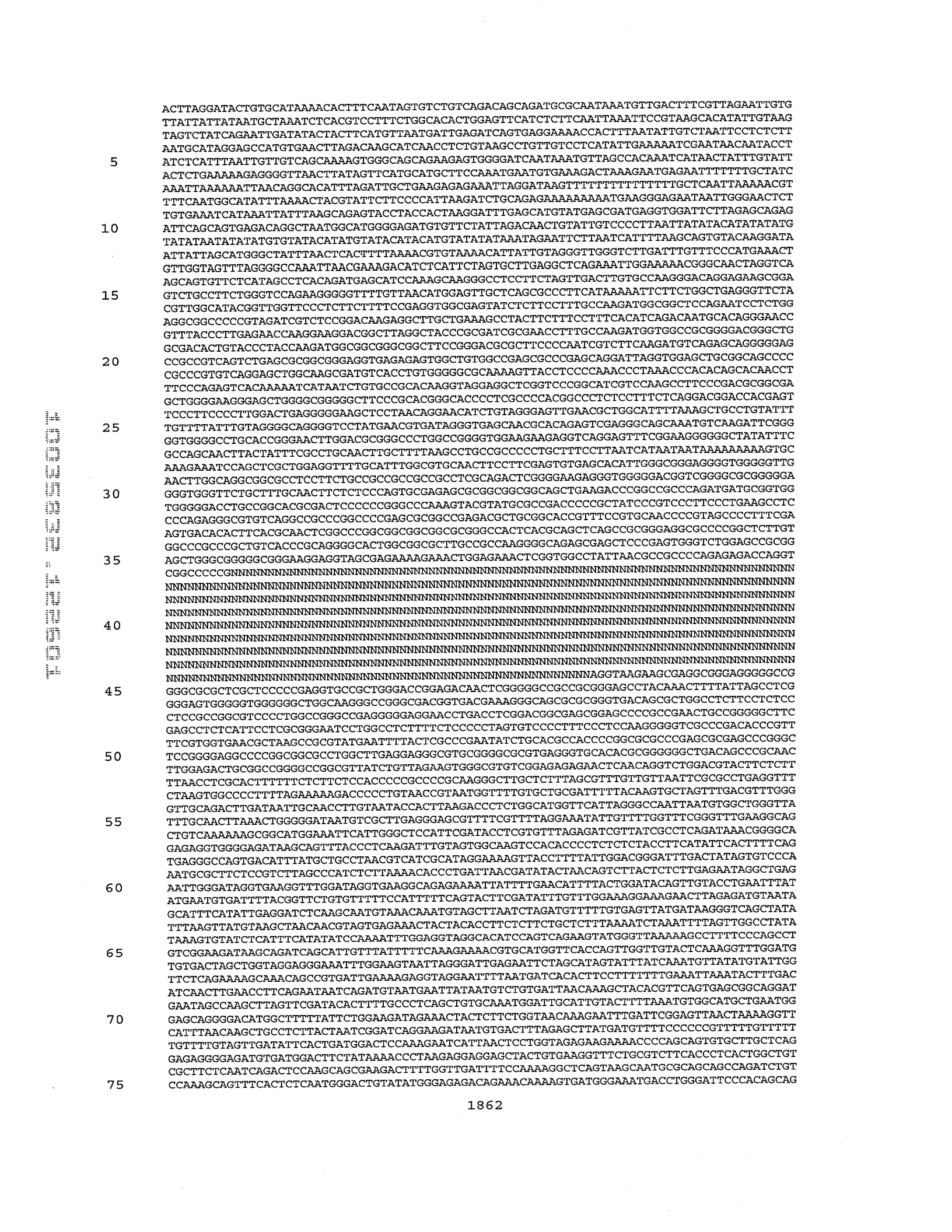
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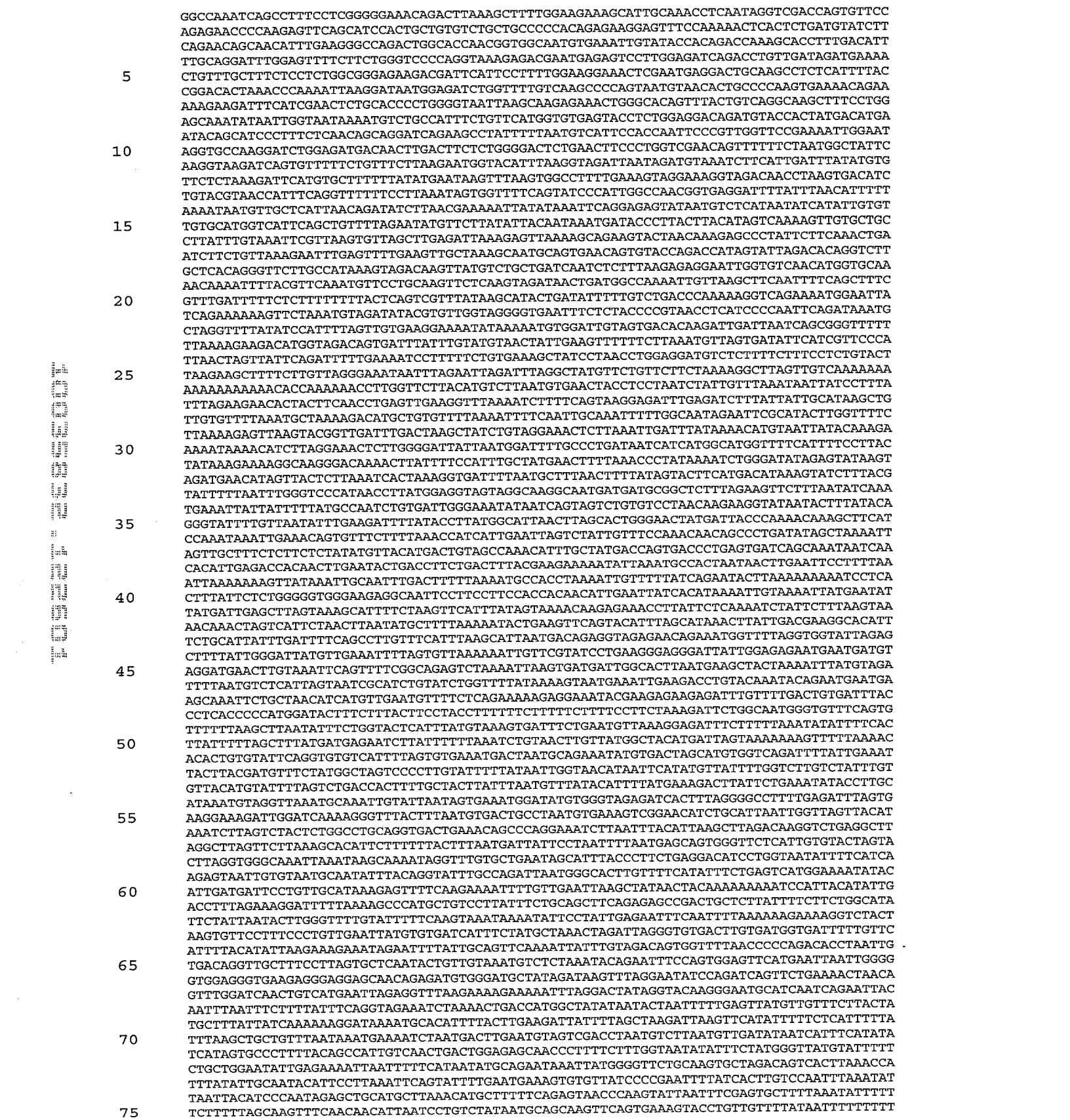
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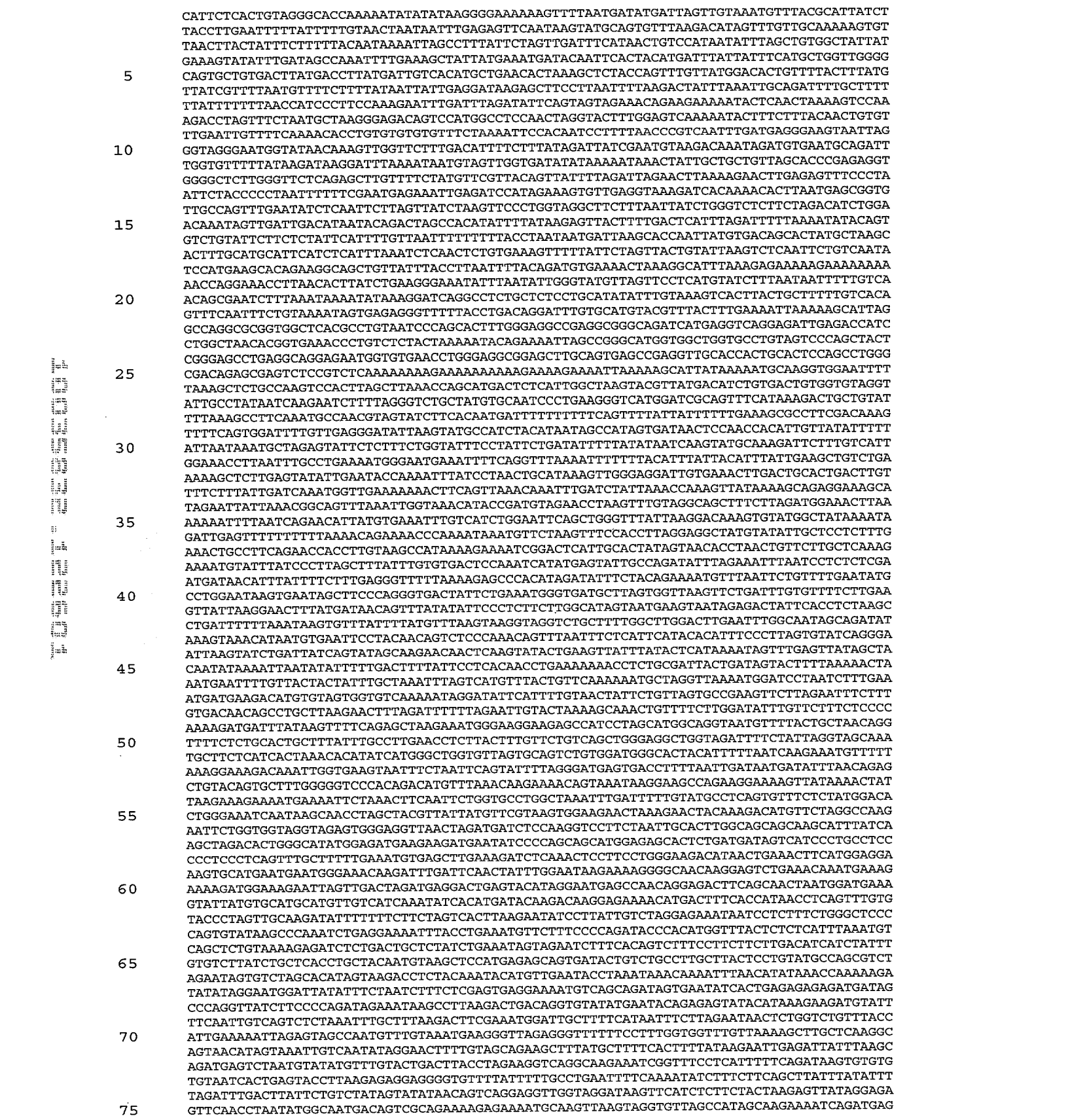
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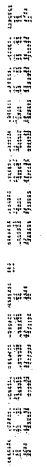
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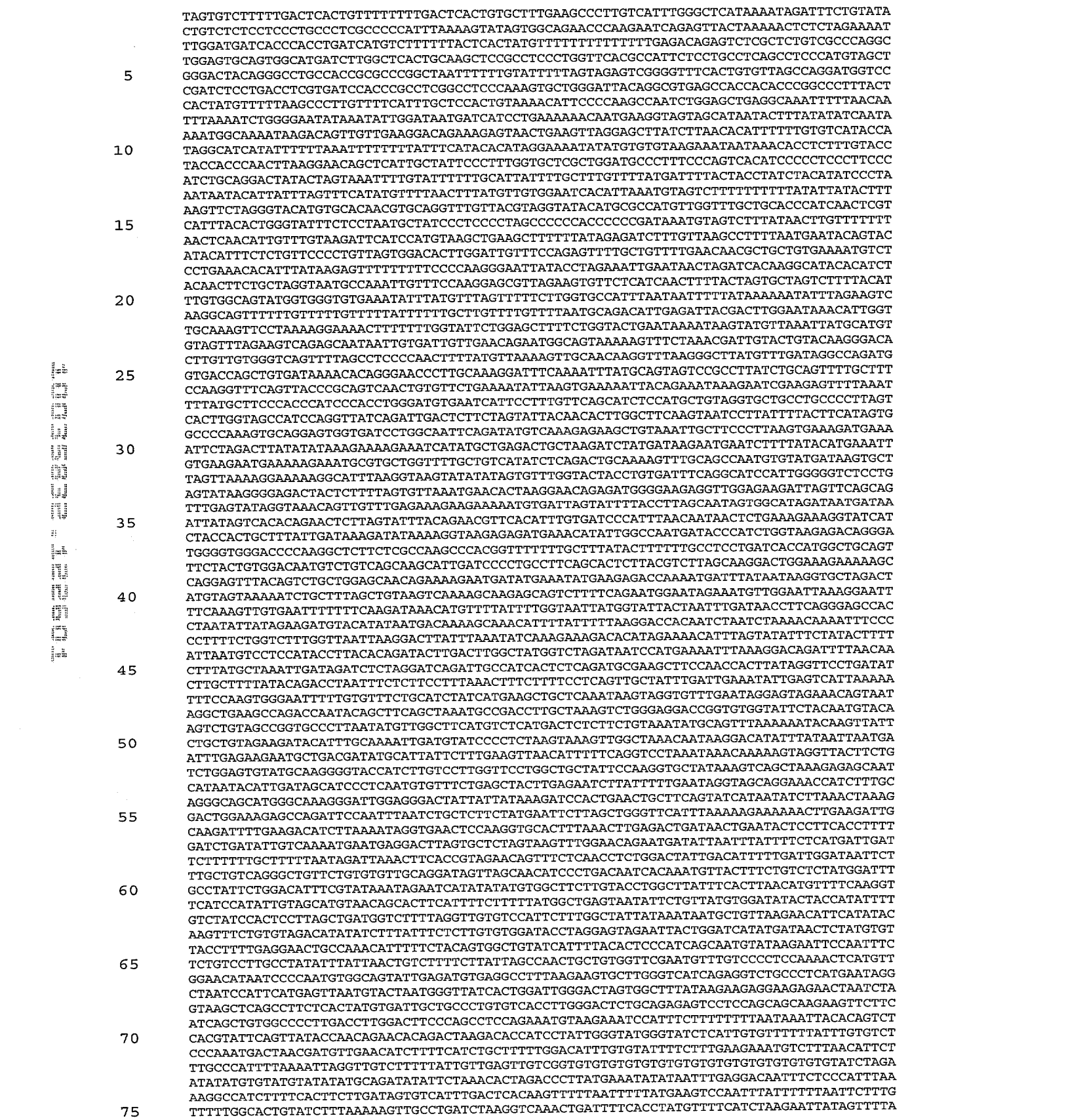


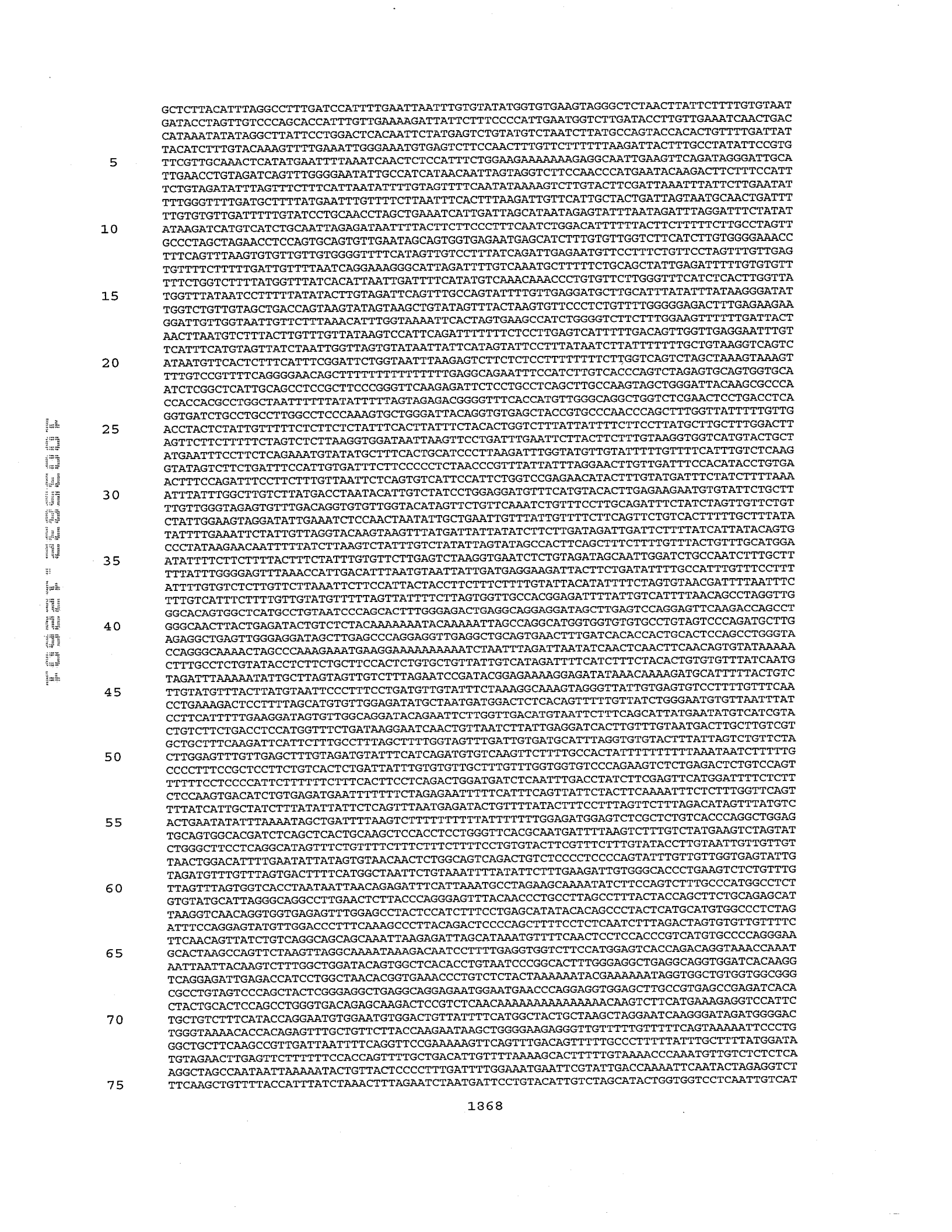
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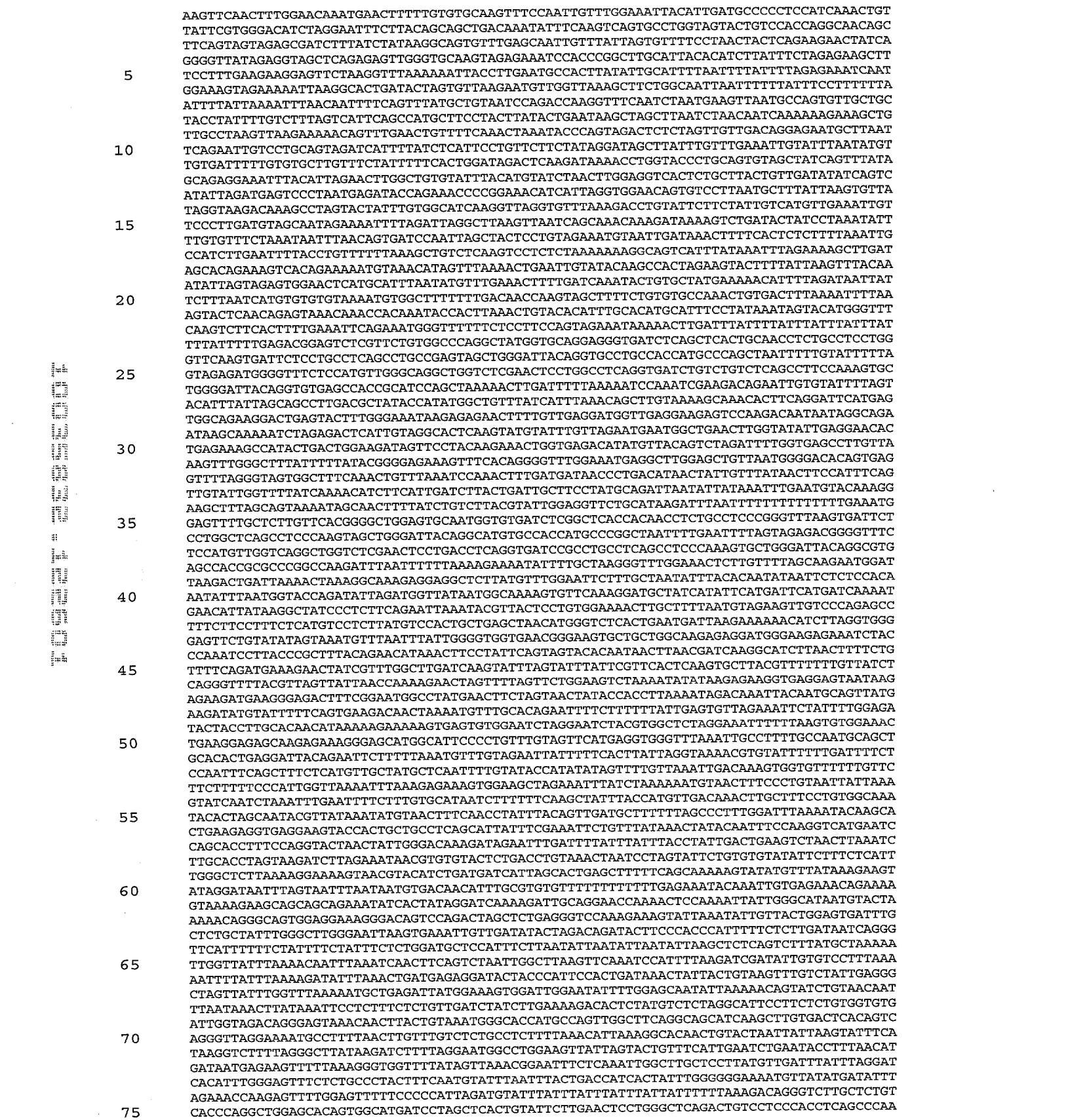


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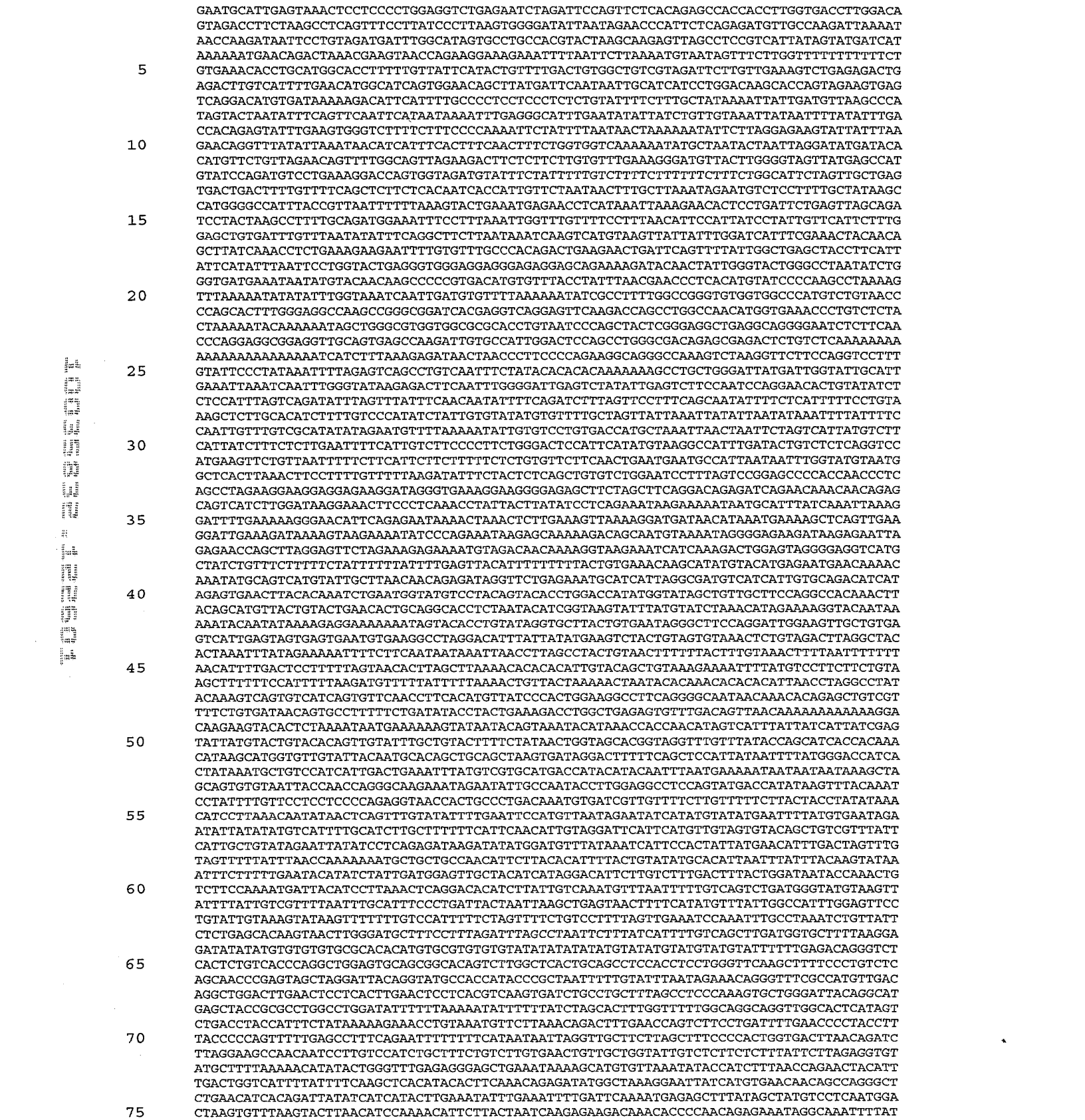


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Art Unit: 1635

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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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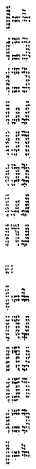
Table 90

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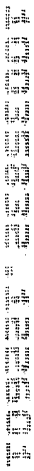
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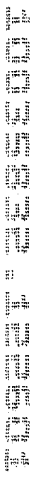
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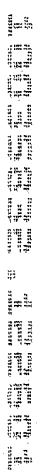
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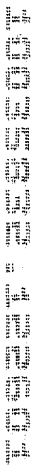
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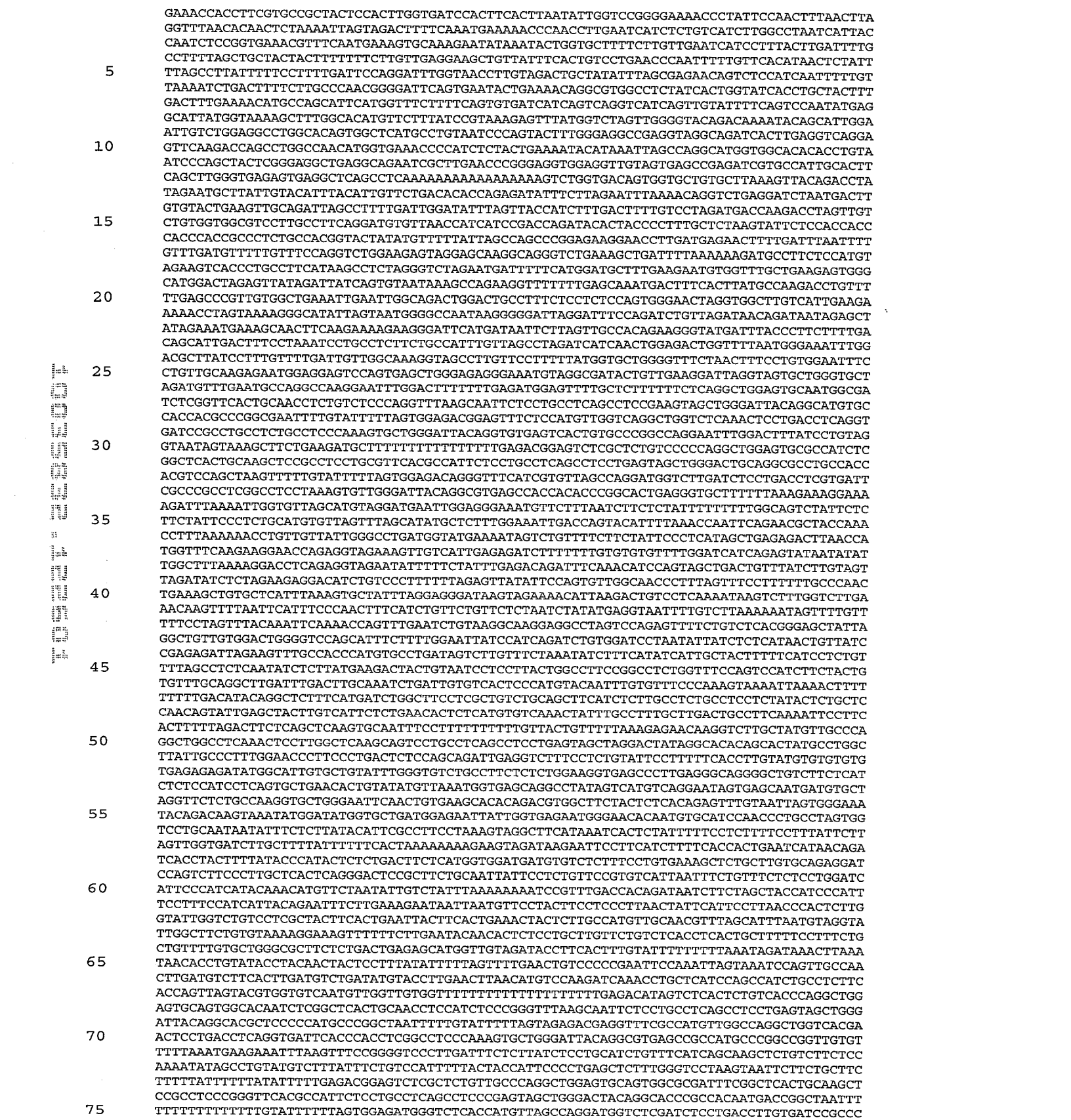
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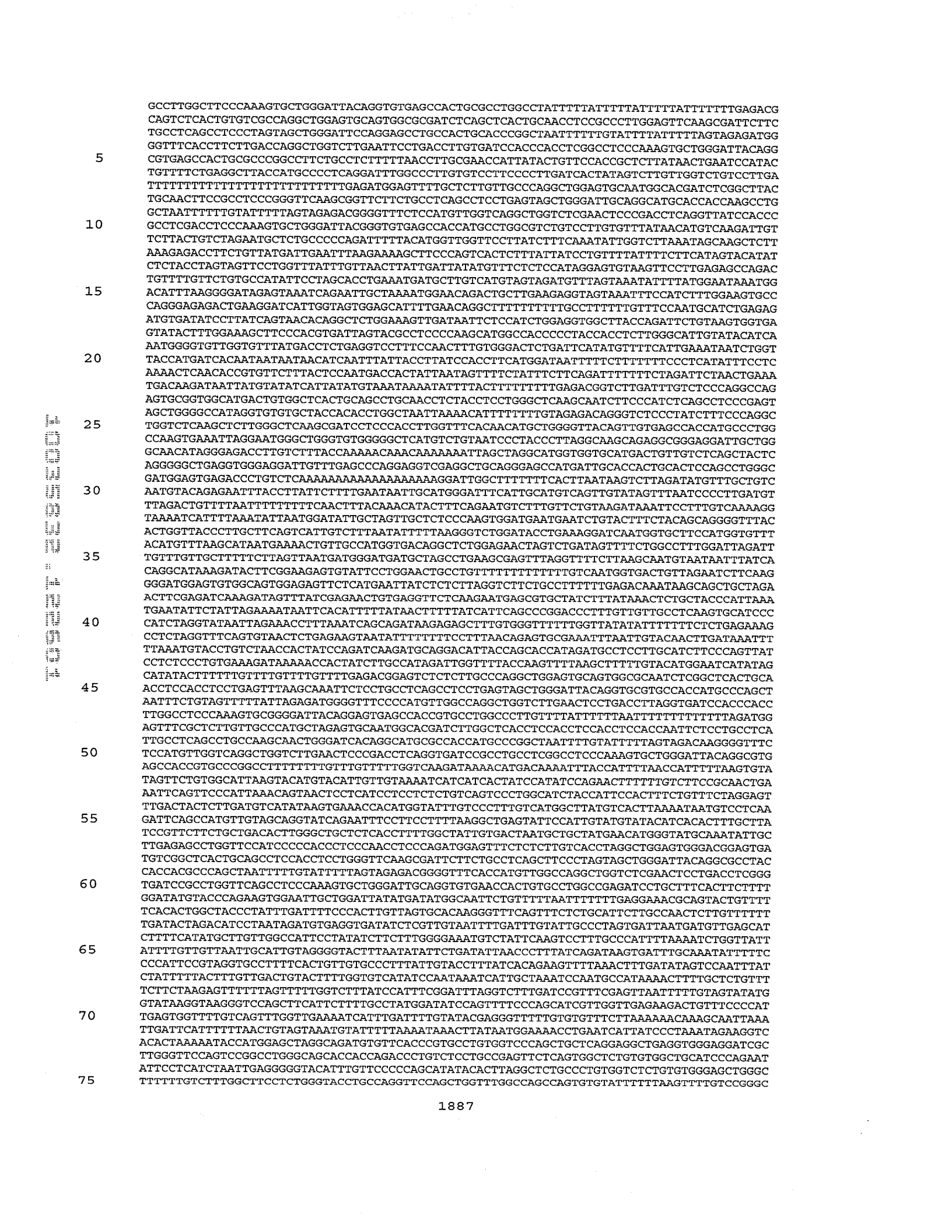
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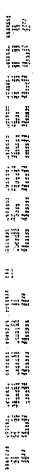


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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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Table 91

MOUSE NOMENCLATURE
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Celera mCG12243

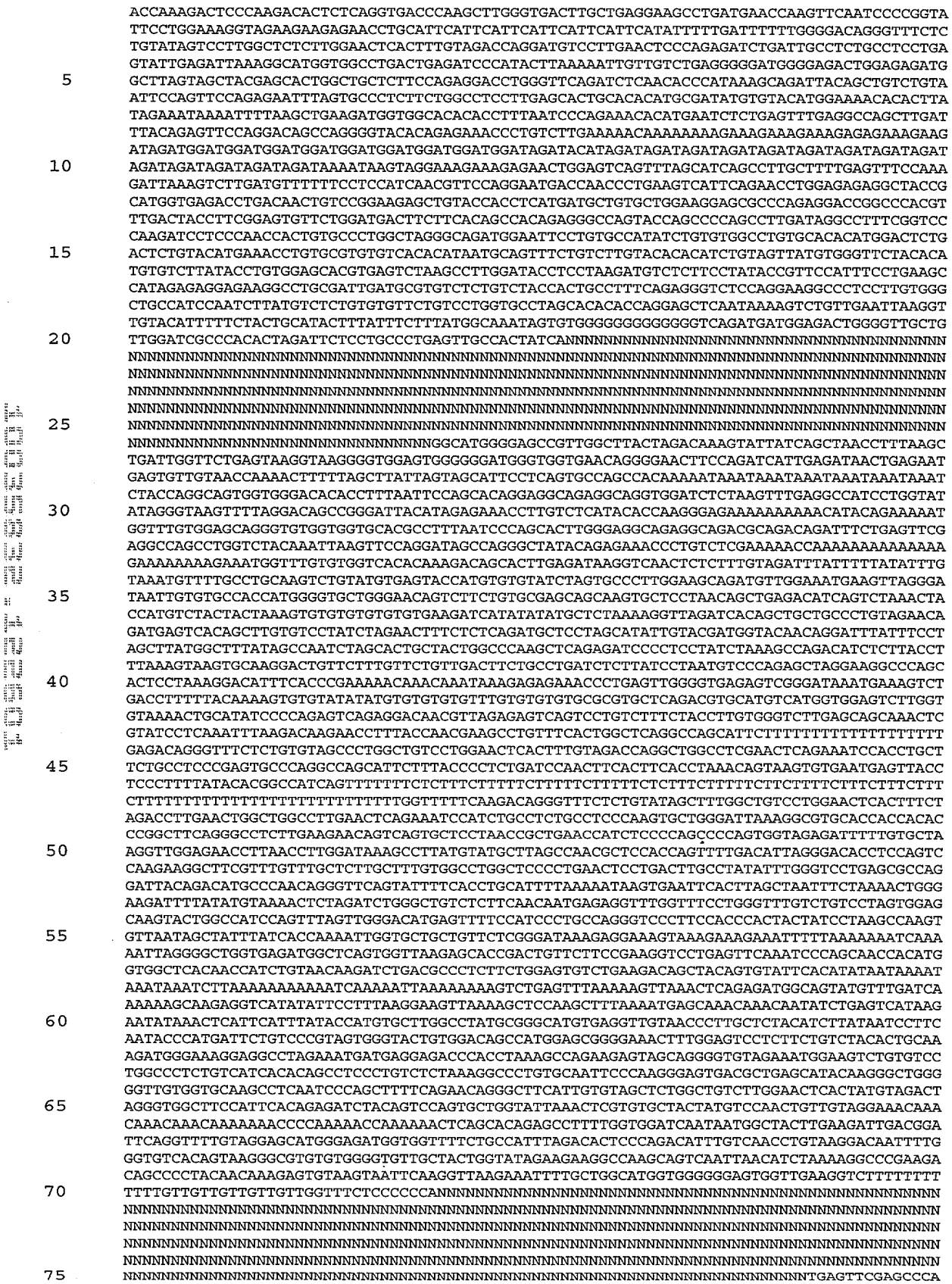
HUMAN NOMENCLATURE
HGNC LCK
Celera hCG41609

MOUSE SEQUENCE - GENOMIC
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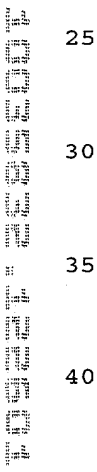
MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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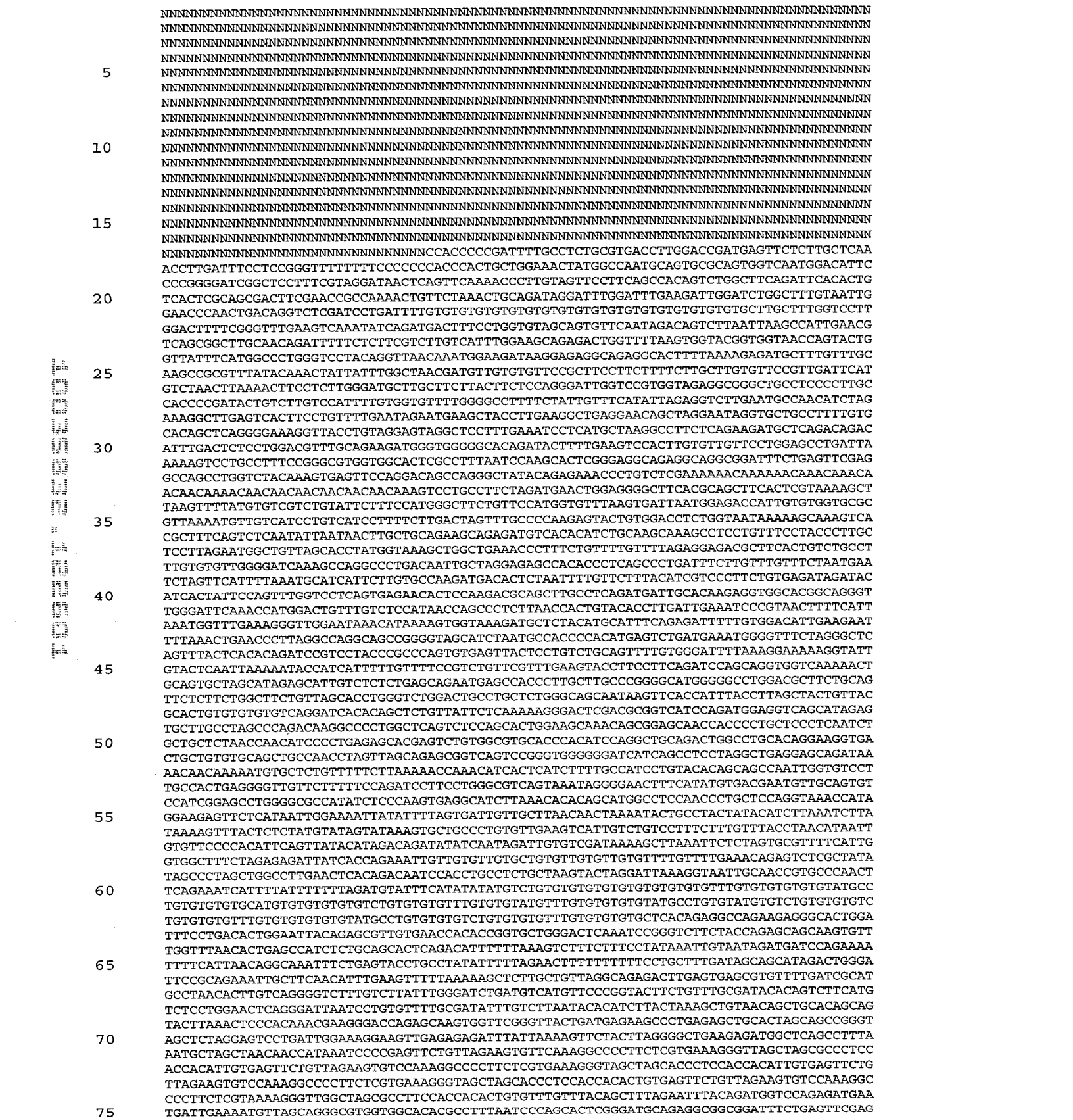
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Table 92

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Celera mCG19236

HUMAN NOMENCLATURE
HGNC GIT2
Celera hCG38510

MOUSE SEQUENCE - GENOMIC
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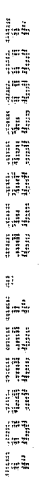
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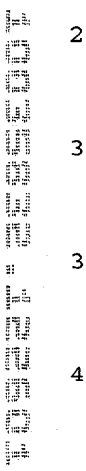
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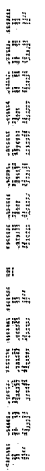
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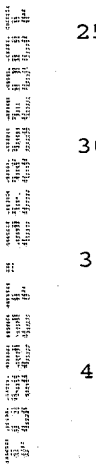
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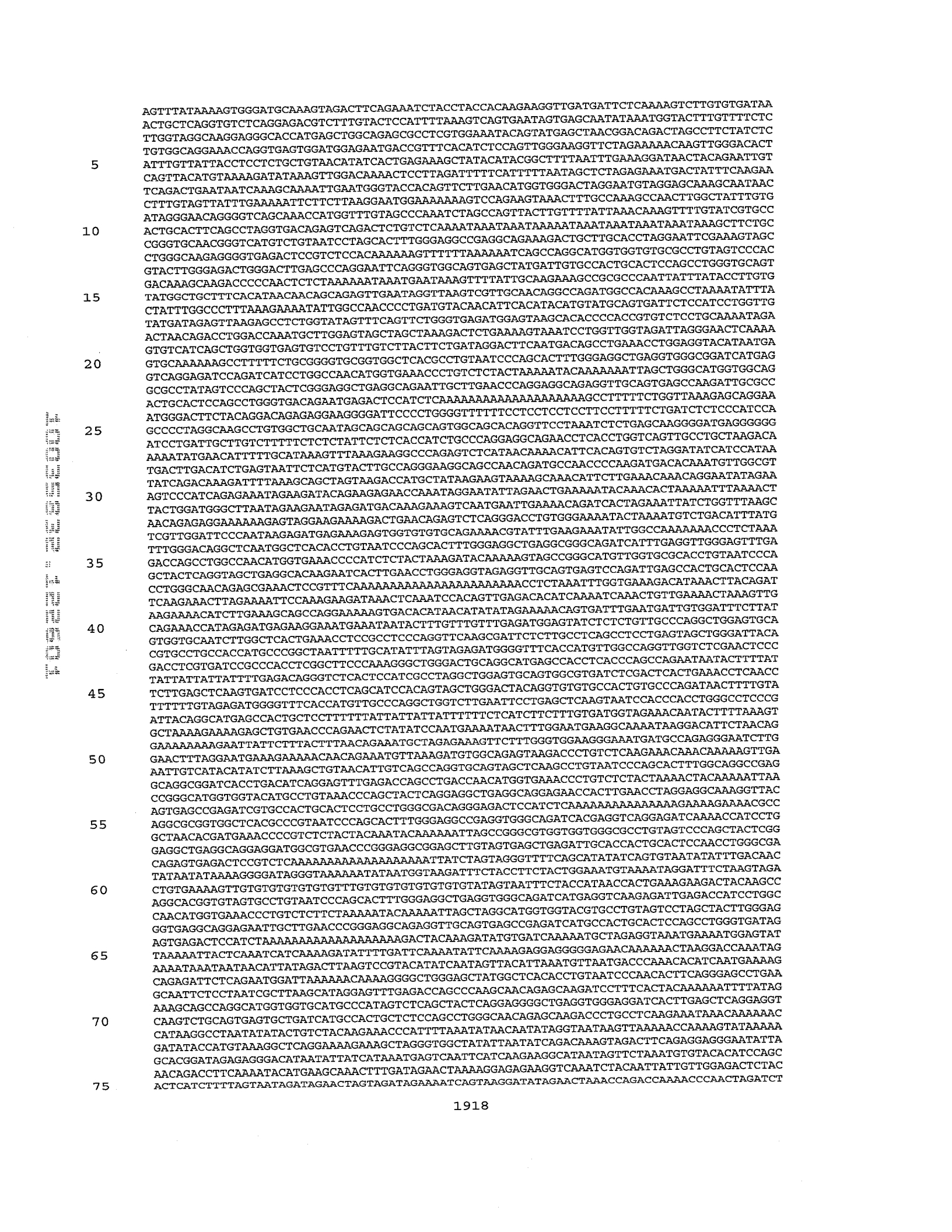
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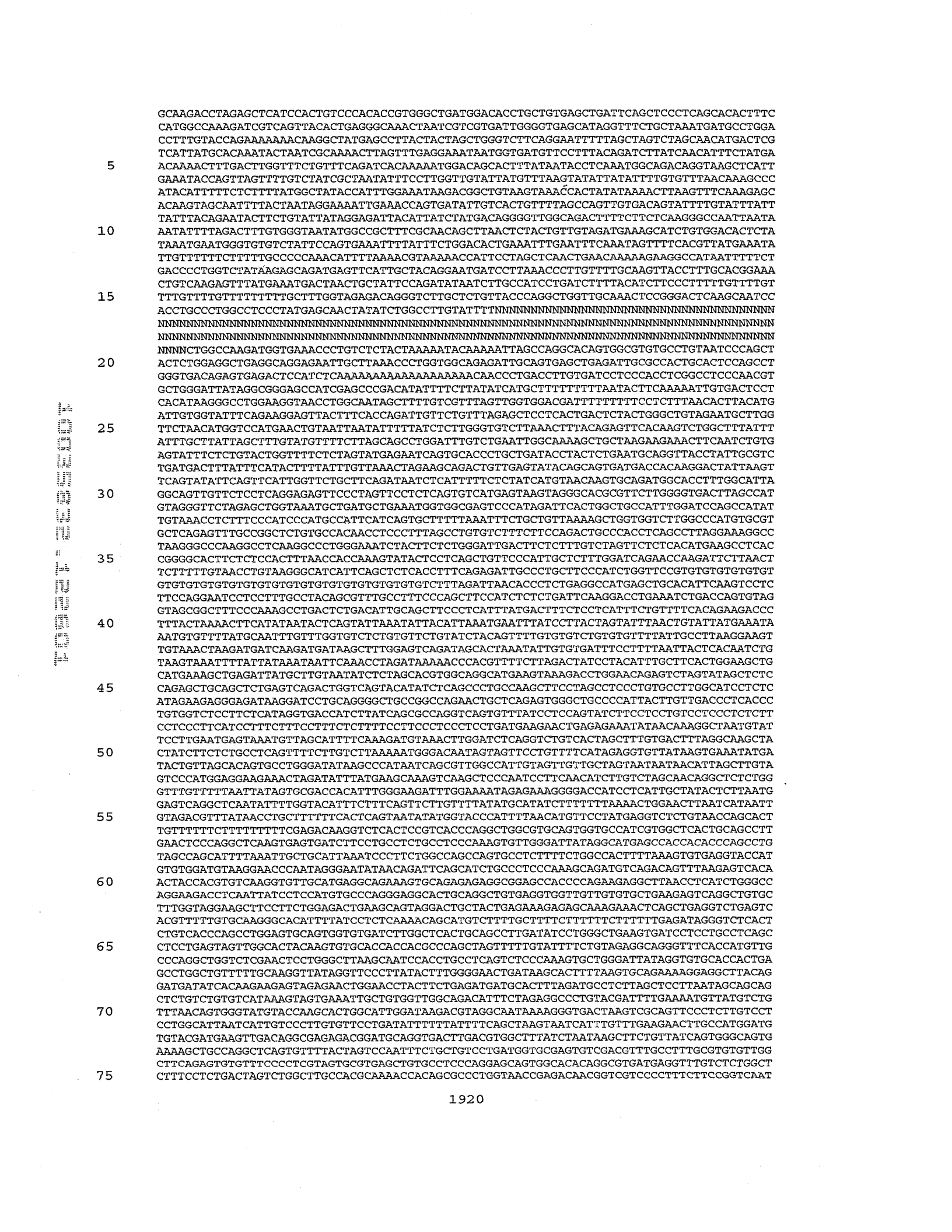


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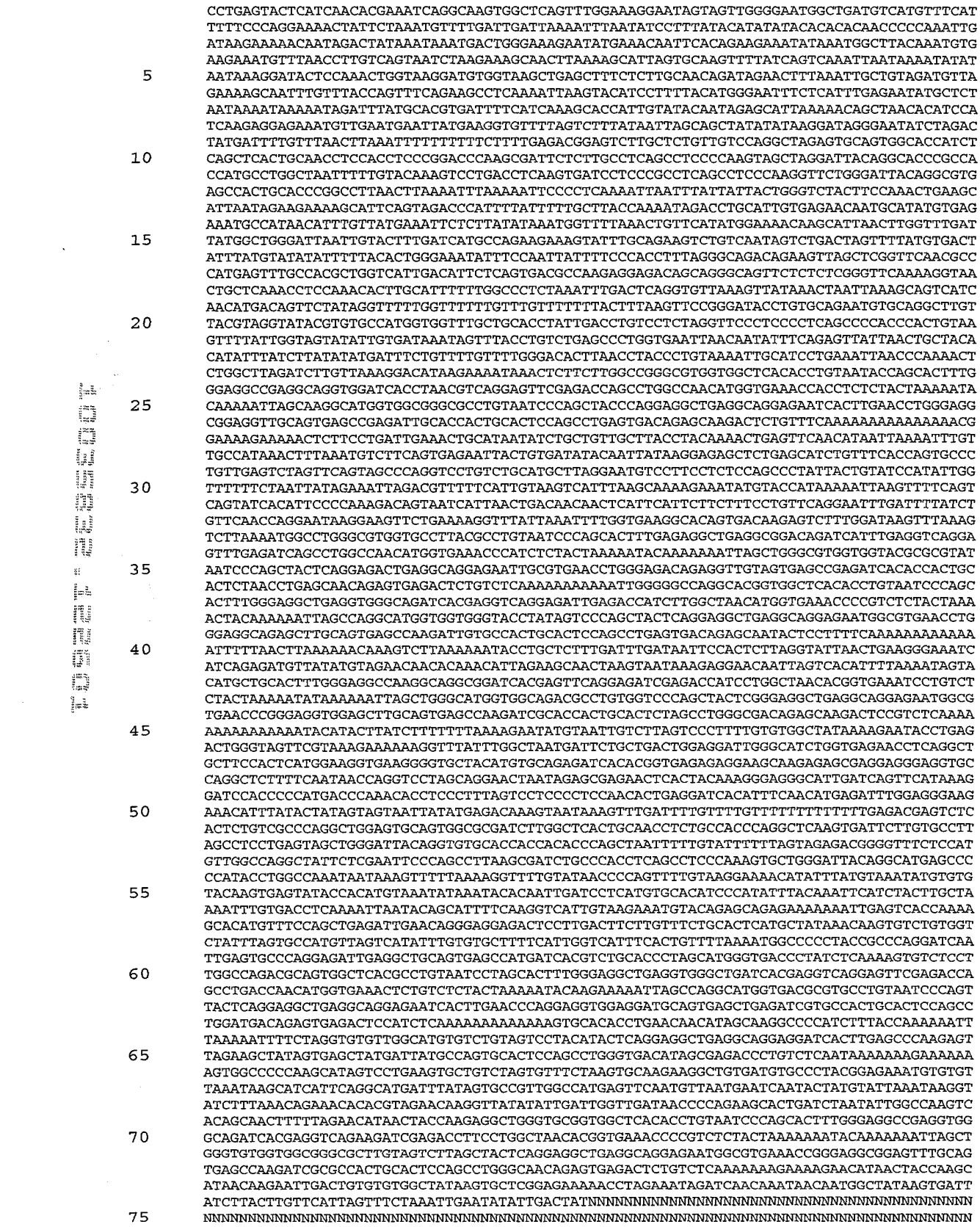


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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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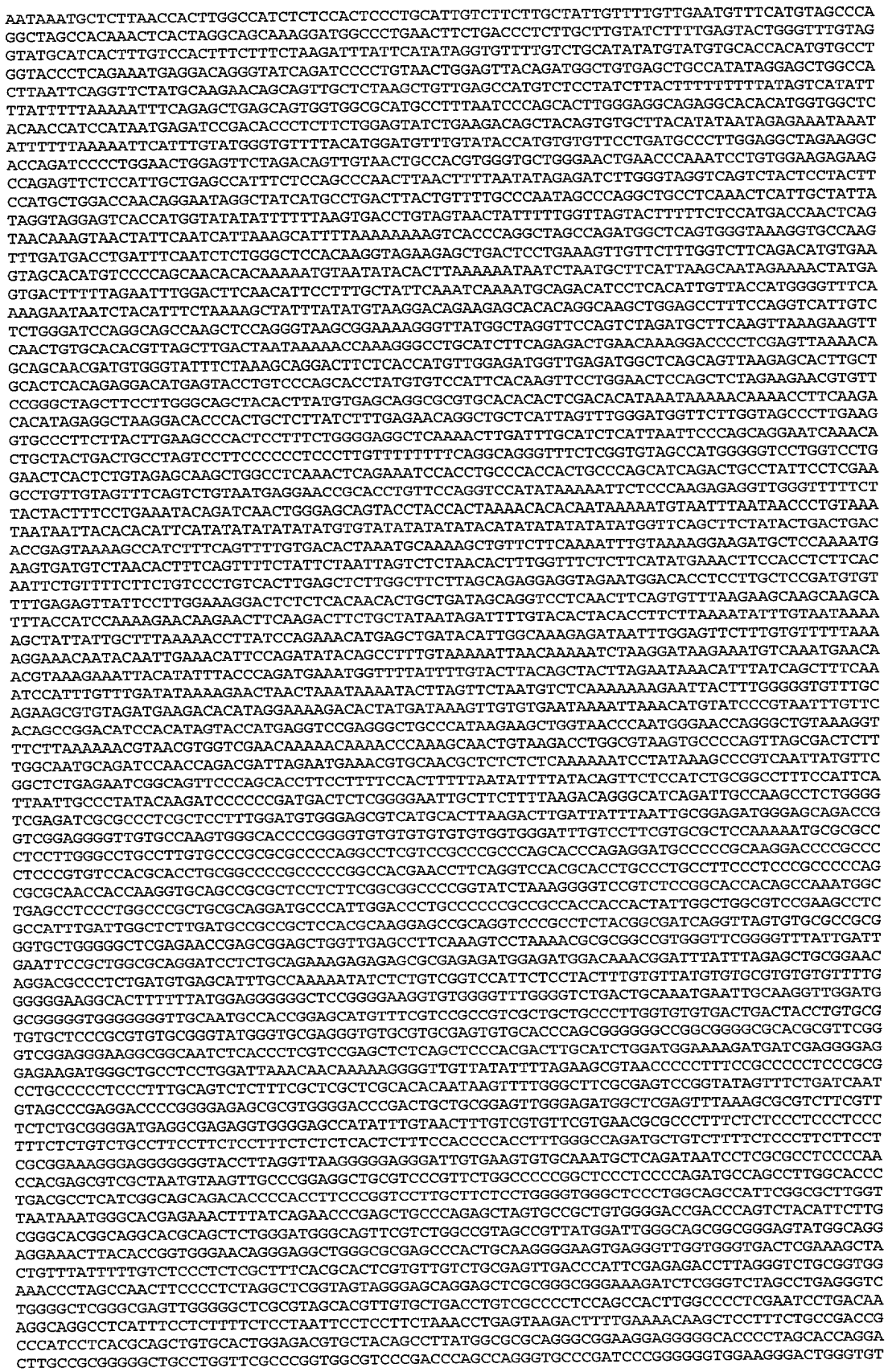
Table 93

MOUSE NOMENCLATURE
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HUMAN NOMENCLATURE
HGNC N/A
Celera hCG23810

MOUSE SEQUENCE - GENOMIC

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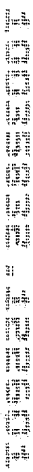


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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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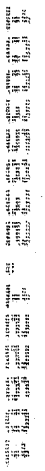
Table 94

MOUSE NOMENCLATURE
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Celera mCG9283

HUMAN NOMENCLATURE
HGNC MAP2K5
Celera hCG1787111

MOUSE SEQUENCE - GENOMIC

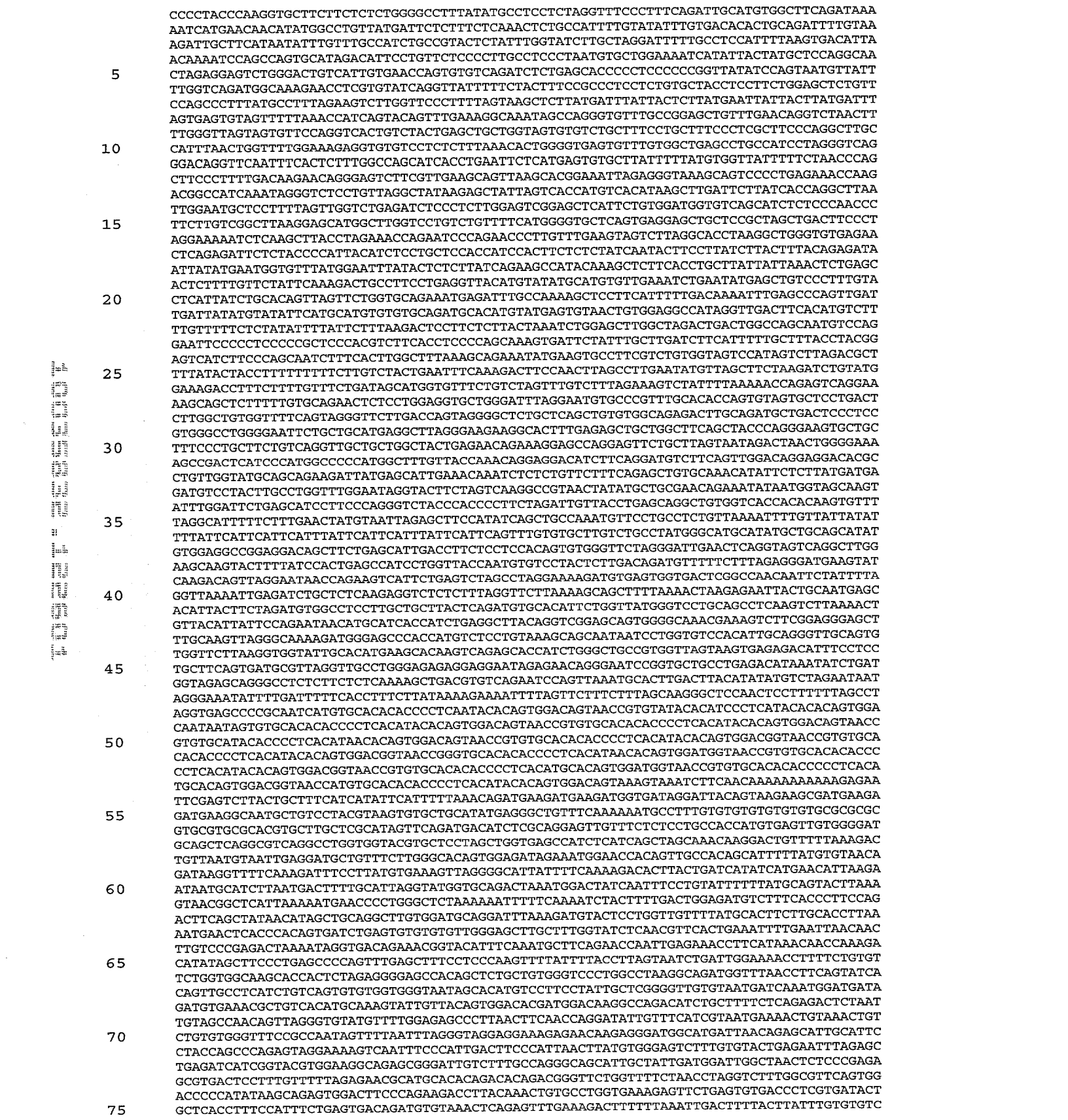
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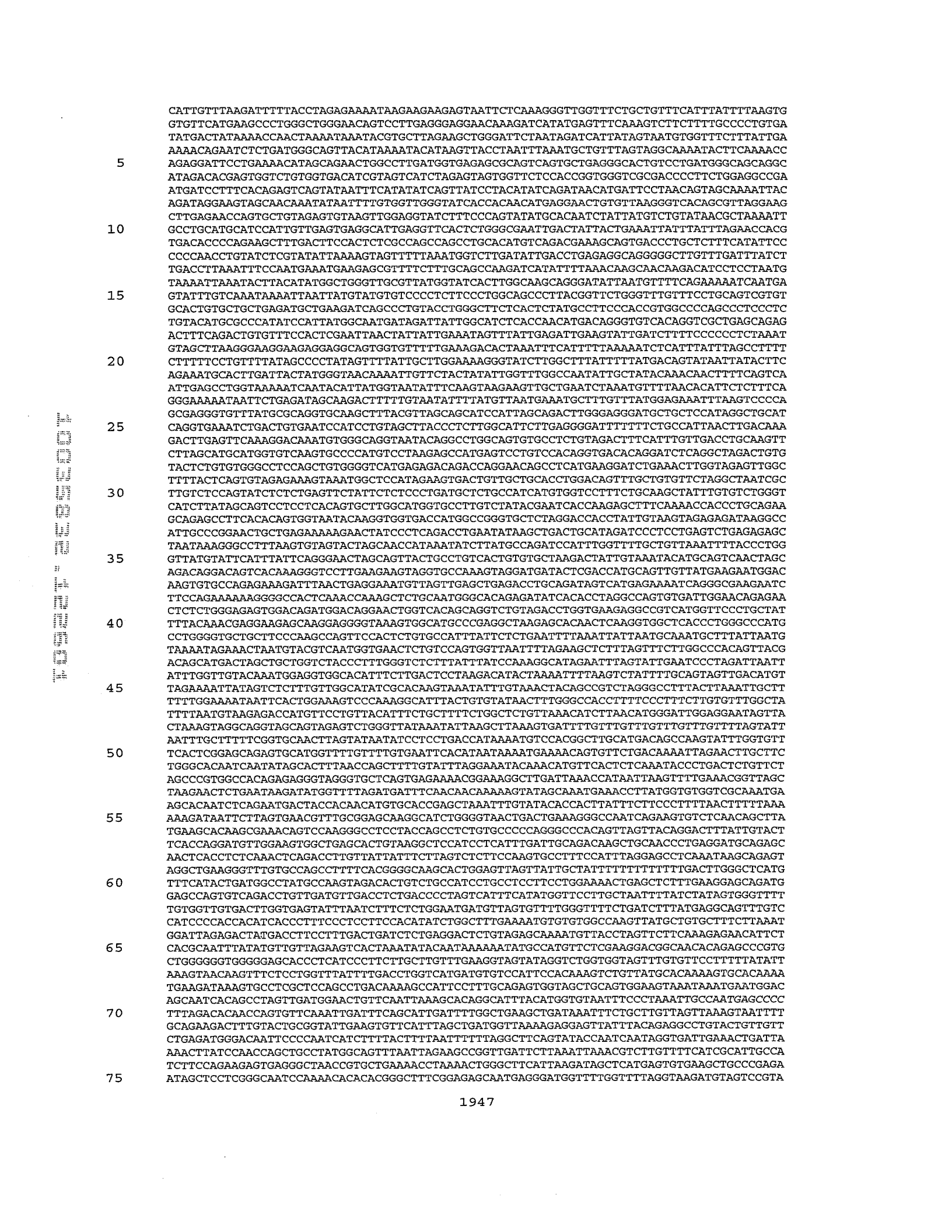
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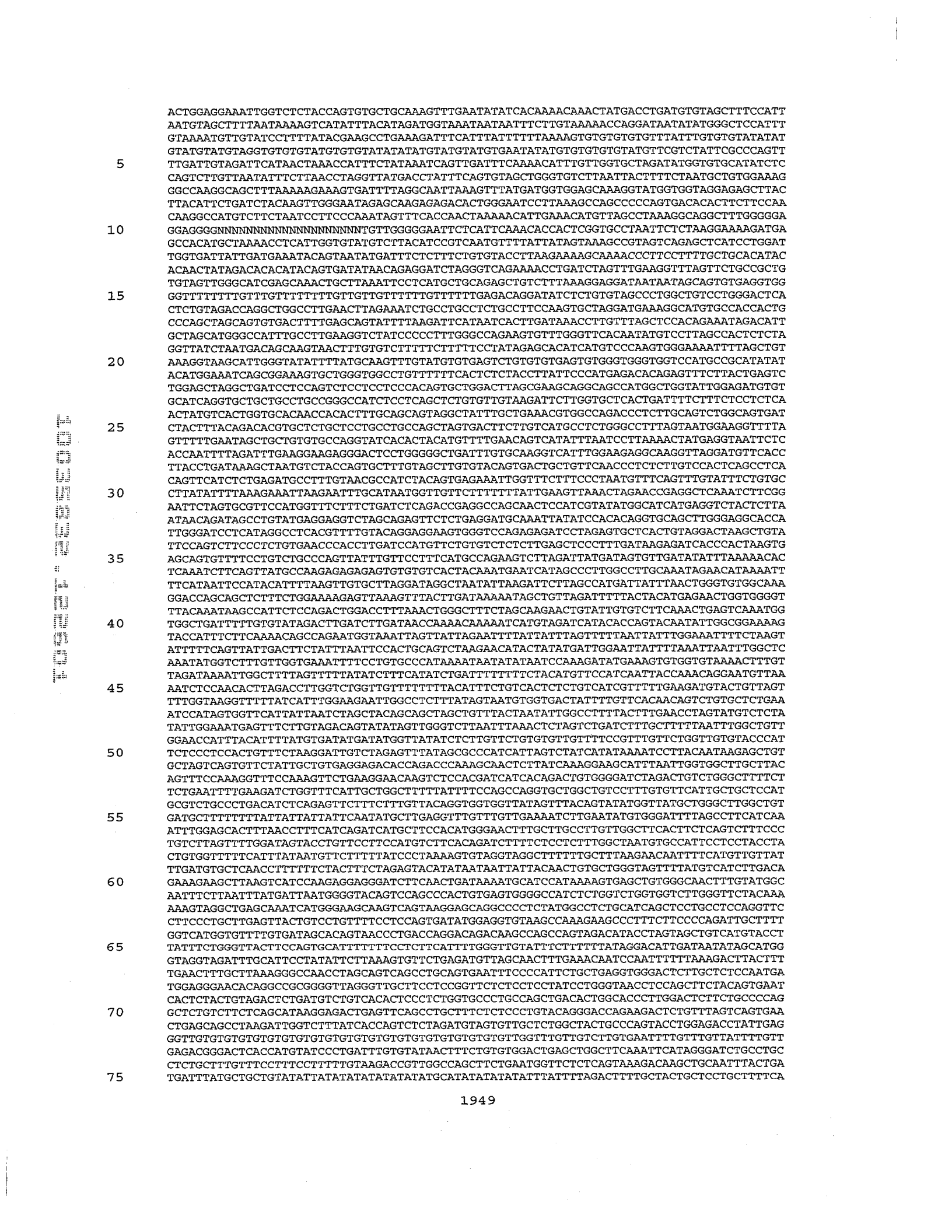
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MOUSE SEQUENCE - mRNA

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MOUSE SEQUENCE - CODING

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HUMAN SEQUENCE - GENOMIC

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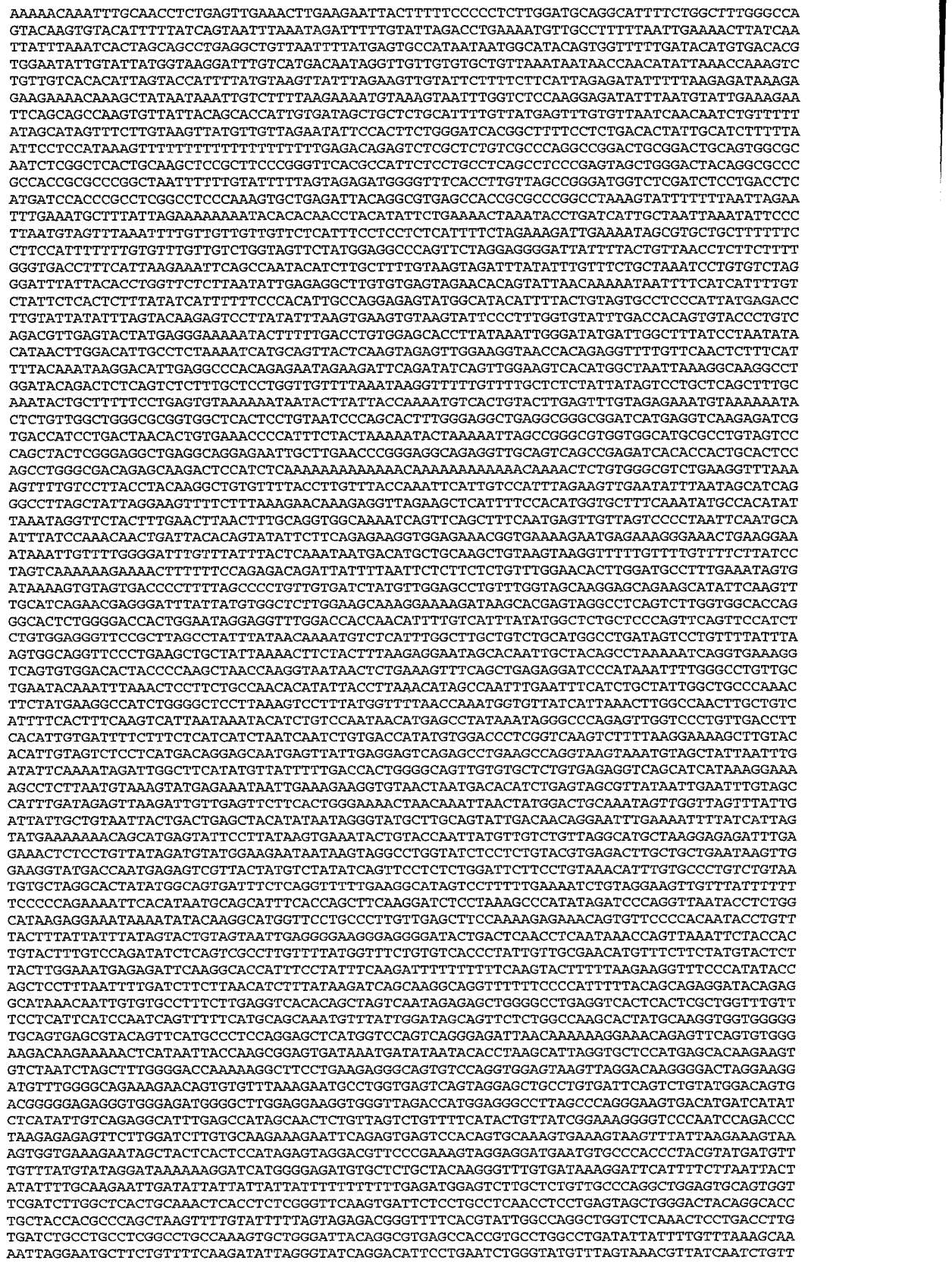
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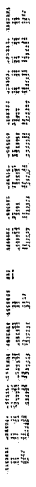
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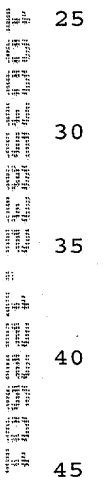
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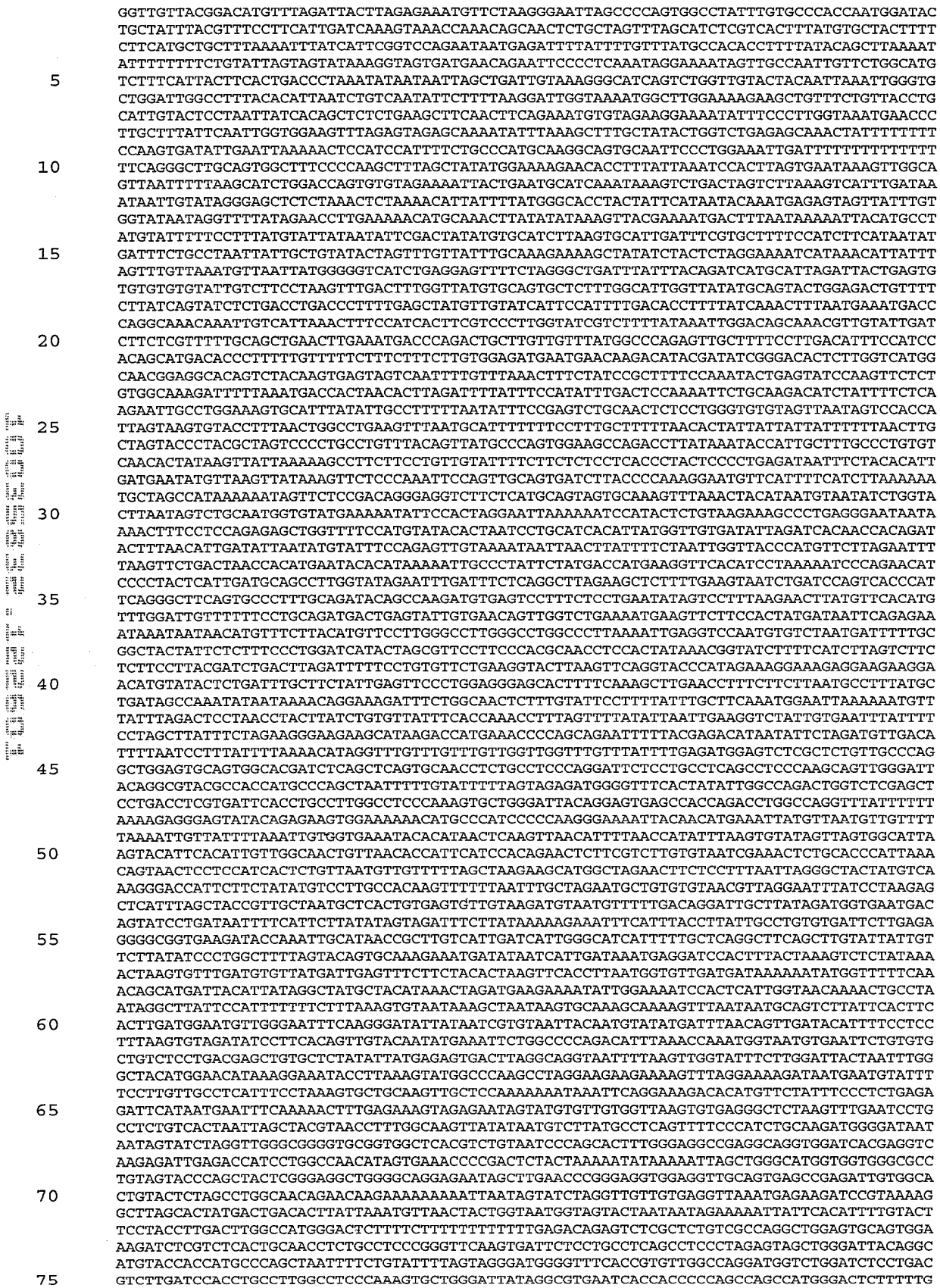
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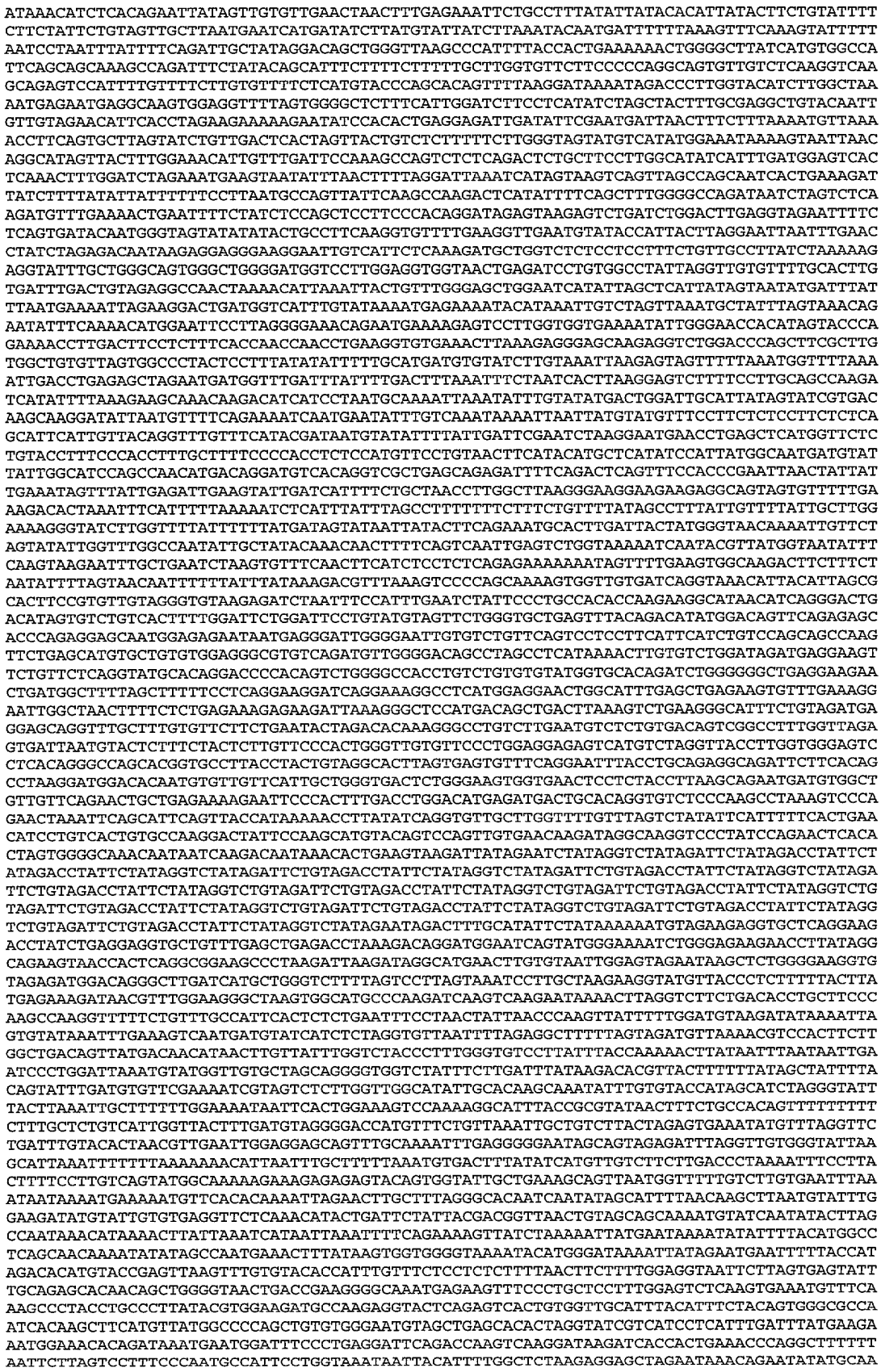


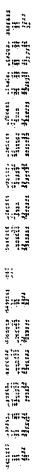
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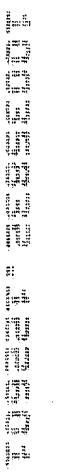


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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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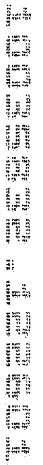
Table 95

MOUSE NOMENCLATURE
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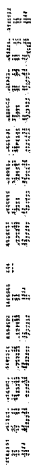
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MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

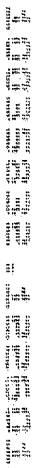
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MOUSE SEQUENCE - CODING

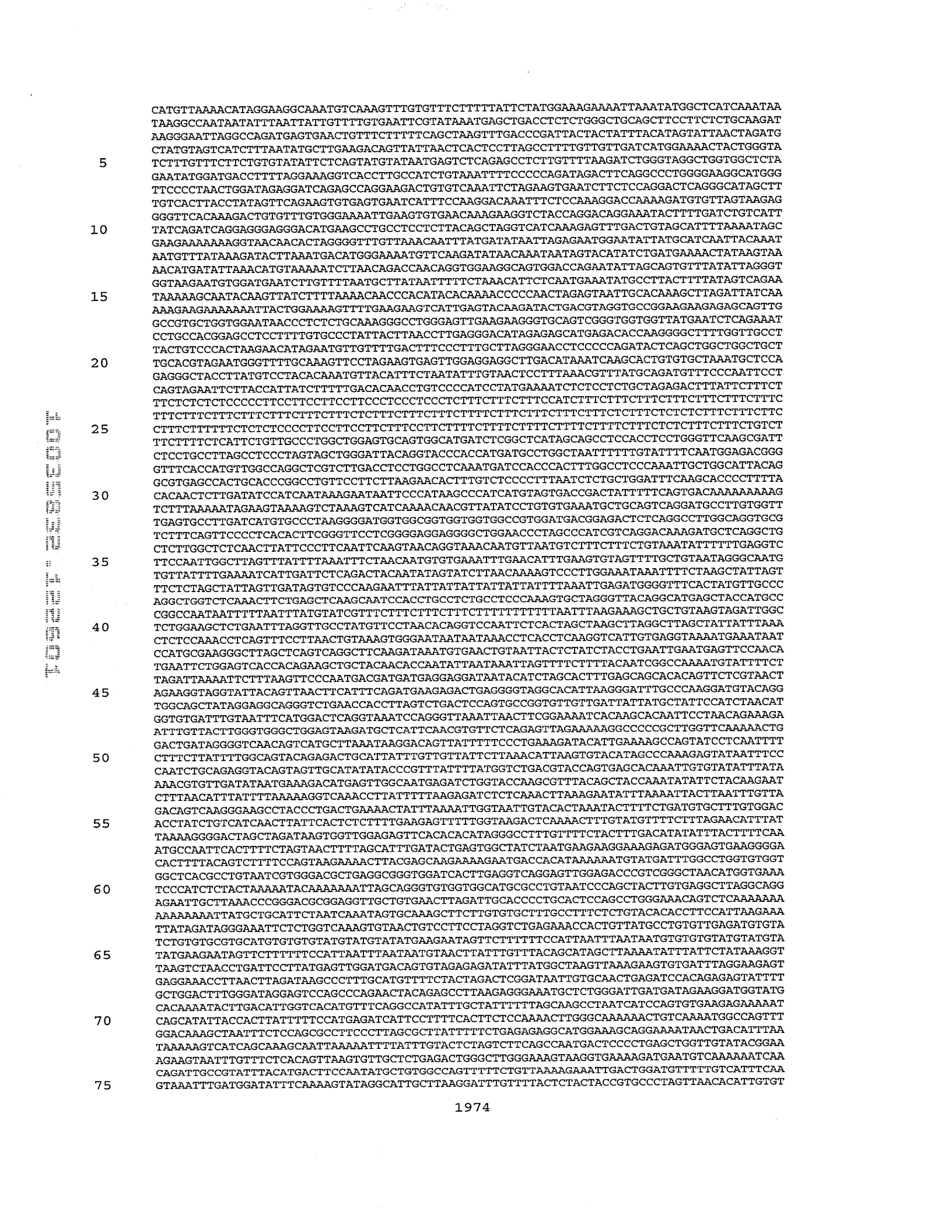
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HUMAN SEQUENCE - GENOMIC

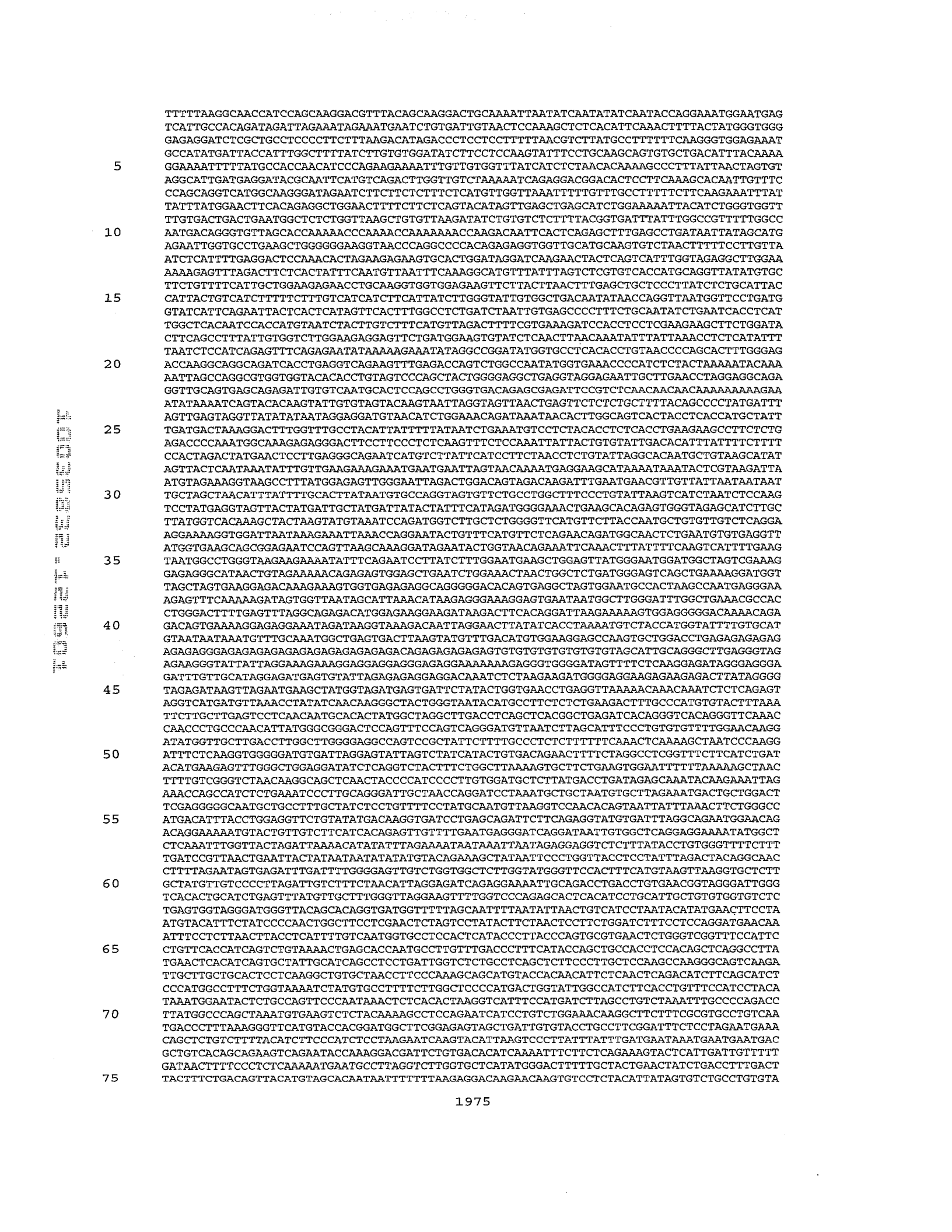
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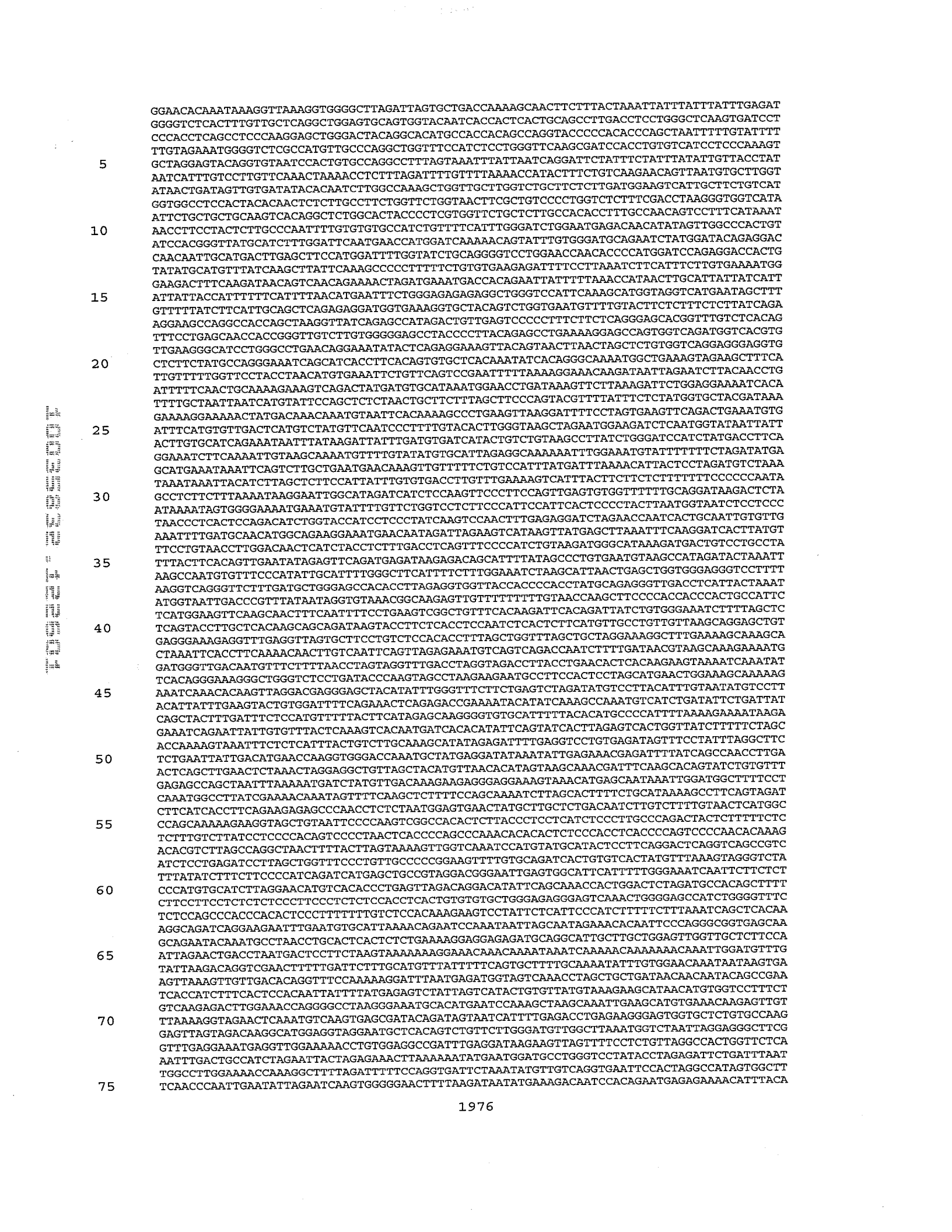
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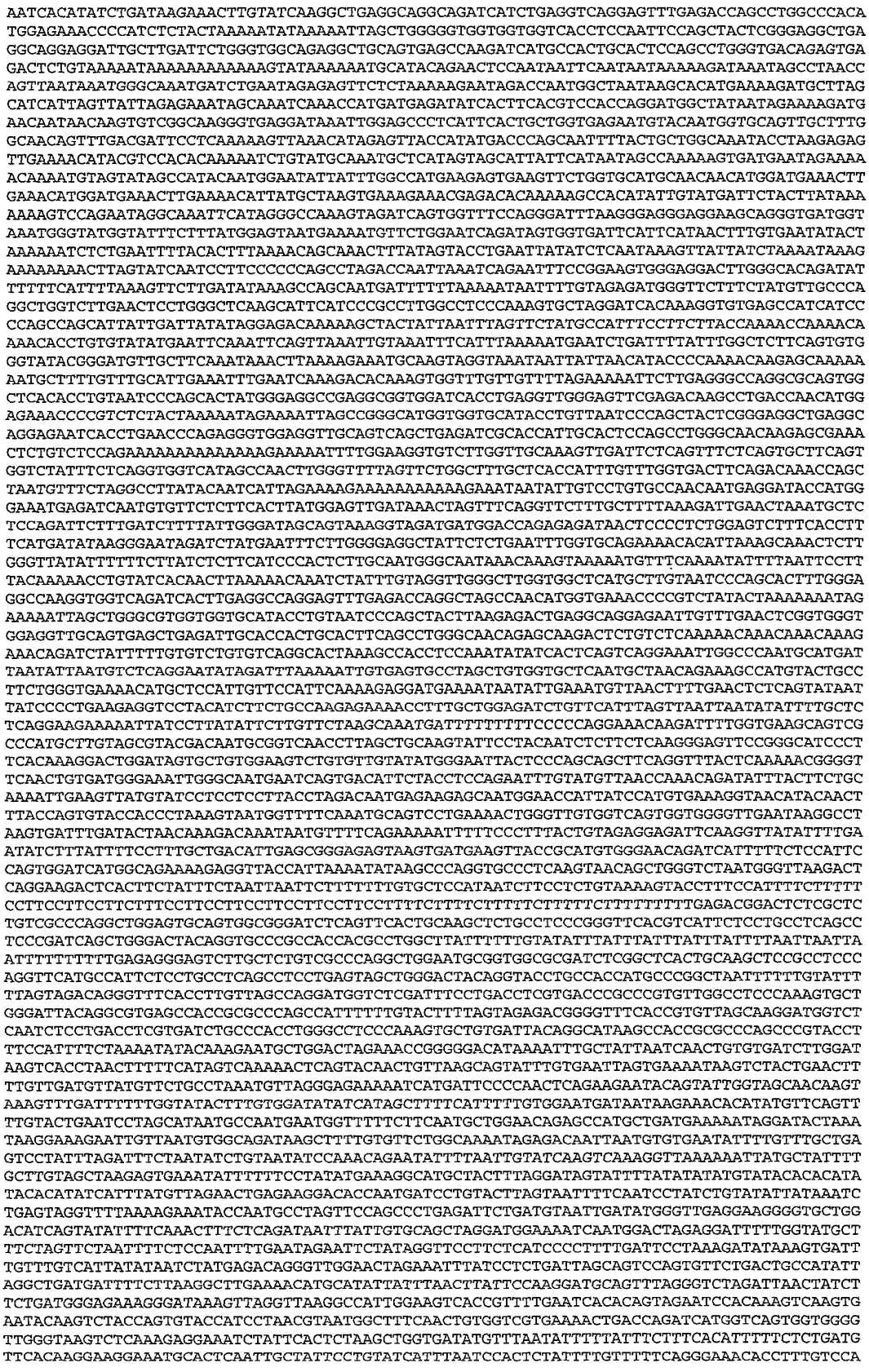


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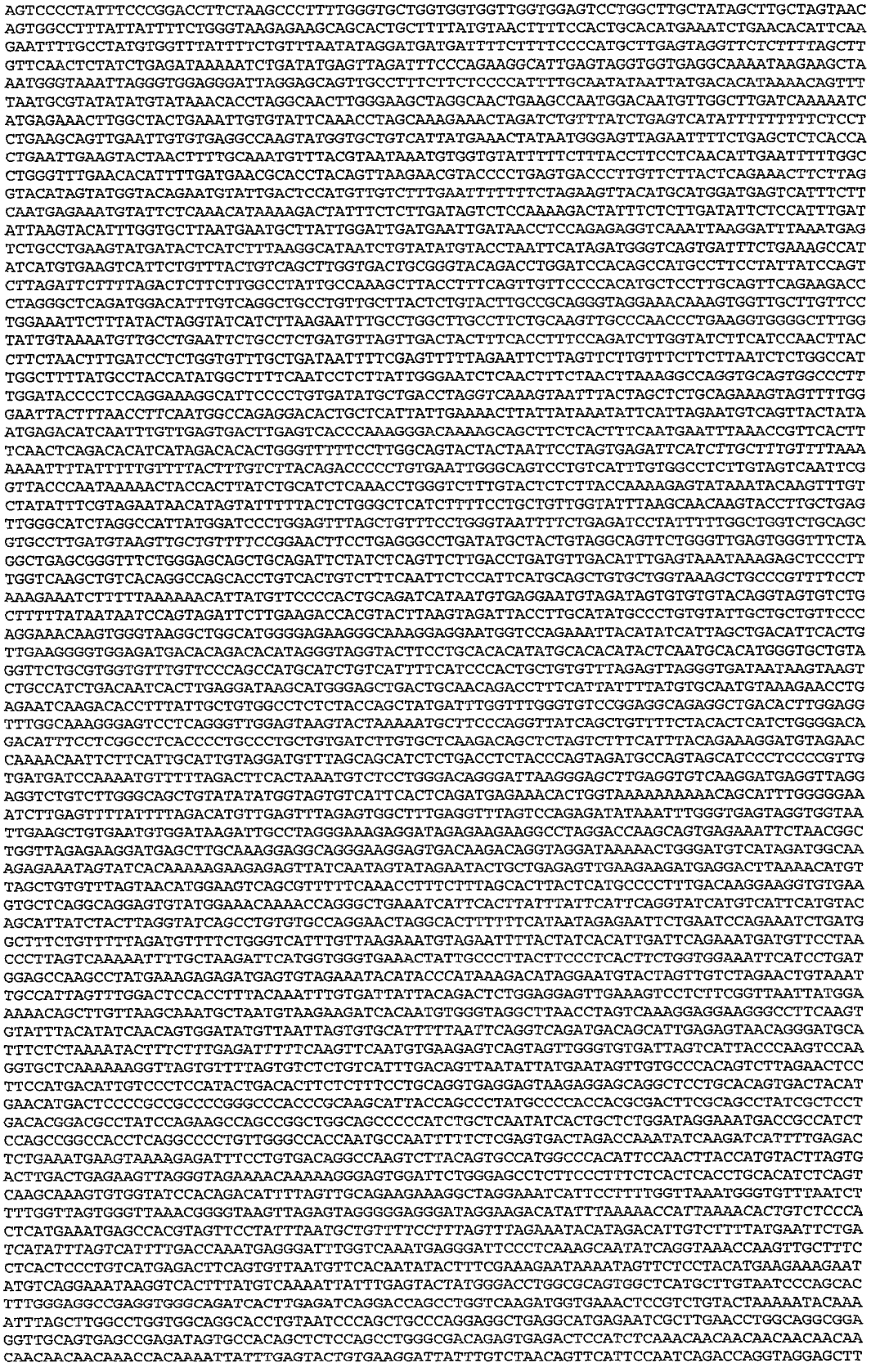


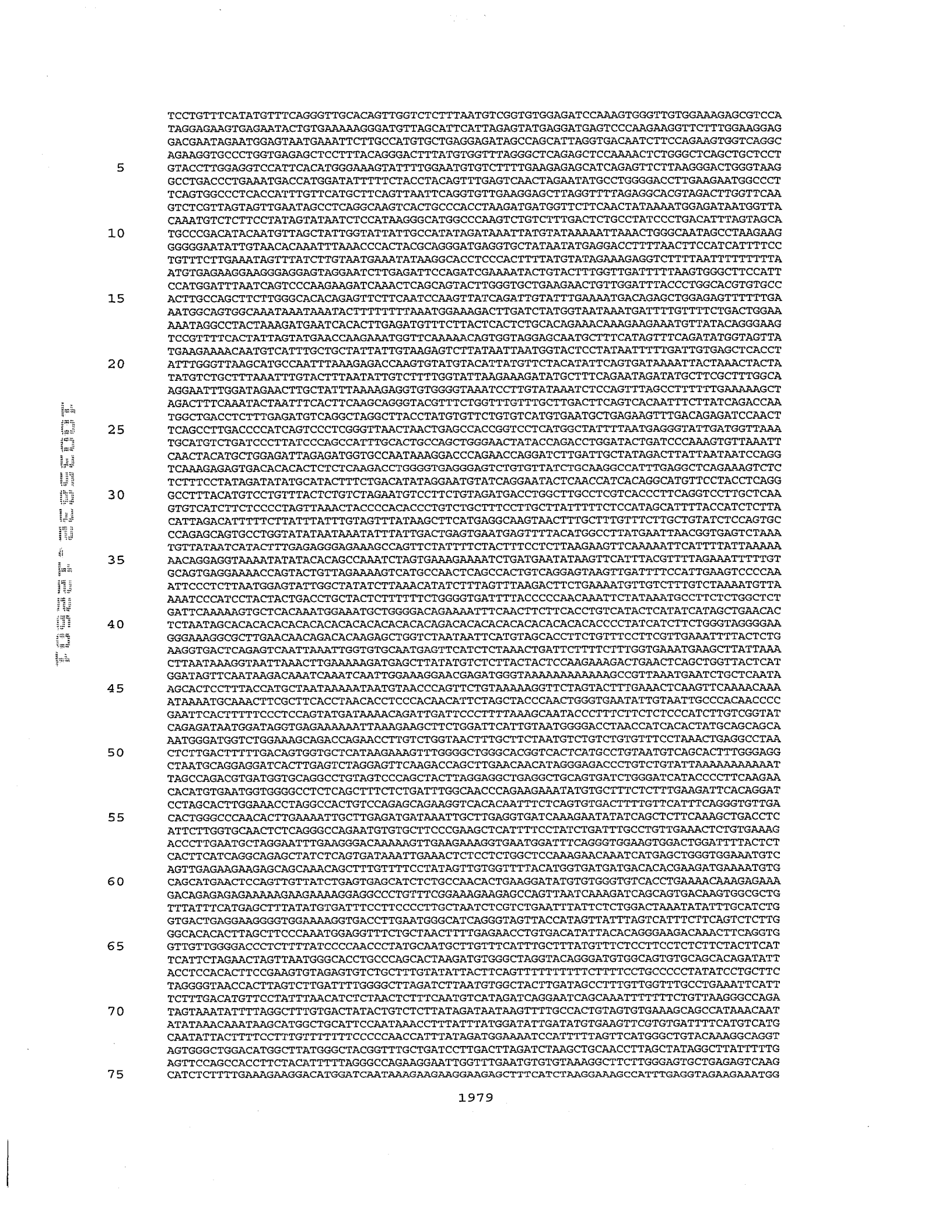
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING

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Table 96

MOUSE NOMENCLATURE
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Celera mCG19301

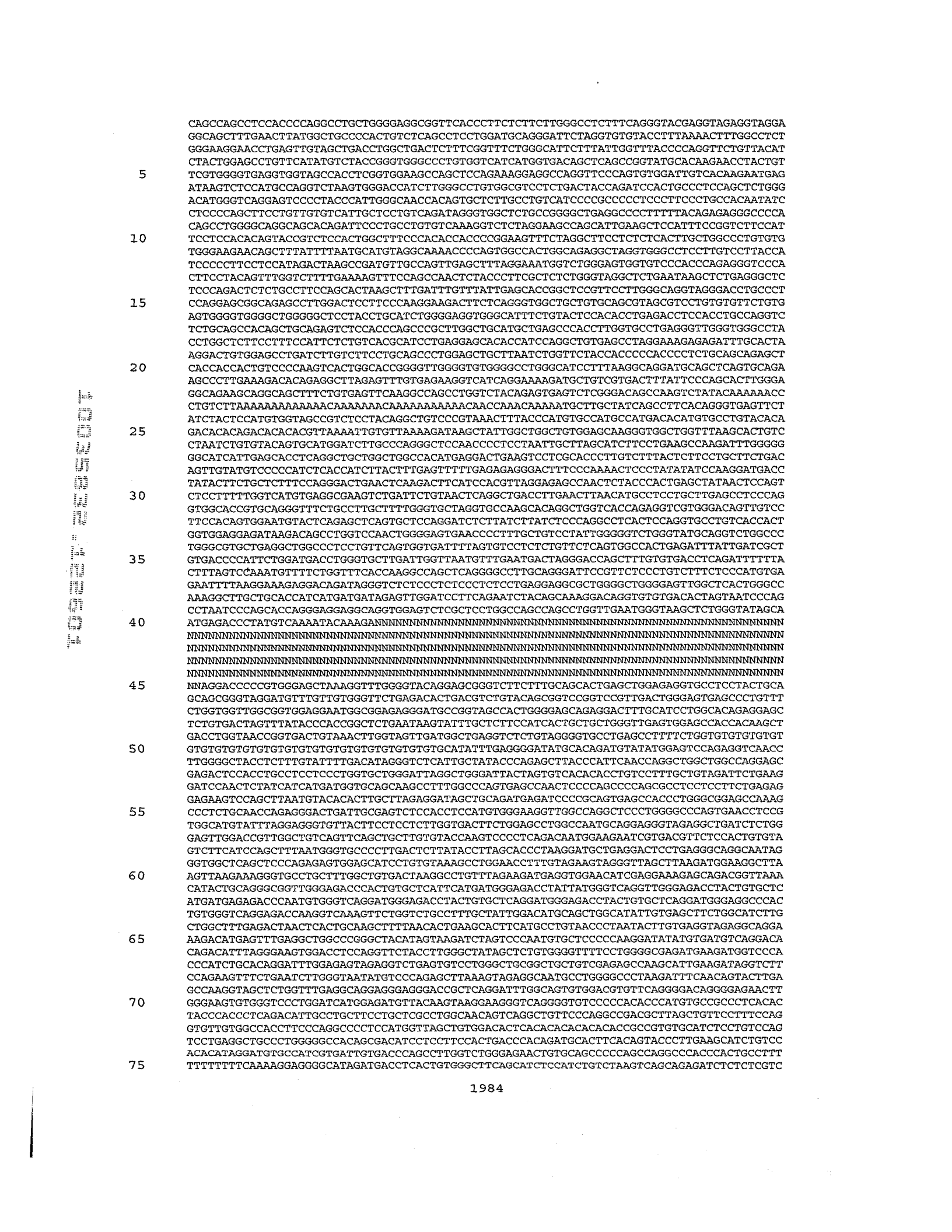
HUMAN NOMENCLATURE
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MOUSE SEQUENCE - GENOMIC

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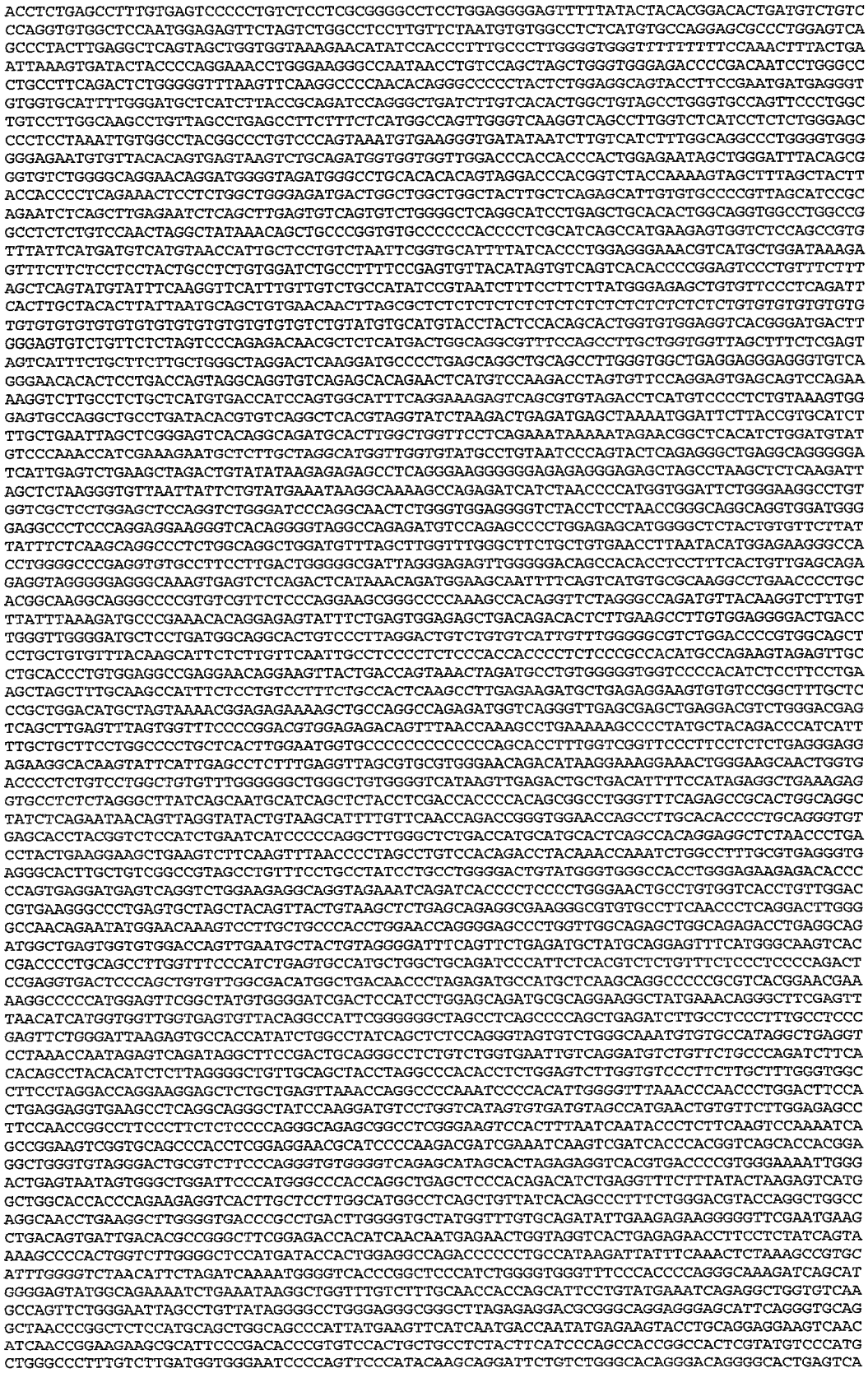


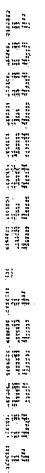
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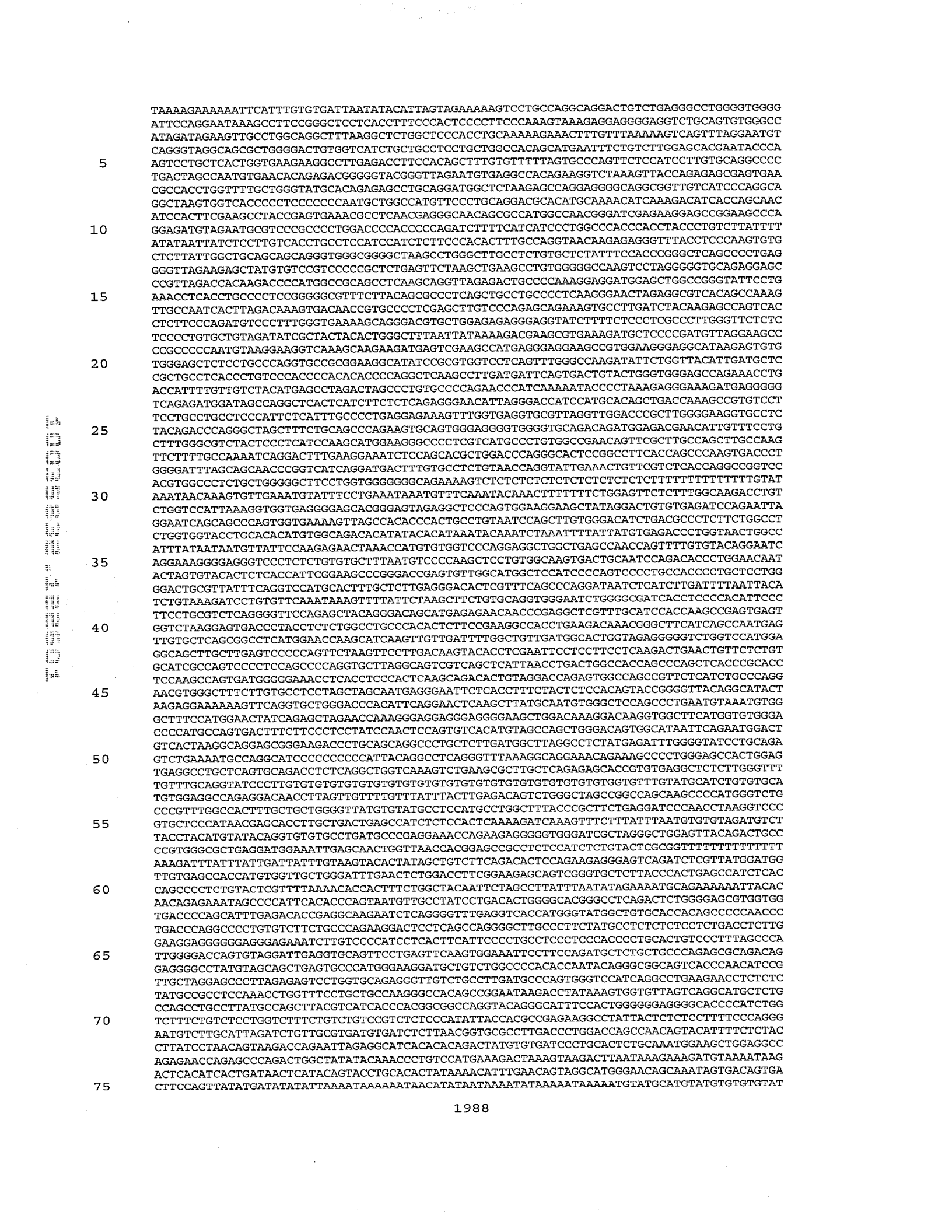
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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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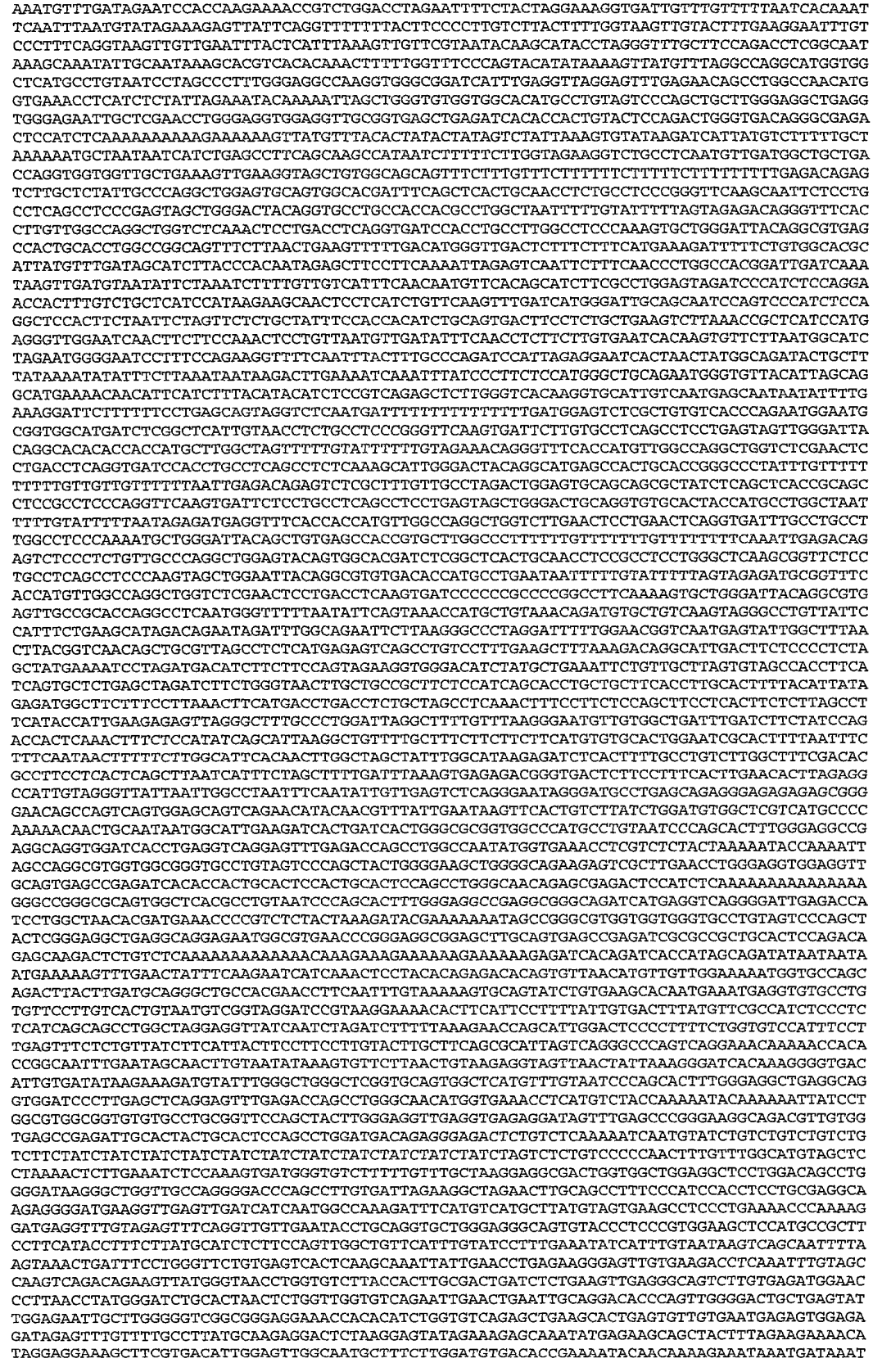
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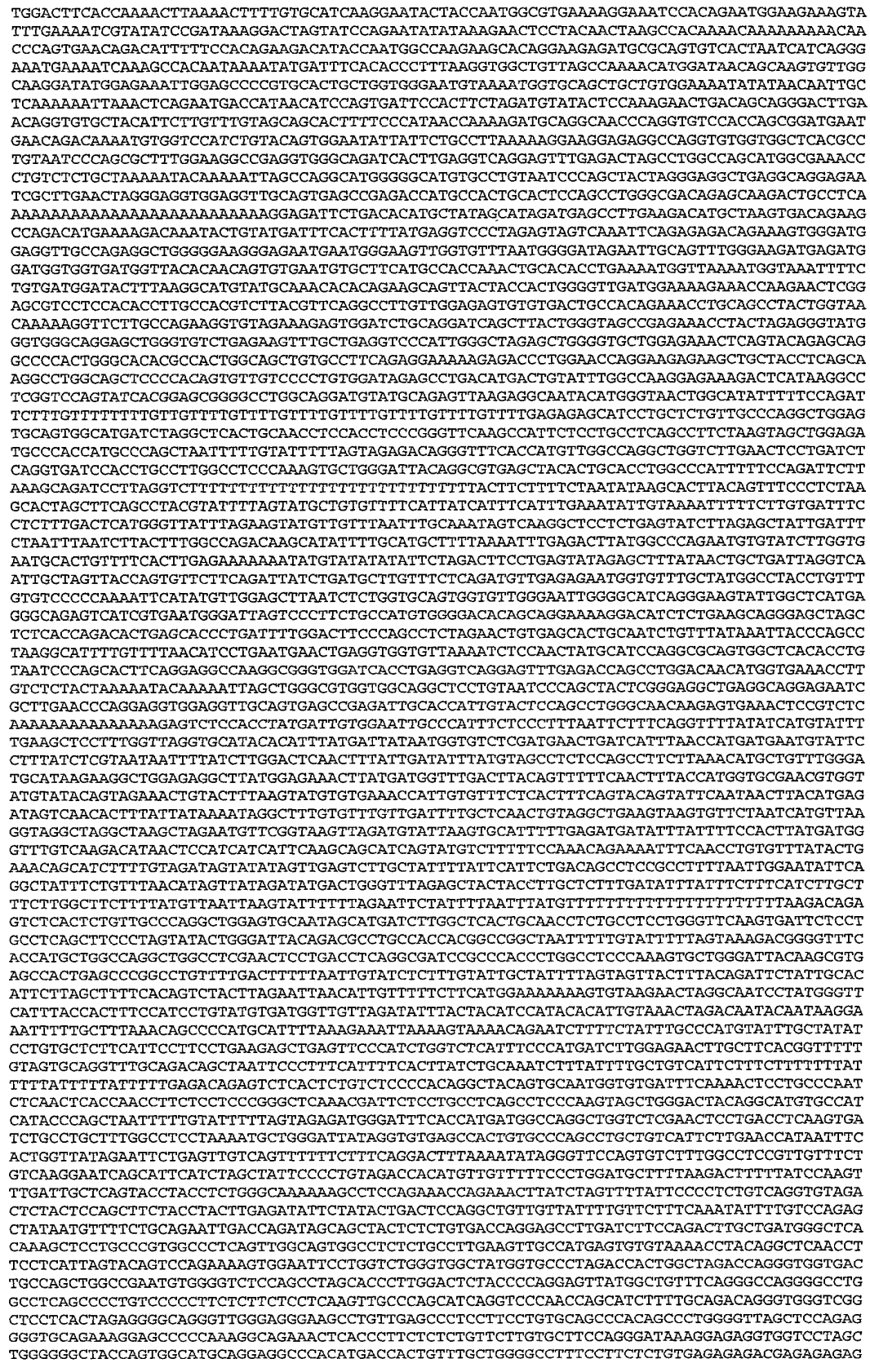
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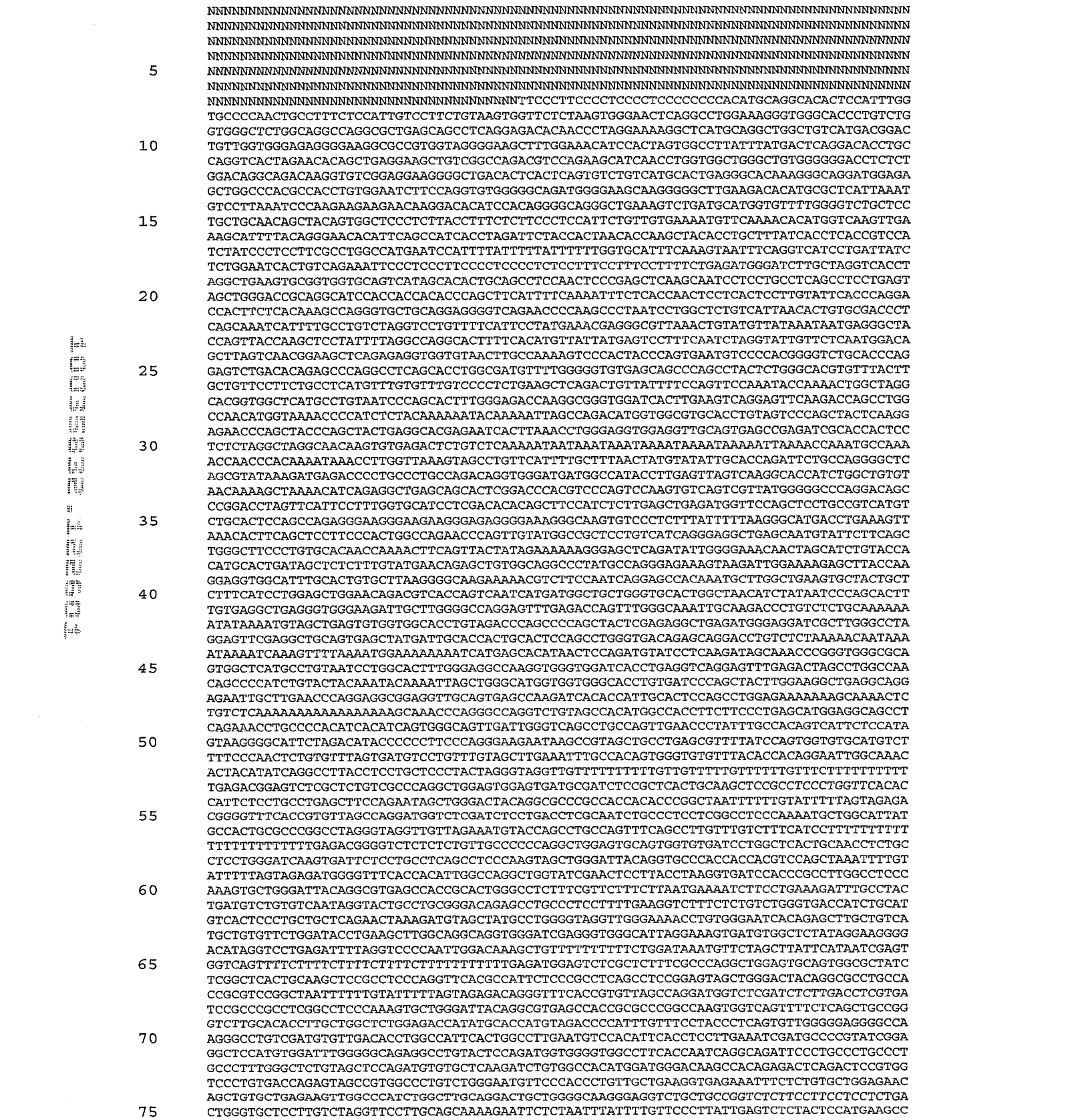


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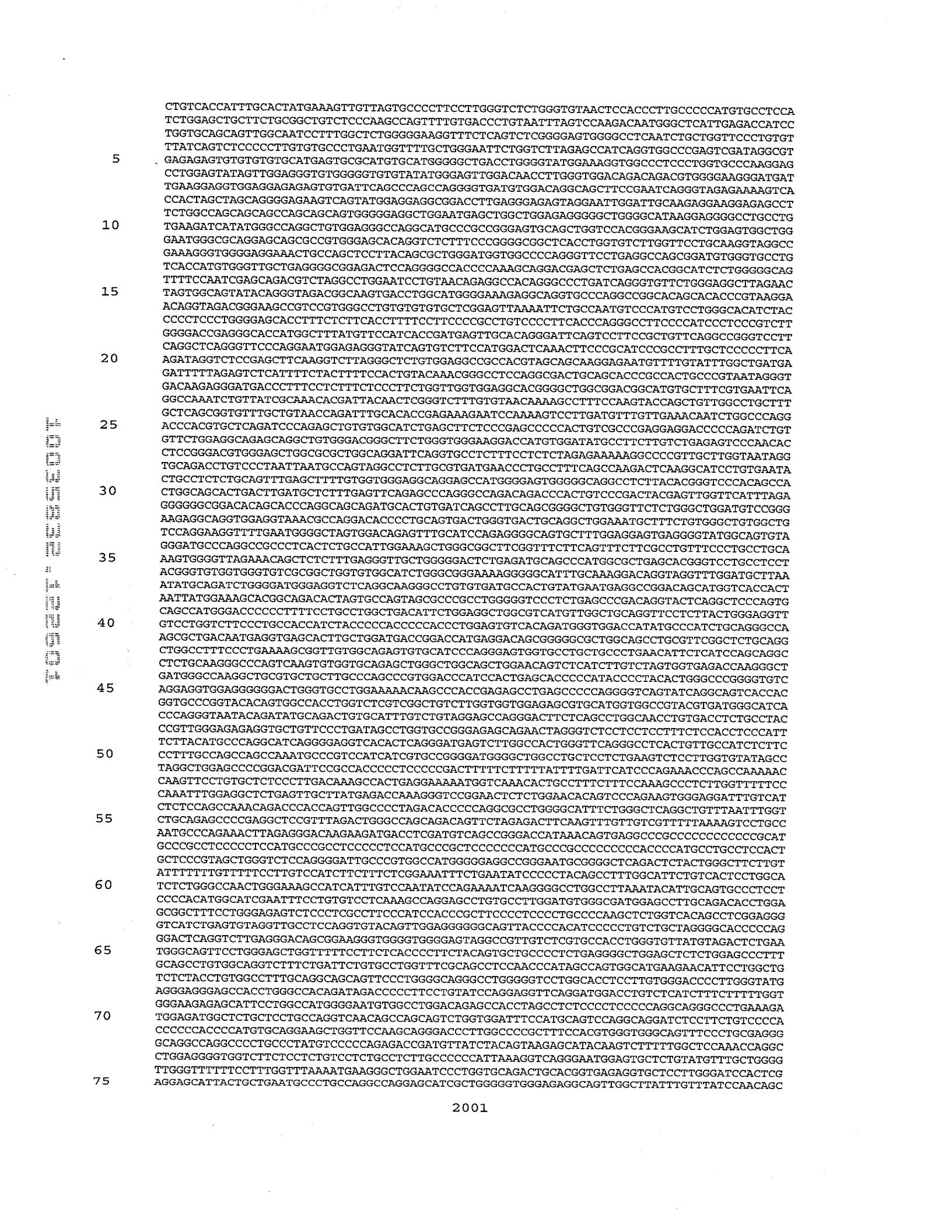
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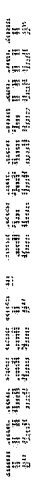
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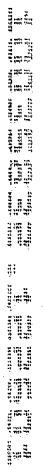
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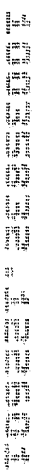
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ATCCCAGCAATGAAACAAGAATCTAGAGTGATGTGATTCCTCCGATGACTTCTCCAACCATCTGGGGTTTTTGTGCGACTCCAAGA
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HUMAN SEQUENCE - mRNA
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HUMAN SEQUENCE - CODING
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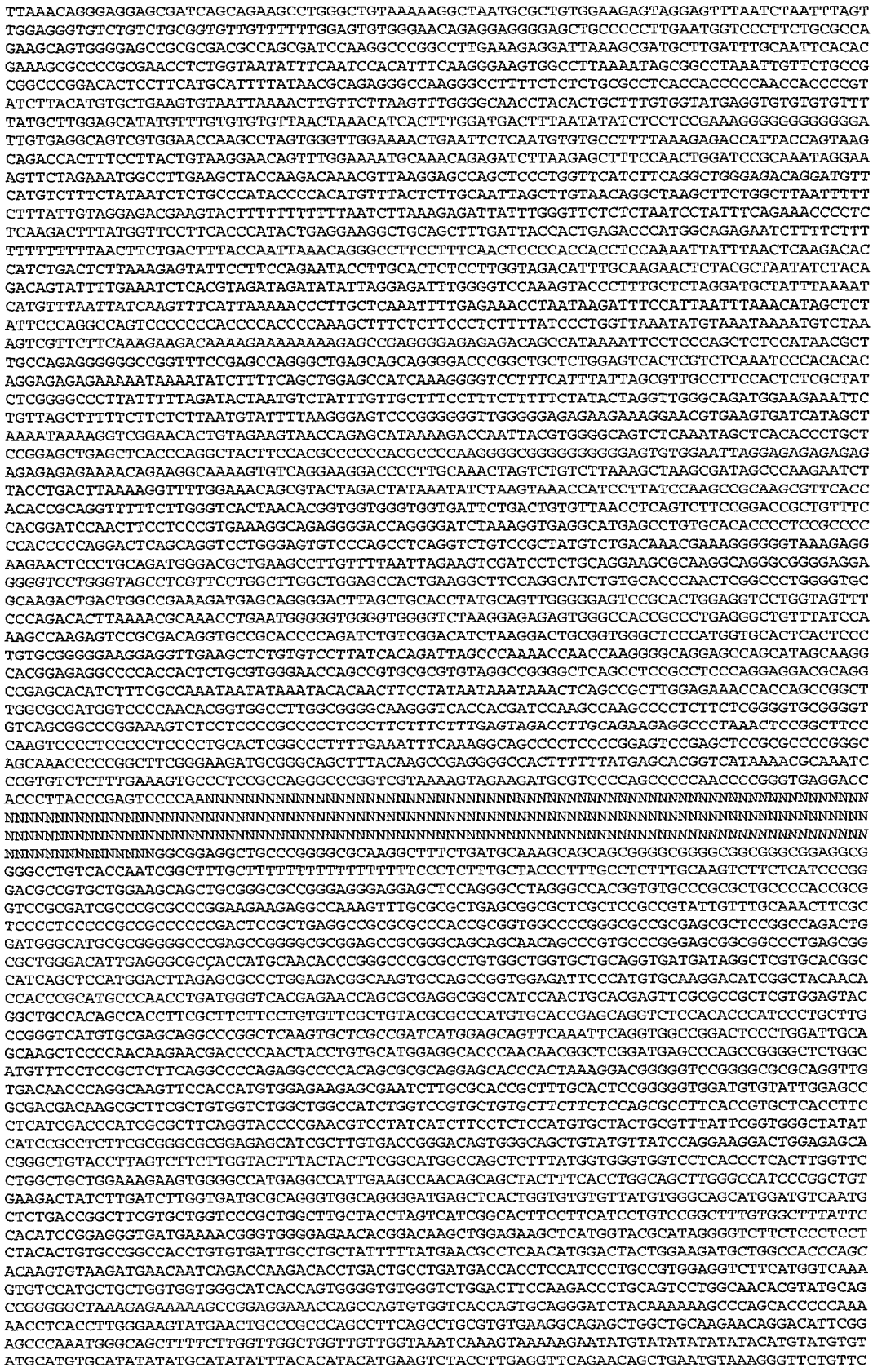
Table 97

MOUSE NOMENCLATURE
ICSGNM Fzd10
Celera mCG51280

HUMAN NOMENCLATURE
HGNC FZD10
Celera hCG21398

MOUSE SEQUENCE - GENOMIC

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MOUSE SEQUENCE - mRNA

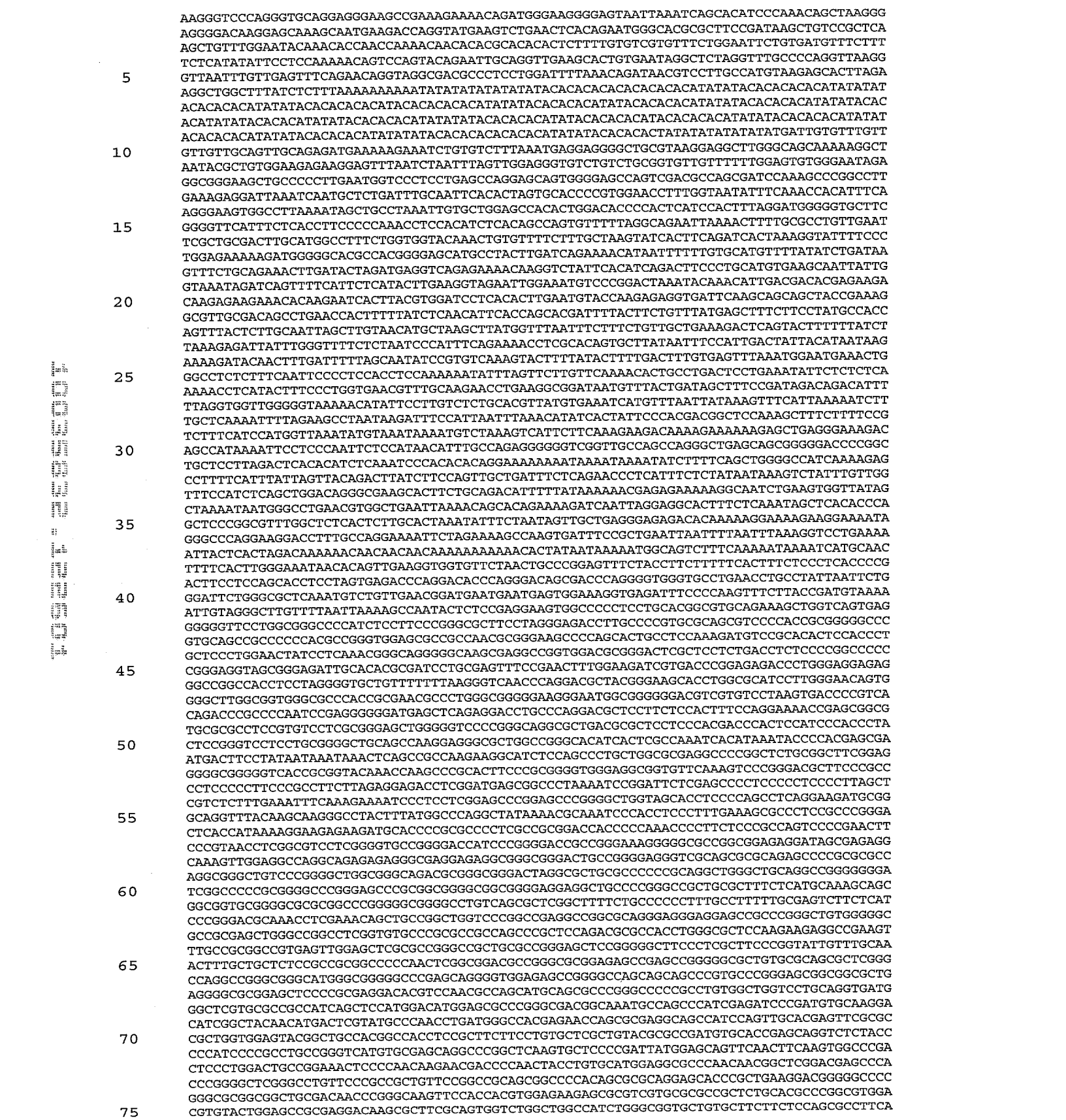
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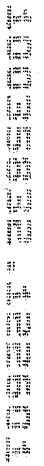
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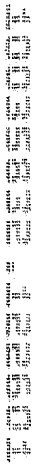
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HUMAN SEQUENCE - mRNA
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Table 98

MOUSE NOMENCLATURE

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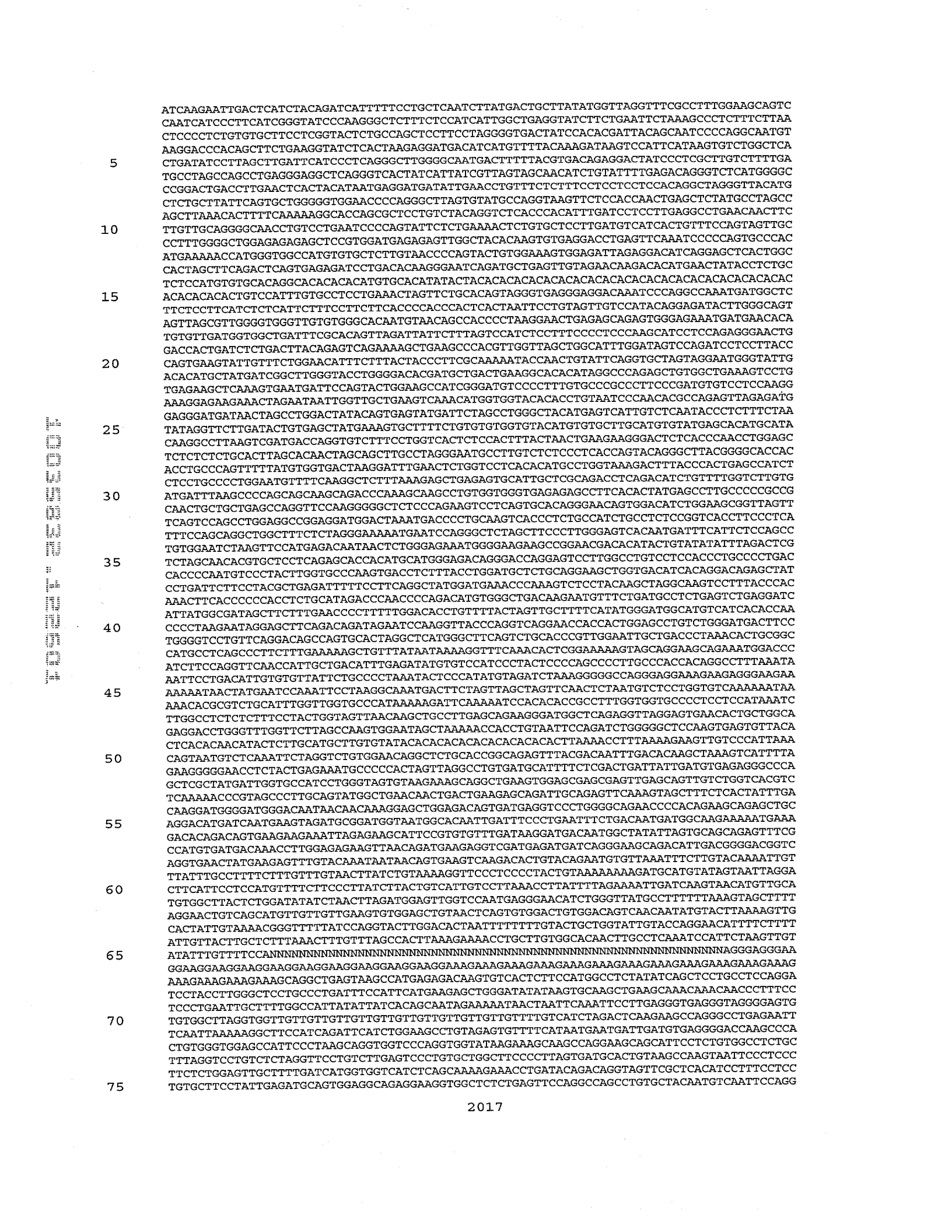
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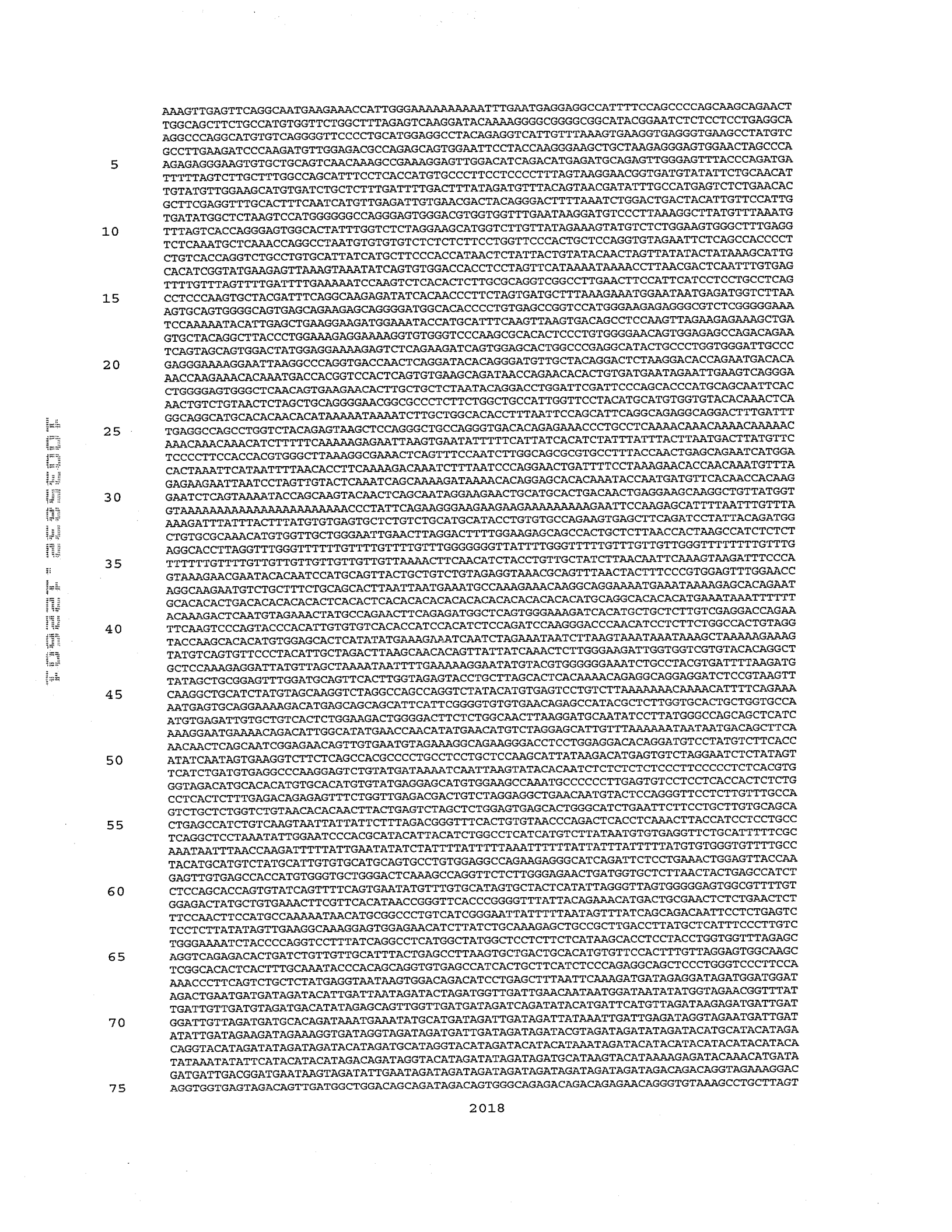
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MOUSE SEQUENCE - GENOMIC

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Replacement Sheet - 35 of 46 pages





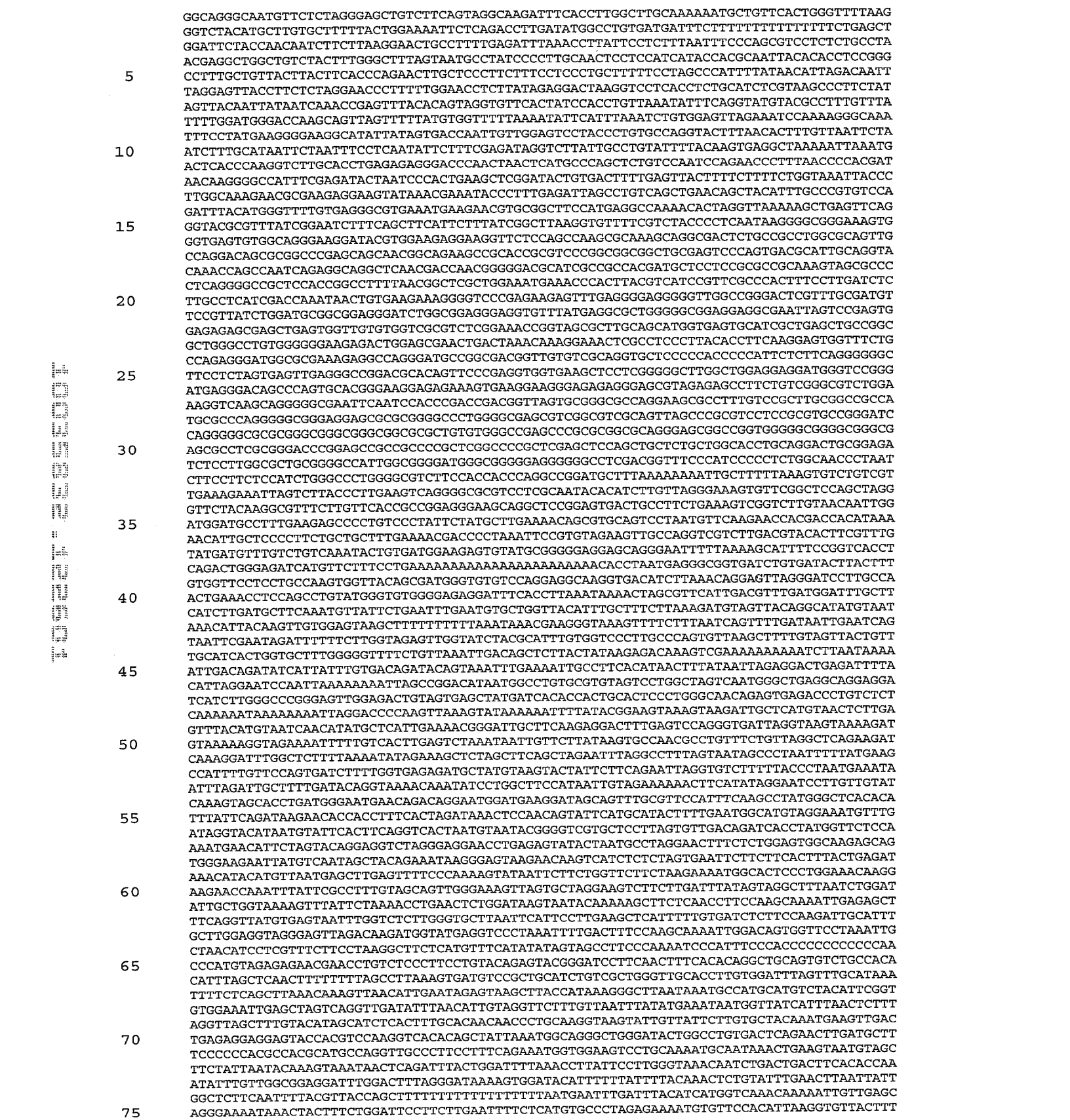
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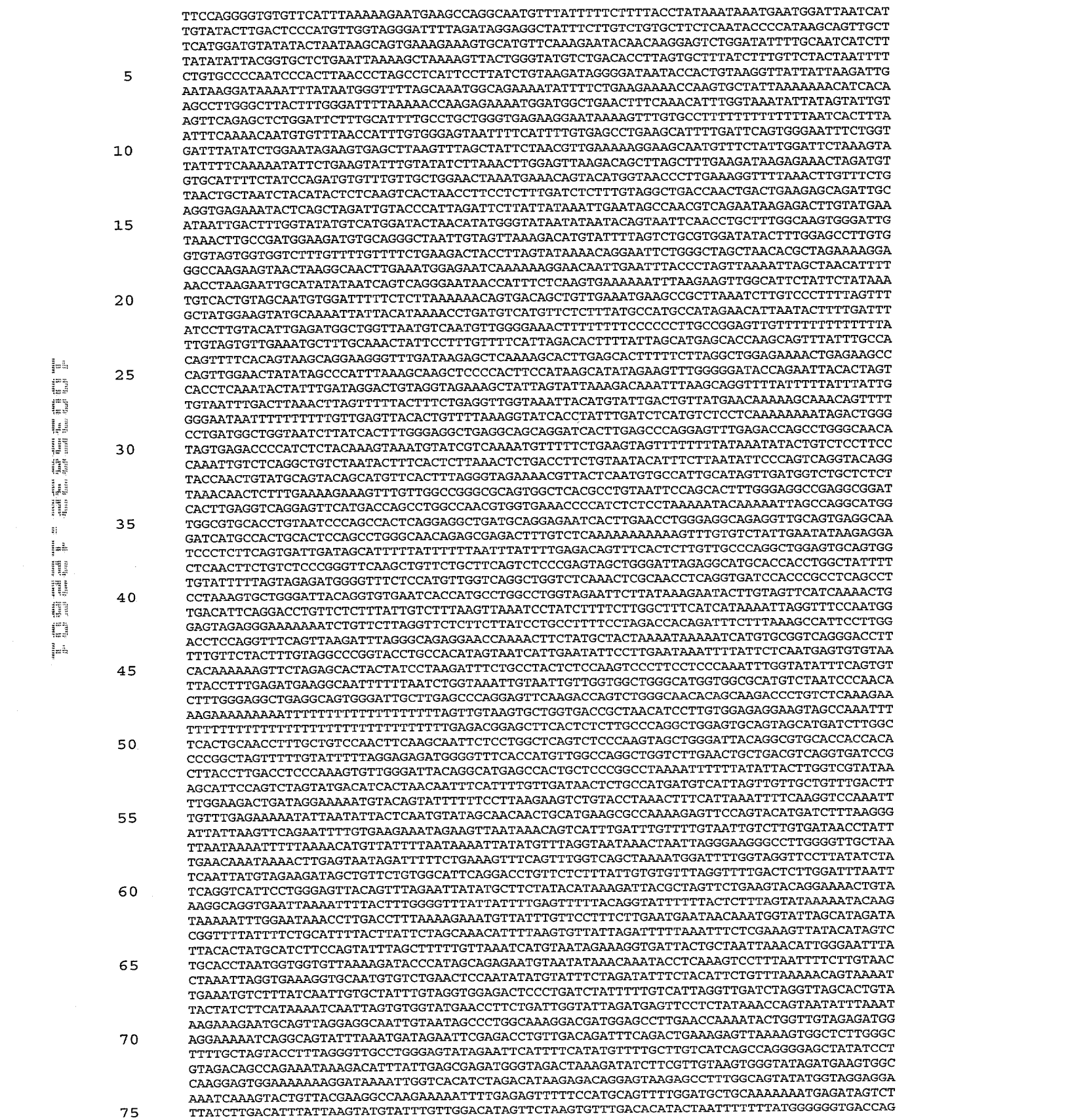
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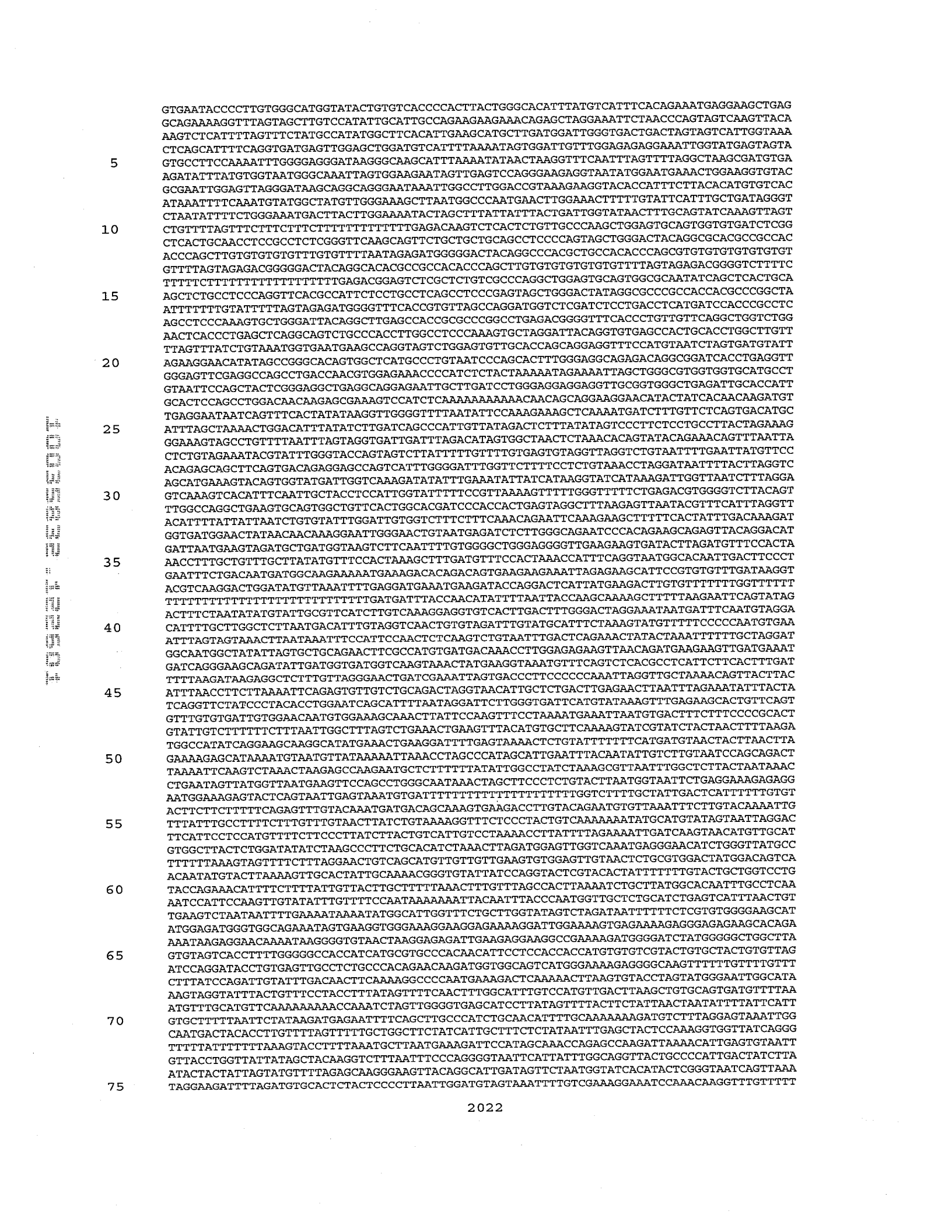
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Application No. 2023200235 Date Filed: 2023-01-17

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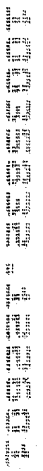
Table 99

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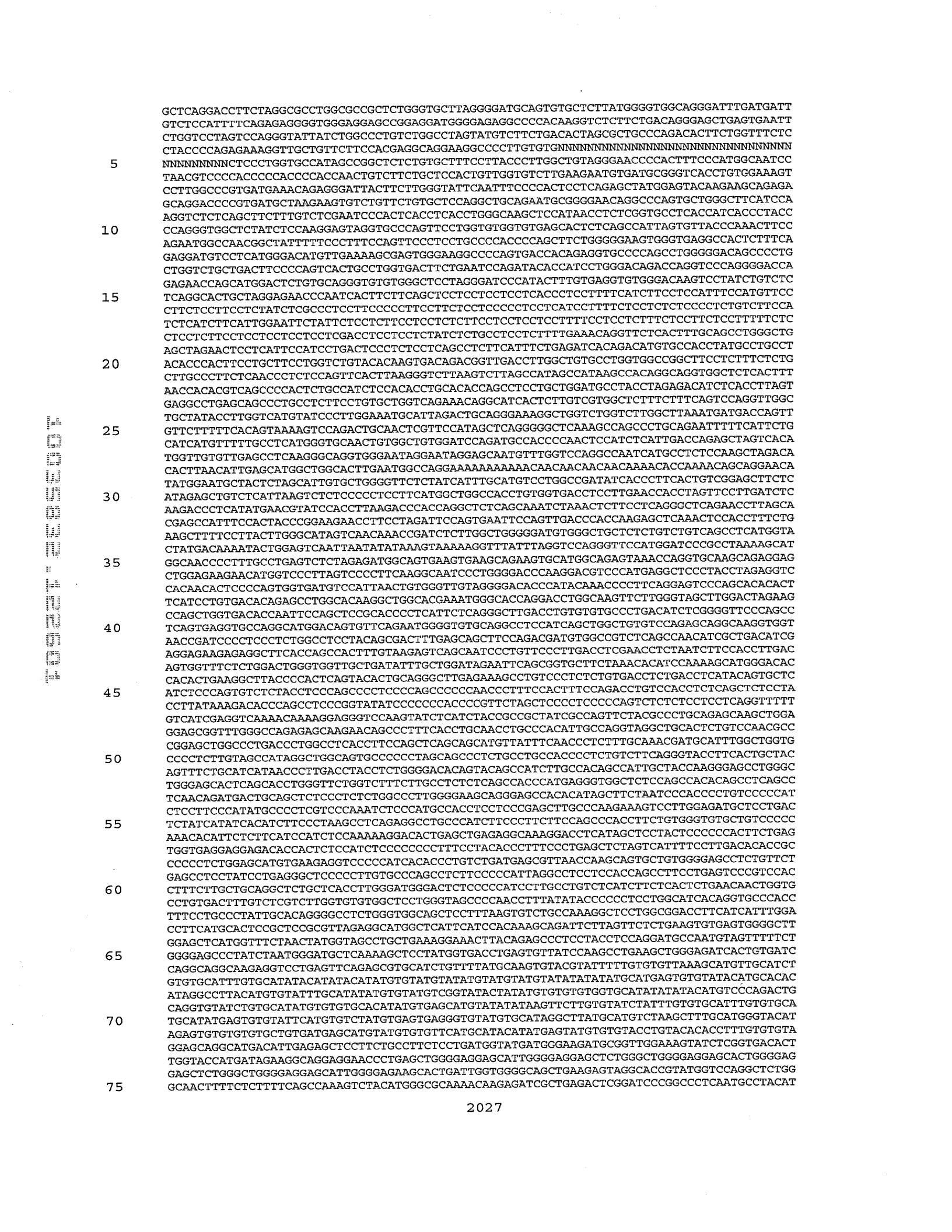
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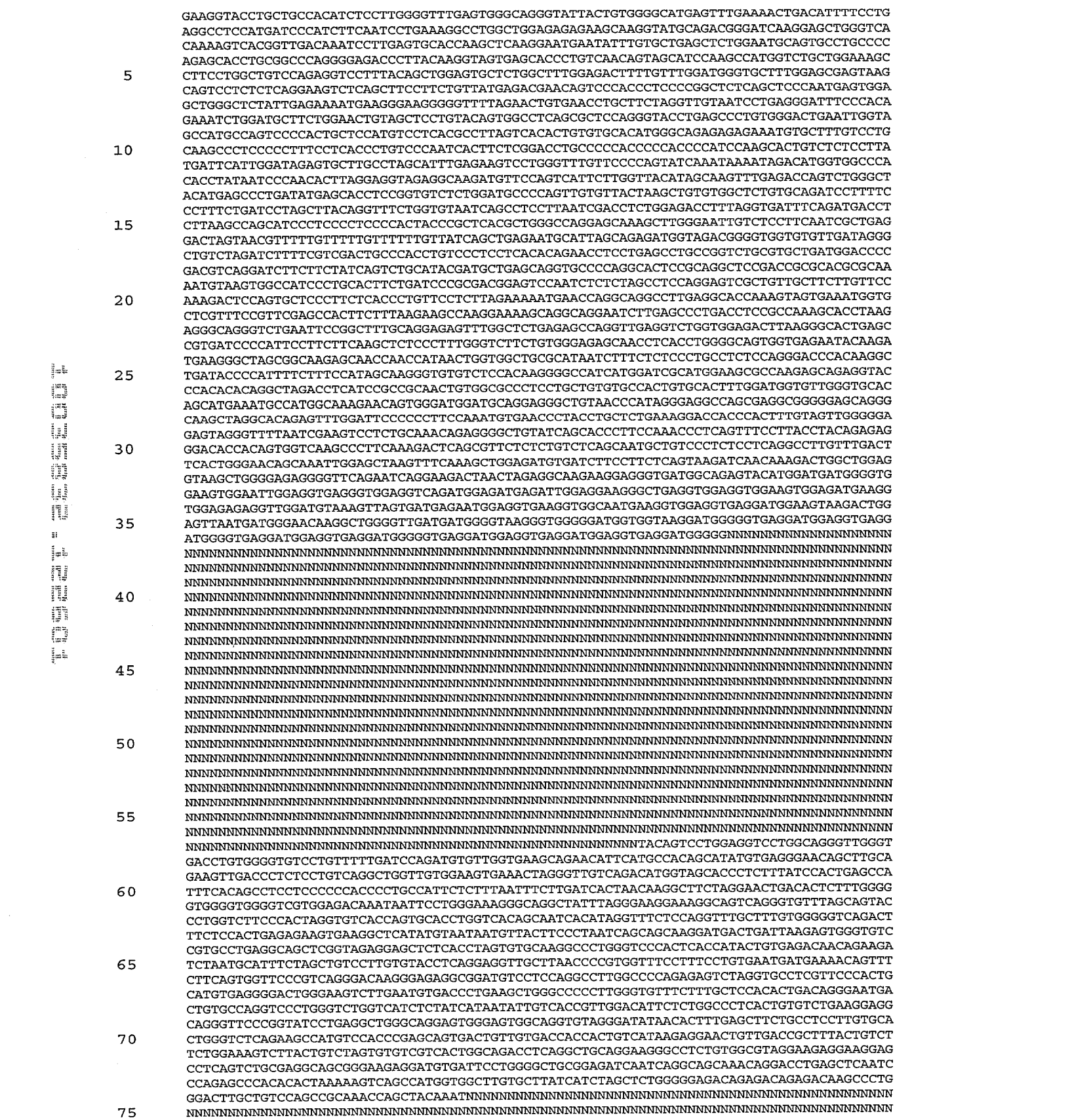
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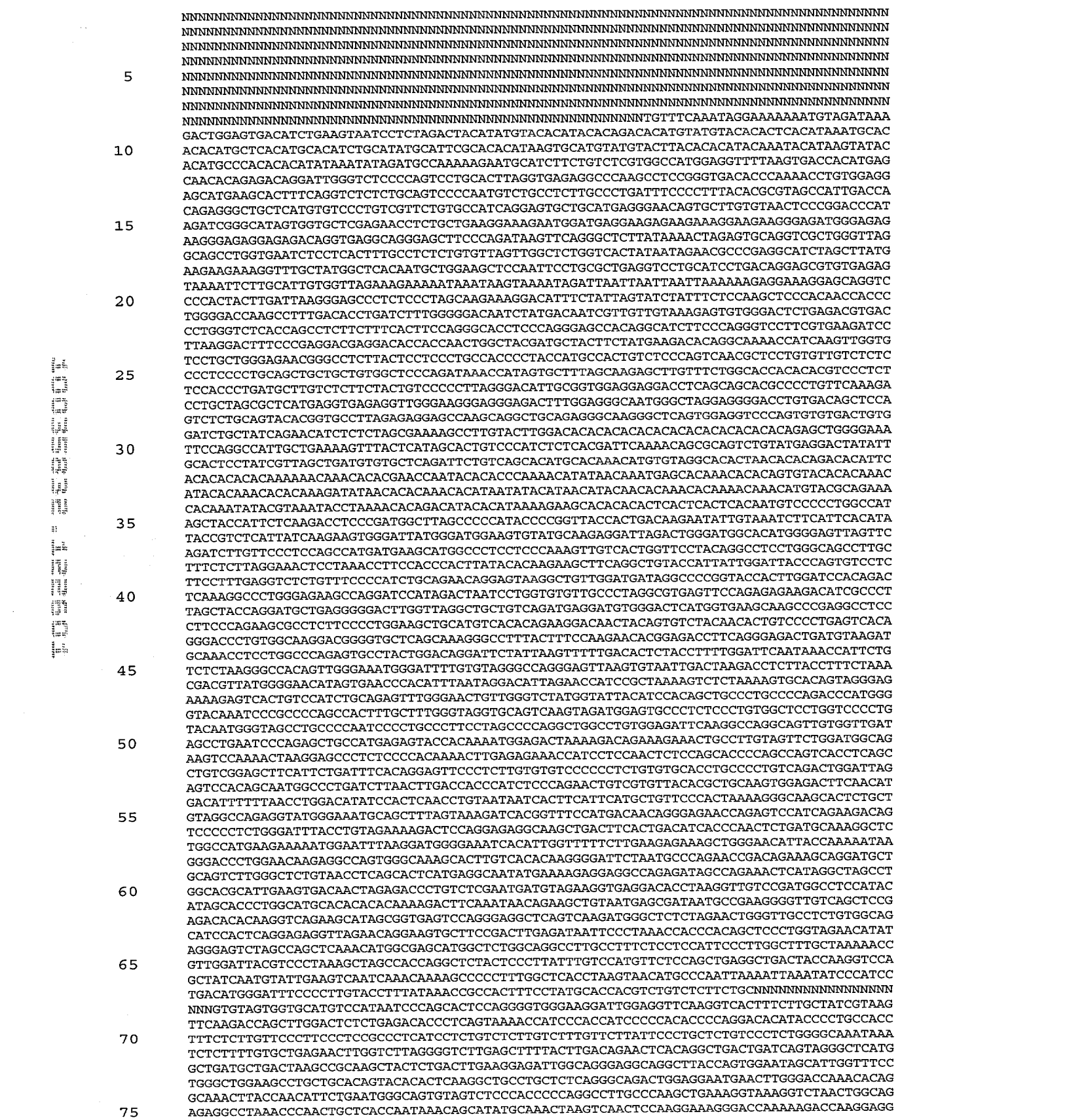


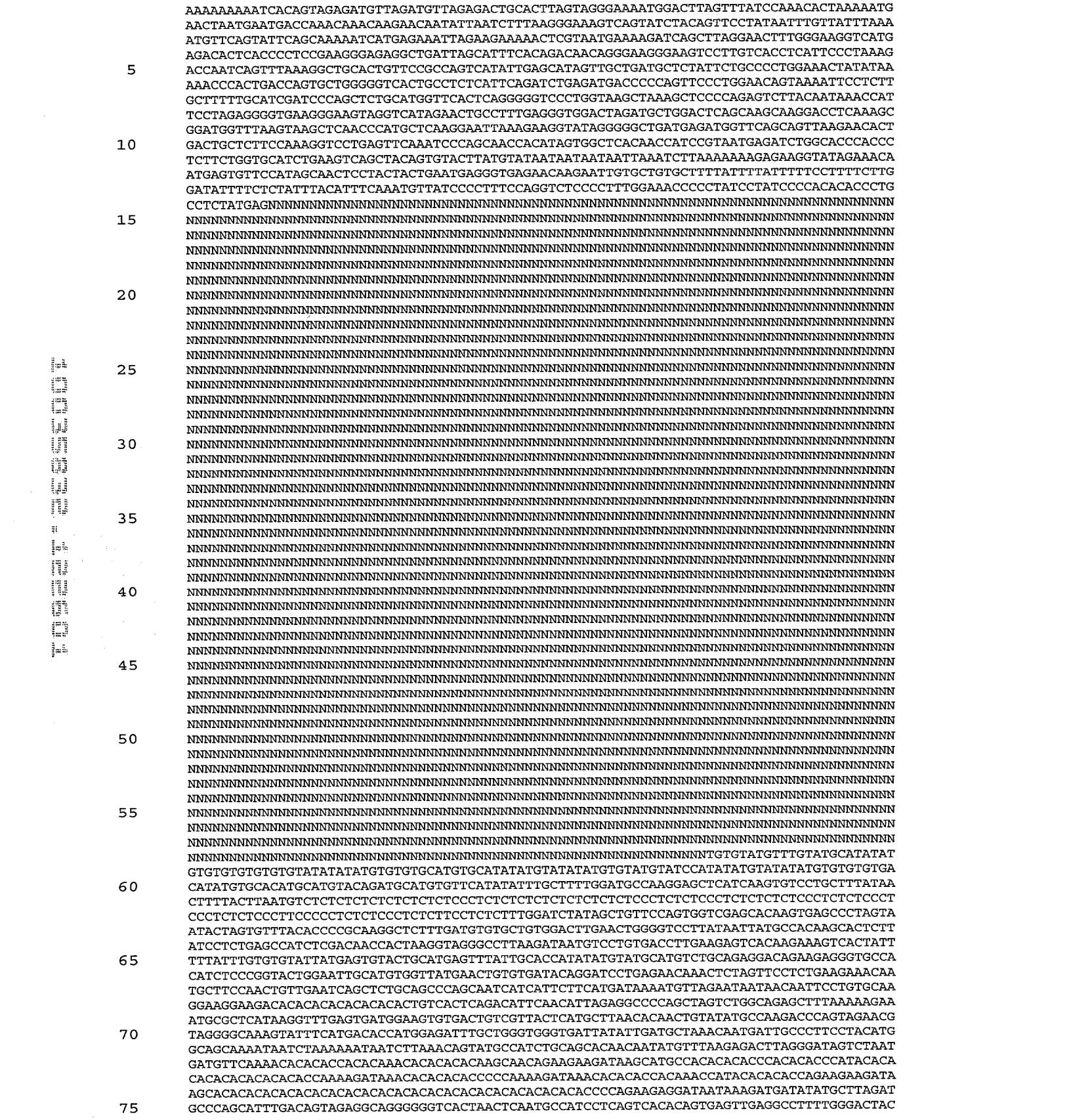
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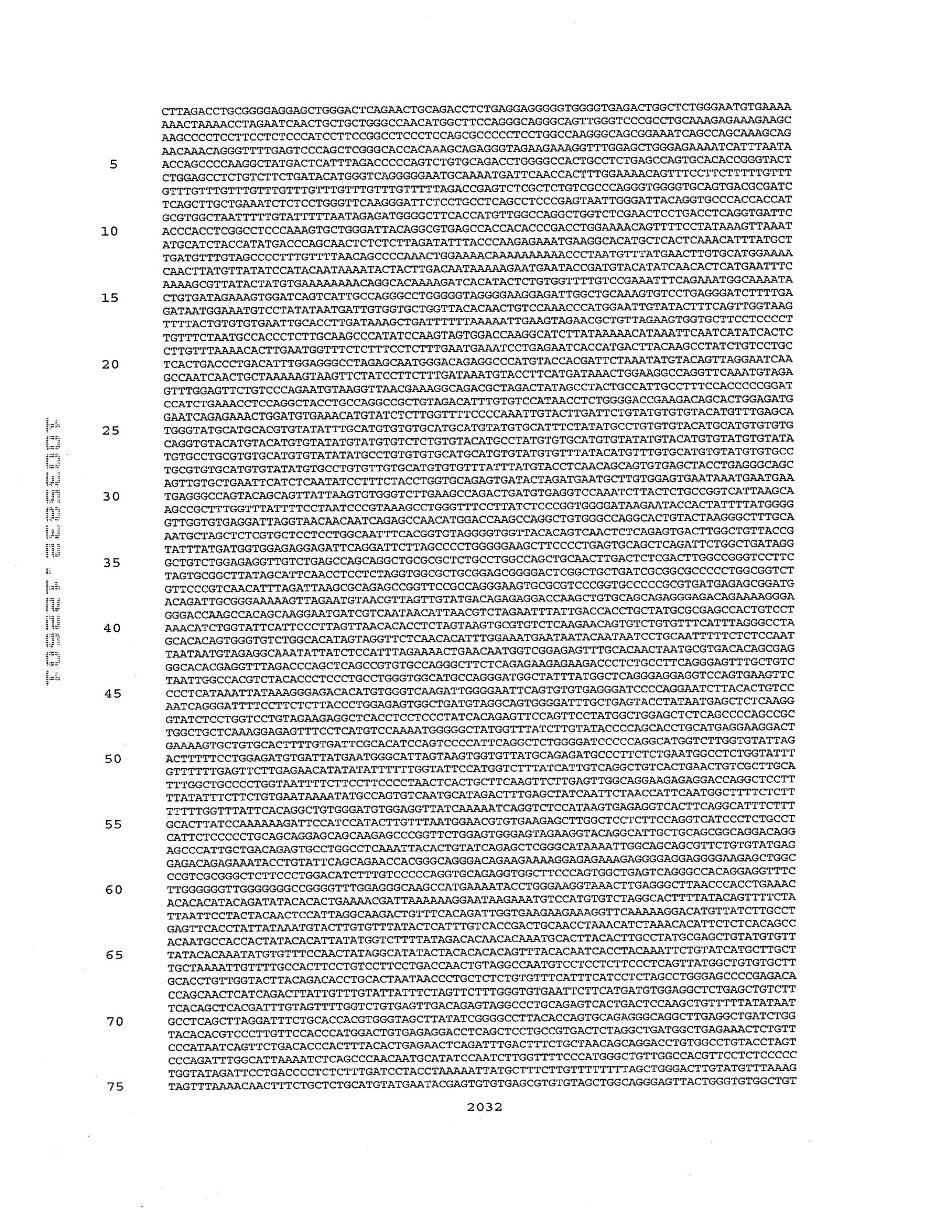


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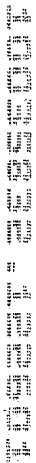
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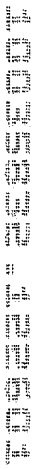
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HUMAN SEQUENCE - mRNA

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HUMAN SEQUENCE - CODING
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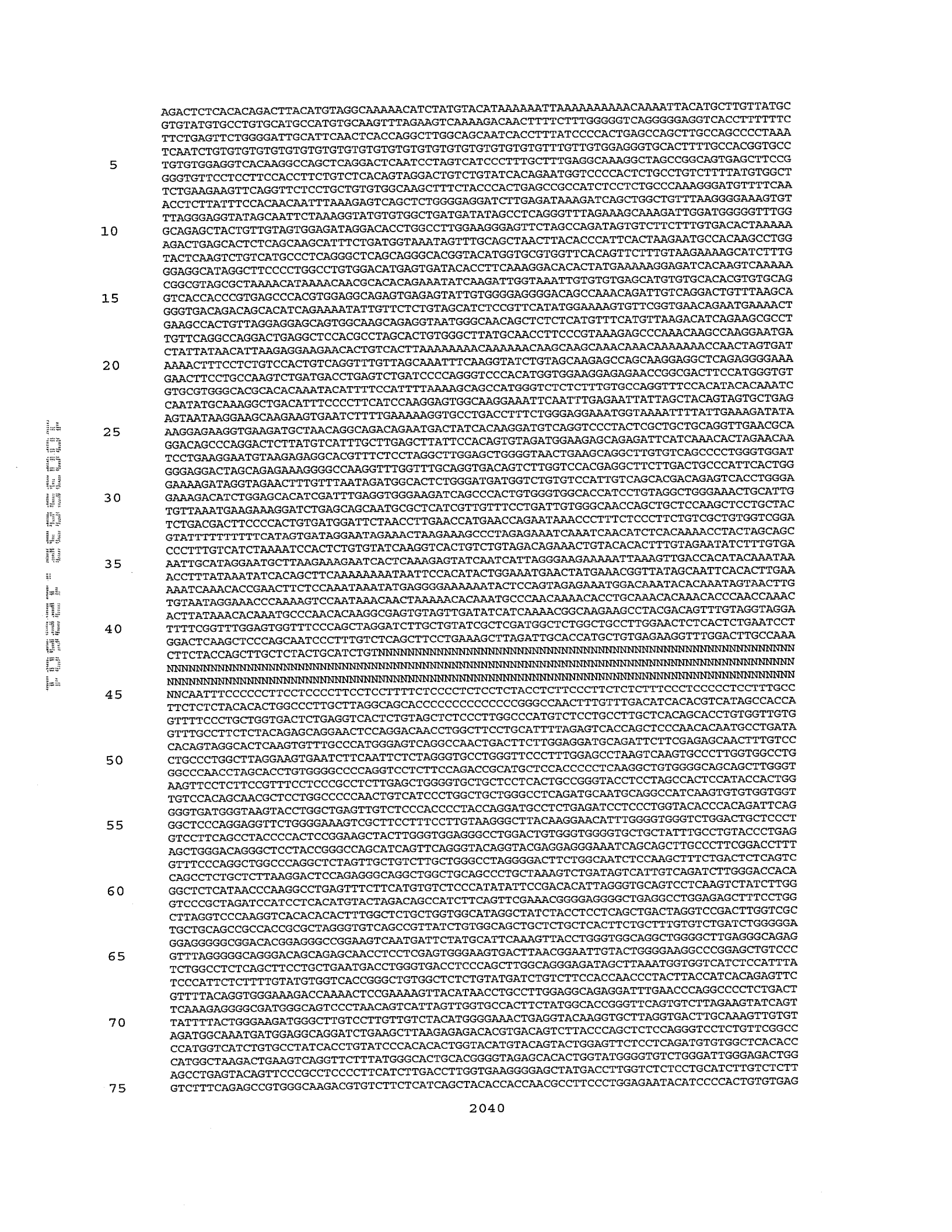
Table 100

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HUMAN NOMENCLATURE
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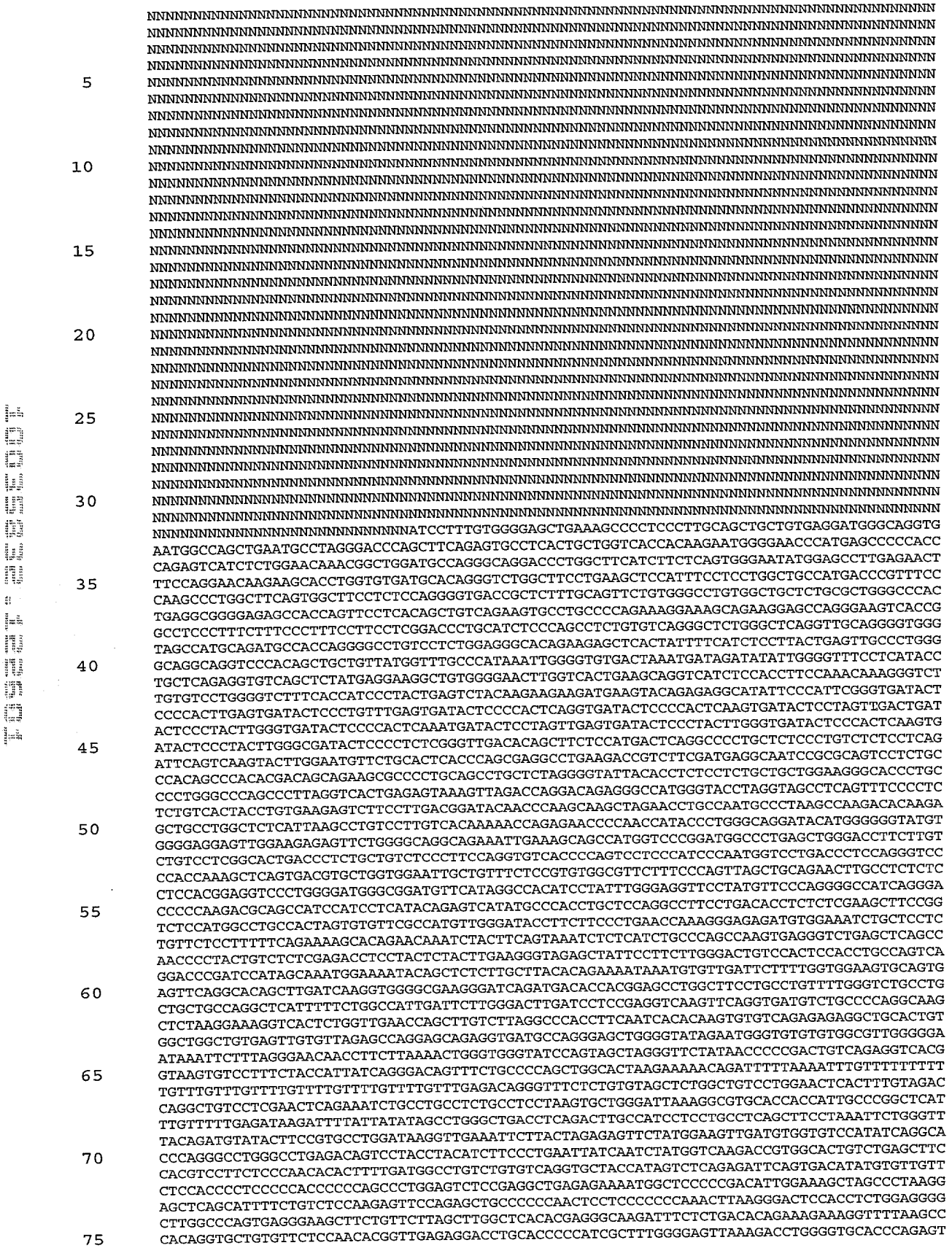
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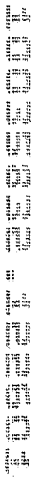
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MOUSE SEQUENCE - mRNA
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MOUSE SEQUENCE - CODING
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HUMAN SEQUENCE - GENOMIC
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